

STIC-Biotech/ChemLib

88836

From: Yaen, Christopher
Sent: Wednesday, March 12, 2003 9:12 AM
To: STIC-Biotech/ChemLib
Subject: 09822698

could you please run a seq search on seq id 5, 24 and 26

thanks

Christopher Yaen
Patent Examiner
US PTO
Art Unit 1642
CM1-Rm 8E18
Mail Box 8E12
703-305-3586

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(STIC)

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

Searcher: Ruhl
Phone: _____
Location: _____
Date Picked Up: 3/12/03
Date Completed: 3/14/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

STIC-Biotech/ChemLib

88803

From: Yaen, Christopher
Sent: Tuesday, March 11, 2003 6:58 PM
To: STIC-Biotech/ChemLib
Subject: 09822698

could you please run a seq search on
seq id no 3 regular search
amino acids 97-110 of seq id no 3 regular and oligo search
amino acids 99-110 of seq id no 3 regular and oligo search
seq id no 1 regular search

thanks

Christopher Yaen
Patent Examiner
US PTO
Art Unit 1642
CM1-Rm 8E18
Mail Box 8E12
703-305-3586

Edward Han
Technical Info. Specialist
STIC/Biotech
CMI 6802 Tel: 305-9203

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MAR 12 2003
(STIC)

Searcher: _____
Phone: _____
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Date Picked Up: 3/13/03
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Online time: _____

TYPE OF SEARCH:
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AA Sequences: 6
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: EUIP
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:30:39 ; Search time 12.3846 Seconds
(without alignments)
33.261 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_l10
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, AA: *
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4: /cgn2_6/prodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/prodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	42.9	95	4	US-08-928-383B-18
2	5	35.7	8	4	US-08-637-732A-34
3	5	35.7	8	4	US-08-637-732A-36
4	5	35.7	14	4	US-08-973-131-75
5	5	35.7	20	1	US-08-103-742-12
6	5	35.7	20	1	US-08-199-508-5
7	5	35.7	22	1	US-07-791-930C-9
8	5	35.7	22	1	US-08-173-515B-12
9	5	35.7	22	3	US-08-329-793-40
10	5	35.7	33	2	US-08-415-788-28
11	5	35.7	34	2	US-08-415-788-11
12	5	35.7	34	2	US-08-415-788-14
13	5	35.7	34	2	US-08-415-788-18
14	5	35.7	34	2	US-08-415-788-24
15	5	35.7	41	2	US-08-415-788-5
16	5	35.7	41	2	US-08-415-788-41
17	5	35.7	56	4	US-07-741-453A-47
18	5	35.7	58	4	US-09-605-785-553
19	5	35.7	116	2	US-08-428-197-10
20	5	35.7	116	5	PCT-US93-10555-10
21	5	35.7	187	4	US-09-117-257-23
22	5	35.7	187	4	US-08-945-476-23
23	5	35.7	187	4	US-09-489-352-23
24	5	35.7	188	4	US-09-117-257-44
25	5	35.7	188	4	US-09-489-352-44
26	5	35.7	264	4	US-08-856-841-14
27	5	35.7	325	1	US-08-118-270-30

28	5	35.7	325	5	PCT-US93-08528-30	Sequence 30, Appl
29	5	35.7	329	1	US-08-348-792-12	Sequence 12, Appl
30	5	35.7	329	2	US-08-462-738-12	Sequence 12, Appl
31	5	35.7	329	4	US-09-199-955-12	Sequence 12, Appl
32	5	35.7	329	4	US-08-880-875-12	Sequence 12, Appl
33	5	35.7	343	1	US-08-348-792-10	Sequence 10, Appl
34	5	35.7	343	2	US-08-462-738-10	Sequence 10, Appl
35	5	35.7	343	4	US-09-199-955-10	Sequence 10, Appl
36	5	35.7	343	4	US-08-880-875-10	Sequence 10, Appl
37	5	35.7	356	4	US-08-259-451-17	Sequence 17, Appl
38	5	35.7	359	1	US-08-181-271A-98	Sequence 98, Appl
39	5	35.7	359	1	US-08-449-315-98	Sequence 98, Appl
40	5	35.7	359	1	US-08-444-803-98	Sequence 98, Appl
41	5	35.7	359	1	US-08-047-413-15	Sequence 15, Appl
42	5	35.7	359	1	US-08-449-043-98	Sequence 98, Appl
43	5	35.7	359	1	US-08-456-265A-98	Sequence 98, Appl
44	5	35.7	359	1	US-08-455-416-98	Sequence 98, Appl
45	5	35.7	359	1	US-08-455-244-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-08-928-383B-18
; Sequence 18, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cossackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-928-383B-18

Query Match 42.9%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HTGGGV 8

Db 88 HTGGV 93
|||||
US-08-637-732A-34
RESULT 2
; Sequence 34, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant p11c Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 8 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-34
Query Match 35.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 1 HTGGG 5
RESULT 3
US-08-637-732A-36
; Sequence 36, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant p11c Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia

; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-36
Query Match 35.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 1 HTGGG 5
RESULT 4
US-08-973-131-75
; Sequence 75, Application US/08973131
; Patent No. 6326166
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Joel L.
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Chimeric DNA-binding proteins
; FILE REFERENCE: APV-022.02
; CURRENT APPLICATION NUMBER: US/08/973,131
; CURRENT FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: PCT/US95/16982
; EARLIER FILING DATE: 1995-12-29
; EARLIER APPLICATION NUMBER: 08/366,083
; EARLIER FILING DATE: 1994-12-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric motif
US-08-973-131-75
Query Match 35.7%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 3 HTGGG 7
RESULT 5
US-08-103-742-12
; Sequence 12, Application 08/103742

```
; Patent No. 5420244
; GENERAL INFORMATION:
; APPLICANT: RUDOLPH, DONNA L.
; APPLICANT: LAL, RENU B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; MYELOPATHY AND ADULT T-CELL LEUKEMIA
; TITLE OF INVENTION: DIAGNOSING HTLV-I ASSOCIATED
; MYELOPATHY AND ADULT T-CELL LEUKEMIA
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/103,742
; FILING DATE: 06 AUG 1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRATT, GWENDOLYN D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.080
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-103-742-12

Query Match 35.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WDPID 13
Db 11 WDPID 15

RESULT 6
US-08-199-508-5
; Sequence 5, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,508
; FILING DATE: February 18, 1994

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,536
; FILING DATE: February 23, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5717058ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 121 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; US-08-199-508-5

Query Match 35.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WDPID 13
Db 8 WDPID 12

RESULT 7
US-07-791-930C-9
; Sequence 9, Application US/07791930C
; Patent No. 5360726
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: Polypeptides Enabling Sorting
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,930C
; FILING DATE: 1991 No. 5360726member 12
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/612,200
; FILING DATE: No. 5360726member 13, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5360726e
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION: Peptide
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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-07-791-930C-9

Query Match 35.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWVD 10
Db 3 GGWVD 7

RESULT 8
US-08-173-515B-12
; Sequence 12, Application US/08173515B
; Patent No. 5525713
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: DNA Encoding Polypeptides
; TITLE OF INVENTION: Enabling Sorting of proteins to
; TITLE OF INVENTION: vacuoles of plants.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,515B
; FILING DATE: 1993 December 23
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,930
; FILING DATE: 1991 No. 5525713member 12
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELE: No. 5525713e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22

;
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-08-173-515B-12

Query Match 35.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWVD 10
Db 3 GGWVD 7

RESULT 9
US-08-329-799-40
; Sequence 40, Application US/08329799
; Patent No. 6054637
; GENERAL INFORMATION:
; APPLICANT: Boller, Thomas
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Ryals, John
; TITLE OF INVENTION: No. 6054637el Signal Sequences
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,799
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,521
; FILING DATE: 13-JUN-1991
; APPLICATION NUMBER: CH 2007/90-9
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: GA/5-18123/A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614
 ; TELEFAX: (919)541-8689
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-329-799-40

Query Match 35.7%; Score 5; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGVD 10
 Db 3 GGVD 7

RESULT 10
 US-08-415-788-28
 ; Sequence 28, Application US/08415788
 ; Patent No. 5834591
 ; GENERAL INFORMATION:
 ; APPLICANT: NORMARK, STAFFAN
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
 ; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,788
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,465
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCHWENNING, LYNN E.
 ; REGISTRATION NUMBER: 37,233
 ; REFERENCE/DOCKET NUMBER: 29500-20046.20
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-415-788-28

Query Match 35.7%; Score 5; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGG 7
 Db 13 HTGG 17

RESULT 11
 US-08-415-788-11
 ; Sequence 11, Application US/08415788
 ; Patent No. 5834591
 ; GENERAL INFORMATION:
 ; APPLICANT: NORMARK, STAFFAN
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
 ; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,788
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,465
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCHWENNING, LYNN E.
 ; REGISTRATION NUMBER: 37,233
 ; REFERENCE/DOCKET NUMBER: 29500-20046.20
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-415-788-11

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 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGG 7
 Db 13 HTGG 17

RESULT 12
 US-08-415-788-14
 ; Sequence 14, Application US/08415788
 ; Patent No. 5834591
 ; GENERAL INFORMATION:
 ; APPLICANT: NORMARK, STAFFAN
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
 ; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

QY 3 HTGG 7
 Db 13 HTGG 17

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,788
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,465
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCHWENNING, LYNN E.
 ; REGISTRATION NUMBER: 37,233
 ; REFERENCE/DOCKET NUMBER: 29500-20046.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-415-788-14

Query Match 35.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
 Db 13 HTGGG 17

RESULT 13
 US-08-415-788-18
 ; Sequence 18, Application US/08415788
 ; Patent No. 5834591
 ; GENERAL INFORMATION:
 ; APPLICANT: NORMARK, STAFFAN
 ; APPLICANT: JONSSON, ANN-BETH
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
 ; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,788
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,465
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCHWENNING, LYNN E.
 ; REGISTRATION NUMBER: 37,233
 ; REFERENCE/DOCKET NUMBER: 29500-20046.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-415-788-18

Query Match 35.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
 Db 13 HTGGG 17

RESULT 14
 US-08-415-788-24
 ; Sequence 24, Application US/08415788
 ; Patent No. 5834591
 ; GENERAL INFORMATION:
 ; APPLICANT: NORMARK, STAFFAN
 ; APPLICANT: JONSSON, ANN-BETH
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
 ; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,788
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,465
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCHWENNING, LYNN E.
 ; REGISTRATION NUMBER: 37,233
 ; REFERENCE/DOCKET NUMBER: 29500-20046.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-415-788-24

Query Match 35.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
 Db 13 HTGGG 17

RESULT 15
 US-08-415-788-5
 ; Sequence 5, Application US/08415788

; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-788-5

Query Match 35.7%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7

Db 24 HTGGG 28

Search completed: March 13, 2003, 15:34:10
Job time : 13.3846 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:59 ; Search time 33.9231 seconds
(without alignments)
54.992 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGGWDPIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	14	100.0	121	AAE12706	Human PH1 Fab anti
2	14	100.0	381	AAE12707	Human b1vPH1-IL-2
3	14	100.0	451	AAE12715	Human recombinant
4	13	92.9	14	AAE12740	Human PH1 Fab anti
5	13	92.9	14	AAE12762	Human PH1 Fab anti
6	13	92.9	14	AAE12770	Human PH1 Fab anti
7	12	85.7	14	AAE12718	Human PH1 Fab anti
8	12	85.7	14	AAE12719	Human PH1 Fab anti
9	12	85.7	14	AAE12741	Human PH1 Fab anti
10	12	85.7	14	AAE12744	Human PH1 Fab anti

11	12	85.7	14	22	AAE12748	Human PH1 Fab anti
12	12	85.7	14	22	AAE12751	Human PH1 Fab anti
13	12	85.7	14	22	AAE12754	Human PH1 Fab anti
14	12	85.7	14	22	AAE12755	Human PH1 Fab anti
15	12	85.7	14	22	AAE12759	Human PH1 Fab anti
16	12	85.7	14	22	AAE12761	Human PH1 Fab anti
17	12	85.7	14	22	AAE12765	Human PH1 Fab anti
18	12	85.7	14	22	AAE12767	Human PH1 Fab anti
19	12	85.7	14	22	AAE12774	Human PH1 Fab anti
20	11	78.6	14	22	AAE12743	Human PH1 Fab anti
21	11	78.6	14	22	AAE12746	Human PH1 Fab anti
22	11	78.6	14	22	AAE12747	Human PH1 Fab anti
23	11	78.6	14	22	AAE12753	Human PH1 Fab anti
24	11	78.6	14	22	AAE12756	Human PH1 Fab anti
25	11	78.6	14	22	AAE12757	Human PH1 Fab anti
26	11	78.6	14	22	AAE12758	Human PH1 Fab anti
27	11	78.6	14	22	AAE12763	Human PH1 Fab anti
28	11	78.6	14	22	AAE12764	Human PH1 Fab anti
29	11	78.6	14	22	AAE12766	Human PH1 Fab anti
30	11	78.6	14	22	AAE12768	Human PH1 Fab anti
31	11	78.6	16	22	AAE12734	Human PH1 Fab anti
32	10	71.4	14	22	AAE12720	Human PH1 Fab anti
33	10	71.4	14	22	AAE12742	Human PH1 Fab anti
34	10	71.4	14	22	AAE12749	Human PH1 Fab anti
35	10	71.4	14	22	AAE12772	Human PH1 Fab anti
36	10	71.4	16	22	AAE12735	Human PH1 Fab anti
37	9	64.3	14	22	AAE12745	Human PH1 Fab anti
38	9	64.3	14	22	AAE12769	Human PH1 Fab anti
39	8	57.1	14	22	AAE12771	Human PH1 Fab anti
40	8	57.1	14	22	AAE12773	Human PH1 Fab anti
41	7	50.0	16	22	AAE12722	Human PH1 Fab anti
42	7	50.0	16	22	AAE12723	Human PH1 Fab anti
43	7	50.0	16	22	AAE12724	Human PH1 Fab anti
44	7	50.0	16	22	AAE12725	Human PH1 Fab anti
45	7	50.0	16	22	AAE12726	Human PH1 Fab anti

ALIGNMENTS

RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX
AC AAE12706;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody variable heavy chain region (VH).
XX
KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
OS Homo sapiens.
XX
FH Key
FH Region
FT
FT Location/Qualifiers
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
FT /note= "VH domain"
FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

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FT XX WO200175110-A2. /note= "Framework region 4"
PN XX
XX XX
XX PD 11-OCT-2001.
XX XX
XX 30-MAR-2001; 2001WO-US10589.
XX PF
XX PR 30-MAR-2000; 2000US-0538913.
XX XX
XX PA (DYAX-) DYAX CORP.
XX PI
XX PI Hoogenboom HRJM, Henderikx MPG;
XX XX
XX DR WPI: 2001-626437/72.
XX DR N-PSDB; AAD20731.
XX XX
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1
XX XX
XX PS Claim 2; Page 94-95; 126pp; English.
XX XX
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC detection method selected from enzyme-linked immunosorbent assay,
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
XX CC antibody VH region.
XX SQ Sequence 121 AA;
XX
XX Query Match 100.0%; Score 14; DB 22; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-07;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 AKHTGGGVWDPIDY 14
XX | | | | | | | | | | | | | | | |
XX Db 97 AKHTGGGVWDPIDY 110
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XX RESULT 2
XX AAEL2707
XX ID AAEL2707 standard; Protein; 381 AA.
XX AC
XX AC AAEL2707;
XX XX
XX DT 04-JAN-2002 (first entry)
XX DE
XX DE Human b1vPH1-IL-2 immunocytokine protein.
XX XX
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200175110-A2.
XX XX
XX PD 11-OCT-2001.
XX XX
XX PF 30-MAR-2001; 2001WO-US10589.
XX XX
XX SQ

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PR 30-MAR-2000; 2000US-0538913.
XX XX
XX PA (DYAX-) DYAX CORP.
XX XX
XX PI Hoogenboom HRJM, Henderikx MPG;
XX XX
XX DR WPI: 2001-626437/72.
XX DR N-PSDB; AAD20732.
XX XX
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1
XX XX
XX PS Claim 9; Page 95-97; 126pp; English.
XX XX
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC detection method selected from enzyme-linked immunosorbent assay,
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human b1vPH1-IL-2
XX CC immunocytokine protein. b1vPH1 is mucin specific binding portion.
XX SQ Sequence 381 AA;
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XX Query Match 100.0%; Score 14; DB 22; Length 381;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-07;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AKHTGGGVWDPIDY 14
XX | | | | | | | | | | | | | | | |
XX Db 97 AKHTGGGVWDPIDY 110
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XX RESULT 3
XX AAEL2715
XX ID AAEL2715 standard; Protein; 451 AA.
XX AC
XX AC AAEL2715;
XX XX
XX DT 04-JAN-2002 (first entry)
XX DE
XX DE Human recombinant immunoglobulin (Ig) heavy chain region.
XX XX
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX KW heavy chain region; cancer; breast; ovary; lung; bladder;
XX KW cytostatic; therapy; immunoglobulin; Ig.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200175110-A2.
XX XX
XX PD 11-OCT-2001.
XX XX
XX PF 30-MAR-2001; 2001WO-US10589.
XX XX
XX PR 30-MAR-2000; 2000US-0538913.
XX XX
XX PA (DYAX-) DYAX CORP.
XX XX
XX PI Hoogenboom HRJM, Henderikx MPG;
XX XX
XX WPI: 2001-626437/72.
XX DR

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DR N-PSDB; AAD20745.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Claim 12; Page 106-108; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human recombinant immunoglobulin

CC (Ig) heavy chain region (variable VH and CH constant heavy chain).

XX

SQ Sequence 451 AA;

Query Match 100.0%; Score 14; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 4.3e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14

Db 97 AKHTGGVWDPIDY 110

|||||

RESULT 4

AAE12740

ID AAE12740 standard; peptide; 14 AA.

XX

AC AAE12740;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

PA (DYAX-) DYAX CORP.

XX

PI Hoogenboom HRJM, Henderikx MPG;

XX

DR WPI; 2001-626437/72.

XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX its portion for binding to an epitope of the protein core of mucin-1 -

PS Example 2; Page 119; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX

SQ Sequence 14 AA;

Query Match 92.9%; Score 13; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.5e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPID 13

Db 1 AKHTGGVWDPID 13

|||||

RESULT 5

AAE12762

ID AAE12762 standard; peptide; 14 AA.

XX

AC AAE12762;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #29.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

PA (DYAX-) DYAX CORP.

XX

PI Hoogenboom HRJM, Henderikx MPG;

XX

DR WPI; 2001-626437/72.

XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 Db 1 AKHTGGGVWDPI 12

RESULT 8
 AAEL12719
 ID AAEL12719 standard; peptide; 14 AA.
 XX
 AC AAEL12719;

04-JAN-2002 (first entry)

Human PH1 Fab antibody VH region FR3-CDR3 variant #3.

Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 variable heavy chain region; cancer; breast; ovary; lung; bladder;
 cytostatic; therapy; PH1 antibody; variant.

OS Homo sapiens.

Key Location/Qualifiers
 Region 1..2
 /label= Framework_region_3
 Region 3..14
 /label= Complementarity_determining_region_3

WO200175110-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10589.

30-MAR-2000; 2000US-0538913.

(DYAX-) DYAX CORP.

Hoogenboom HRJM, Henderikx MPG;

WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1

Claim 2; Page 75; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 Db 1 AKHTGGGVWDPI 12

RESULT 9
 AAEL12741
 ID AAEL12741 standard; peptide; 14 AA.
 XX
 AC AAEL12741;

04-JAN-2002 (first entry)

Human PH1 Fab antibody VH region FR3-CDR3 variant #8.

Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 variable heavy chain region; cancer; breast; ovary; lung; bladder;
 cytostatic; therapy; PH1 antibody; variant.

OS Homo sapiens.

Key Location/Qualifiers
 Region 1..2
 /label= Framework_region_3
 Region 3..14
 /label= Complementarity_determining_region_3

WO200175110-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10589.

30-MAR-2000; 2000US-0538913.

(DYAX-) DYAX CORP.

Hoogenboom HRJM, Henderikx MPG;

WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1
 Example 2; Page 119; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

RESULT 10

AAE12744

ID AAE12744 standard; peptide; 14 AA.

XX AC AAE12744;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #11.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytotstatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2 /label= Framework_region_3

XX FT Region 3..14 /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPT; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 119; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

RESULT 11

AAE12748

ID AAE12748 standard; peptide; 14 AA.

XX AC AAE12748;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytotstatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2 /label= Framework_region_3

XX FT Region 3..14 /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPT; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 120; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 12

AAE12751
 ID AAE12751 standard; peptide; 14 AA.

XX
 AC AAE12751;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #18.

XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key

FT Region Location/Qualifiers

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX
 PI Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX

PS Example 2; Page 121; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 13

AAE12754
 ID AAE12754 standard; peptide; 14 AA.

XX
 AC AAE12754;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #21.

XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key

FT Region Location/Qualifiers

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX
 PI Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 121; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 DB 1 AKHTGGGVWDPI 12

RESULT 14
 AAEL2755
 ID AAEL2755 standard; peptide; 14 AA.
 XX
 AC AAEL2755;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #22.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 122; 126pp; English.

XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 DB 1 AKHTGGGVWDPI 12

RESULT 15
 AAEL2759
 ID AAEL2759 standard; peptide; 14 AA.
 XX
 AC AAEL2759;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #26.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 122; 126pp; English.

XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX
SQ

Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

Search completed: March 13, 2003, 15:31:41

Job time : 33.9231 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 51.7192 Seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-1
 Perfect score: 592
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 s

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10:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	592	100.0	113	22	AAE12705	Human PHL Fab anti
2	592	100.0	220	22	AAE12714	Human recombinant
3	592	100.0	381	22	AAE12707	Human biyPHL-IL-2
4	540	91.2	239	21	AAV82615	Human PThrp monocl
5	537	90.7	239	21	AAV82616	Human PThrp monocl
6	534	90.2	262	23	ABP46070	Human PThrp monocl
7	528	89.2	239	21	AAV82617	Human BLYS binding
8	528	89.2	239	21	AAV82618	Human PThrp monocl
9	527	89.0	239	21	AAV82610	Human PThrp monocl
10	524	88.5	112	19	AAW53586	Light chain of a h

11	523.5	88.4	114	21	AA95186	Anti-platelet glyco
12	523.5	88.4	131	21	AA95226	Anti-platelet glyco
13	522	88.2	112	17	AA95218	Human IgM GM607 va
14	521	88.0	239	21	AA92611	Human p7Hrp monoc
15	520	87.8	239	21	AA92614	Human p7Hrp monoc
16	519.5	87.8	113	21	AA95221	Anti-platelet glyco
17	518.5	87.6	113	21	AA95220	Anti-platelet glyco
18	517.5	87.4	112	21	AA95187	Anti-platelet glyco
19	517.5	87.4	222	22	AAU04972	Synthetic antibody
20	517.5	87.4	222	22	AAU04976	Synthetic antibody
21	517.5	87.4	248	22	AA955590	Anti-hEDRF antibod
22	512.5	86.6	111	21	AA95225	Anti-platelet glyco
23	512.5	86.6	222	22	AAU04974	Synthetic antibody
24	511	86.3	109	20	AA939809	Trk1.6 antibody lig
25	510	86.1	114	18	AAW27544	Human Ab light cha
26	510	86.1	281	18	AAAB27560	Consensus single c
27	507	85.6	112	21	AAAB18883	Amino acid sequenc
28	506	85.5	114	23	ABB57576	HLA-DR-specific pr
29	505	85.3	112	22	AA933587	Human anti-Rh(D) c
30	504	85.1	239	21	AA92619	Human p7Hrp monoc
31	502	84.8	113	15	AA956652	Human p7Hrp monoc
32	501	84.6	112	19	AAW34015	Anti-CMV monoclon
33	501	84.6	139	22	AAAB99117	Human Anti-CD4 ant
34	497	84.0	239	21	AA92612	Human p7Hrp monoc
35	497	84.0	239	21	AA92613	Human p7Hrp monoc
36	488	82.4	143	20	AA934313	IgM antibody CEM 1
37	487	82.3	148	20	AA934309	IgM antibody CEM 1
38	486.5	82.2	260	23	ABP45028	Human Blys binding
39	484.5	81.8	113	17	AAAB98508	Vlkappa for antibo
40	483	81.6	112	23	AAE15713	Mouse monoclonal a
41	483	81.6	116	19	AAW76126	Human ICR-8.1 V-K
42	483	81.6	116	19	AAW71256	Humanised murine a
43	483	81.6	116	20	AAW81450	Humanised antibody
44	483	81.6	116	21	AAAB13046	Protein sequence o
45	483	81.6	116	21	AA92445	Humanised ICR-8.1

ALIGNMENTS

RESULT 1

AAE12705

ID AAE12705 standard; Protein; 113 AA.

XX AAE12705;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody variable light chain region (VL).

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;

XX variable light chain region; cancer; breast; ovary; lung; bladder;

XX cystostatic; therapy; PH1 antibody.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX Region

XX 24..39

XX /label= CDR1

XX /note= "Complementarity determining region 1"

XX Region

XX 55..61

XX /label= CDR2

XX /note= "Complementarity determining region 2"

XX Region

XX 94..102

XX /label= CDR3

XX /note= "Complementarity determining region 3"

XX XX

XX W0200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX XX

ALIGNMENTS

RESULT 1

AAE12705
ID AAE12705 standard; Protein; 113 AA.

AA
AC
AAE12705:

04-JAN-2002 (first entry)

DE Human PH1 Fab antibody variable light chain region (VL):

Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
KW
variable light chain region; cancer; breast; ovary; lung; bladder;
KW
cystostatic; therapy; PH1 antibody.
KW

OS Homo sapiens.

	Key	Location/Qualifiers
FH	Region	24..39
FT		

FT
/label= CDR1
FT
/note= "Complementarity determining region 1"

FT	region	33.1.01	/label= CDR2
FT			

FT /note= "Complementarity determining region 2"

ET /label= CDR3

/Note= "Complementarity determining region 3"

PN WO200175110-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US10589.

XX

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PR 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX
XX N-PSDB; AAD20730.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Claim 3; Page 93; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is anti-MUC1 human PHI Fab
XX antibody VL region.
XX
XX Sequence 113 AA;
SQ
Query Match 100.0%; Score 592; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.2e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
QY 61 SGVPRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
RESULT 2
AAE12714
ID AAE12714 standard; Protein; 220 AA.
XX
XX AAE12714;
XX
XX 04-JAN-2002 (first entry)
XX
XX Human recombinant immunoglobulin (Ig) light chain region.
XX
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX light chain region; cancer; breast; ovary; lung; bladder;
XX cytostatic; therapy; immunoglobulin; Ig.
XX
XX Homo sapiens.
XX
XX WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX

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XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX
XX N-PSDB; AAD20744.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Claim 12; Page 103; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human recombinant immunoglobulin
XX (Ig) light chain region (variable VL and CL constant kappa light chain).
XX
XX Sequence 220 AA;
SQ
Query Match 100.0%; Score 592; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-41;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
QY 61 SGVPRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
RESULT 3
AAE12707
ID AAE12707 standard; Protein; 381 AA.
XX
XX AAE12707;
XX
XX 04-JAN-2002 (first entry)
XX
XX Human bivPHI-IL-2 immunocytokine protein.
XX
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX
XX Homo sapiens.
XX
XX WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX

```

DR N-PSDB; AAD20732.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Claim 9; Page 95-97; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human bivPH1-IL-2
 CC immunocytokine protein. bivPH1 is mucin specific binding portion.
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 592; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3.2e-41;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGSPOLLIYSGSHRA 60
 DB 127 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGSPOLLIYSGSHRA 186
 QY 61 SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 187 SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 4
 AAY82615
 ID AAY82615 standard; Protein; 239 AA.
 XX
 AC AAY82615;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 155
 FT /label= "possible Ala"
 FT /note= "possible Ala"
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (N1SB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.
 DR N-PSDB; AAA13925.
 XX
 CC A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Claim 31; Page 45-46; 88pp; Japanese.
 XX
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.
 XX
 SQ Sequence 239 AA;

Query Match 91.2%; Score 540; DB 21; Length 239;
 Best Local Similarity 90.3%; Pred. No. 3.9e-37;
 Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGSPOLLIYSGSHRA 60
 DB 21 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGSPOLLIYSGSHRA 80
 QY 61 SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 81 SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 133

RESULT 5
 AAY82616
 ID AAY82616 standard; Protein; 239 AA.
 XX
 AC AAY82616;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 5
 FT /label= Val, Ala, Asp, Gly
 FT Misc-difference 13
 FT /note= "possibly Leu"
 FT Misc-difference 25
 FT /label= Ile, Thr, Asn, Ser
 FT Misc-difference 27
 FT /label= Phe, Ser, Tyr, Cys
 FT Misc-difference 216
 FT /note= "possible Val"
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX

PR 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 XX
 XX WPI: 2000-286723/25.
 DR N-PSDB; AA13926.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 XX including metastasis, and pain
 PS Claim 31; Page 48-49; 88pp; Japanese.
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.
 XX
 SQ Sequence 239 AA;
 Query Match 90.7%; Score 537; DB 21; Length 239;
 Best Local Similarity 89.4%; Pred. No. 6, 9e-37;
 Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 21 DIVMXQXPLSLPVTPGEPASISCRSSQSLHNSGYNYLDFWFLQKPGQSPQLLIYLSNRA 80
 QY 61 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPTKVDIKR 113
 DB 81 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQALQTPFTFGPTKVDIKR 133
 RESULT 6
 ABP46070
 ID ABP46070 standard; Protein; 262 AA.
 XX
 AC ABP46070;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 2081.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI: 2002-114799/15.
 DR
 XX
 XX Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 2880-2881; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 262 AA;
 Query Match 90.2%; Score 534; DB 23; Length 262;
 Best Local Similarity 90.3%; Pred. No. 1, 3e-36;
 Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 150 EIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYNYLDFWFLQKPGQSPQLLIYLSNRA 209
 QY 61 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPTKVDIKR 113
 DB 210 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQALQTPFTFGGCTKVEIKR 262
 RESULT 7
 AAY82617
 ID AAY82617 standard; Protein; 239 AA.
 XX
 AC AAY82617;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 XX Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
 DE
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 XX Misc-difference 3 /label= Phe, Leu, Ile, Val
 FT Misc-difference 4 /label= Leu, Pro, His, Arg
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
XX Homo sapiens.
XX
XX OS
XX Key Location/Qualifiers
XX Misc-difference 27 /label= Phe, Ser, Tyr, Cys
XX FT
XX Misc-difference 156
XX FT
XX Misc-difference 164
XX FT
XX Misc-difference 164
XX FT
XX /label= Phe, Leu
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX PR
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISR) JAPAN TOBACCO INC.
XX PA
XX WPI; 2000-286723/25.
XX DR
XX N-PSDB; AAA13920.
XX
XX A human monoclonal antibody to parathyroid hormone related protein.
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 33; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
Query Match 89.0%; Score 527; DB 21; Length 239;
Best Local Similarity 88.5%; Pred. No. 4.6e-36;
Matches 100; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLPVTGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 21 DIVMTQXPLSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 113
DB 81 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQALQTPFTFGPTKVDIKR 133
RESULT 10
AAW53586
ID AAW53586 standard; Protein; 112 AA.
XX
XX AAW53586;
XX
XX 23-JUL-1998 (first entry)
XX
XX Light chain of a human antibody.

XX Light chain; human; humanised immunoglobulin; NOK2; Fas ligand;
KW inhibition; apoptosis; Fas expression; treatment; AIDS; rejection;
KW transplant surgery; autoimmune disease; SLE; RA; diabetes.
XX
XX Homo sapiens.
XX
XX WO9810070-A1.
XX
XX 12-MAR-1998.
XX
XX 27-AUG-1997; 97WO-JP02983.
XX PF
XX 20-SEP-1996; 96JP-0271546.
XX PR
XX 02-SEP-1996; 96JP-0231742.
XX
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Eda Y, Higuchi H, Maeda H, Nakata M, Okumura K;
XX Ushio Y;
XX WPI; 1998-193620/17.
XX
XX Human immunoglobulin or its active fragment specific for Fas ligand
XX - for treatment of AIDS, organ rejection, autoimmune diseases e.g.
XX systemic lupus erythematosus and diabetes
XX
XX Disclosure; Page 261; 348pp; Japanese.
XX
XX The present sequence represents the light chain of a human antibody, and
XX can be used in the humanised immunoglobulin of the invention. The
XX humanised immunoglobulin reacts specifically with a region of a Fas
XX ligand that is important in inhibiting apoptosis induced by cells with
XX Fas expression. The immunoglobulin of the invention can inhibit
XX physiological reactions between a Fas ligand and Fas, typlified by
XX apoptosis. The humanised immunoglobulin is used for treatment of AIDS,
XX rejection following transplant surgery, autoimmune diseases such as
XX SLE or RA, and diabetes.
XX
XX Sequence 112 AA;
Query Match 88.5%; Score 524; DB 19; Length 112;
Best Local Similarity 87.5%; Pred. No. 3.8e-36;
Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLPVTGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 112
DB 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQALQTPFTFGQGTKEIKR 112
RESULT 11
AAAY95186
ID AAY95186 standard; Protein; 114 AA.
XX
XX AAY95186;
XX
XX 29-AUG-2000 (first entry)
XX
XX Anti-platelet glycoprotein Ib human H1b-5 VL.
XX
XX Variable light chain; single chain antibody; scFv; human; H1b-5;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 1..23
XX /note= "framework region 1"


```

FT Region 24..39 "complementarity determining region 1"
FT Region 40..54 /note= "framework region 2"
FT Region 55..61 /note= "complementarity determining region 2"
FT Region 62..93 /note= "framework region 3"
FT Region 94..101 /note= "complementarity determining region 3"
FT Region 102..114 /note= "framework region 4"
PN WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILL/) MILLER J L.
XX Miller JL;
XX WPI: 2000-365744/31.
XX N-PSDB; AAA27664.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Claim 11; Page 77; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) of human single chain antibody (scFv) HIB-5, which is directed
CC against platelet glycoprotein Ib (GPiB). The HIB series of scFv
CC was isolated from a human synthetic VH and VL scFv library by 3
CC rounds of phagemid selection against transfected CHO cells
CC expressing the GPiB alpha component of the GPiB/IX/V complex
CC on their surface, followed by a 4th round of selection against
CC washed human platelets, and 2 final rounds in which attempts were
CC made to displace scFv from washed platelets by flooding with
CC murine monoclonal antibody or mimotope peptide (see AAY95229).
CC Whether displayed as surface proteins on a phagemid or secreted
CC as free scFv by Escherichia coli, the HIB scFv clones are capable
CC of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPiB alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX
XX SQ Sequence 114 AA;
Query Match 88.4%; Score 523.5; DB 21; Length 114;
Best Local Similarity 87.7%; Pred No. 4.2e-36;
Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 EIVLTQSPISLPTVTPGEPASISCRSSQLLSHNGYITLDWYLOKQPSQLLIYGSNRA 60
Dd ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DVVMTQSPISLPTVTPGEPASISCRSSQLLSHNGYINLWYLOKQPSQLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTLTISRVEADGVGYTCMQGLQS-PFTFGGTQVDIKR 113
Dd |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGVPDRFSGSGGTDTLTISRVEADGVGYTCMQALQTPPTFGGTQKLEIKR 114
RESULT 12

```

```

AAY95226
.. ID AAY95226 standard; Protein; 131 AA.
XX AC AAY95226;
XX 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human HIB-5 VL region and linker.
XX KW Variable light chain; single chain antibody; scFv; human; HIB-5;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.
XX OS Chimeric - Synthetic.
XX OS Chimeric - Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..17 /note= "vector-derived linker"
FT Region 18..131 /note= "light chain variable region"
FT Region 18..40 /note= "framework region 1"
FT Region 41..56 /note= "complementarity determining region 1"
FT Region 57..71 /note= "framework region 2"
FT Region 72..78 /note= "complementarity determining region 2"
FT Region 79..110 /note= "framework region 3"
FT Region 111..119 /note= "complementarity determining region 3"
FT Region 120..131 /note= "framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILL/) MILLER J L.
XX Miller JL;
XX WPI: 2000-365744/31.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Disclosure; Fig 8; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) plus linker peptide of human single chain antibody (scFv)
CC HIB-5, which is directed against platelet glycoprotein Ib (GPiB).
CC HIB-5 is composed of a heavy chain variable region and light chain
CC variable region joined via a vector-derived peptide linker. The
CC HIB series of scFv was isolated from a human synthetic VH and VL
CC scFv library by 3 rounds of phagemid selection against transfected
CC CHO cells expressing the GPiB alpha component of the GPiB/IX/V
CC complex on their surface, followed by a 4th round of selection
CC against washed human platelets, and 2 final rounds in which
CC attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or mimotope peptide (see
CC AAY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC

```

CC purposes. They provide a new class of antithrombotic agents,
 CC useful for the prevention of platelet-dependent thrombi in
 CC diseased arteries, bypass grafts, dialysis etc., and can also be
 CC used as diagnostic reagents. Methods of inhibiting aggregation
 CC of platelets, of binding human platelet GPIIb/IIIa and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.

XX
 SQ Sequence 131 AA;

Query Match 88.4%; Score 523.5; DB 21; Length 131;
 Best Local Similarity 87.7%; Pred. No. 4.9e-36;
 Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLSPLPTGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 18 DVMTQSPVLSPLPTGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 77
 QY 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQS-PFTFGGKVDIKR 113
 DB 78 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQTPPTFGGKLEIKR 131

RESULT 13
 AAR95218
 ID AAR95218 standard; protein; 112 AA.
 XX AAR95218;
 DT 16-DEC-1996 (first entry)
 XX Human IgM CM607 variable light chain.
 DE
 XX
 XX Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 24..39
 FT /label= CDR 1.
 FT Domain 55..61
 FT /label= CDR 2.
 FT Domain 89..97
 FT /label= CDR 3.
 XX
 PN W09613594-A1.
 XX
 XX 09-MAY-1996.
 XX
 XX 26-OCT-1995; 95WO-US13811.
 XX
 XX 28-OCT-1994; 94US-0331398.
 XX 28-OCT-1994; 94US-0331396.
 XX 28-OCT-1994; 94US-0331397.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
 PI Padlan EA, Pai L, Pastan I, Willingham M;
 XX WPI; 1996-251462/25.
 XX
 XX Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate
 PT antigen
 XX
 XX Example 13; Figure 11b; 116pp; English.
 PS
 XX A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and
 CC heavy chains of an antibody (Ab) fused together, and an effector

CC molecule, where the fusion protein or Ab has the binding specificity
 CC of monoclonal Ab (MAB) B1, B3 or B5, can be used for the production
 CC of such fusion proteins or antibodies. The fusion proteins can be
 CC used in compositions as an immunotoxin to inhibit tumour cell growth.
 CC The single chain antibody can be used to detect the presence or
 CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a
 CC patient. The antibodies are also useful as multiple targeting
 CC moieties, providing at least 2 kinds of biological activity. They
 CC can also be used in diagnostic assays and for the imaging of tumours
 CC when attached to a radiolabel and for the pathological diagnosis of
 CC tumours. Humanised antibodies are less immunogenic than the mouse
 CC MABs B1, B3 and B5, making them more suitable for long term
 CC treatment.

XX
 SQ Sequence 112 AA;

Query Match 88.2%; Score 522; DB 17; Length 112;
 Best Local Similarity 89.3%; Pred. No. 5.5e-36;
 Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPTGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 1 DIVMTQSPVLSPLPTGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 QY 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQS-PFTFGGKVDIKR 112
 DB 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQTPPTFGGKVEIKR 112

RESULT 14
 AAY82611
 ID AAY82611 standard; protein; 239 AA.
 XX AAY82611;
 XX 02-AUG-2000 (first entry)
 DT Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
 XX
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 XX hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 OS Homo sapiens.
 XX
 XX JP2000080100-A.
 PN 21-MAR-2000.
 XX
 XX 12-OCT-1998; 98JP-0304793.
 XX
 XX 17-JUN-1998; 98JP-0188196.
 XX 26-JUN-1998; 98JP-0196729.
 XX
 XX (NISB) JAPAN TOBACCO INC.
 XX
 XX WPI; 2000-286723/25.
 DR N-PSDB; AAA13921.
 XX
 XX A human monoclonal antibody to parathyroid hormone related protein, -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 XX Claim 31; Page 34-35; 88pp; Japanese.
 XX
 XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment

CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 88.0%; Score 521; DB 21; Length 239;
Best Local Similarity 86.7%; Pred. No. 1.4e-35;
Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPVLPVTPGEPATISCRSSQSLHNRGNVLDWFLQKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGVSGTDFTLRIISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGVSGTDFTLKLSRVEADVGLYCMQALQIPFTFGPGTKVDIKR 133
RESULT 15
AAY82614
ID AAY82614 standard; Protein; 239 AA.
XX
AC AAY82614;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Misc-difference 25
FT /label= Ile, Thr, Asn, Ser
FT Misc-difference 27
FT /label= Phe, Ser, Tyr, Cys
FT Misc-difference 117
FT /label= Leu, Ile, Val
FT Misc-difference 146
FT /label= Phe, Ser, Tyr, Cys
FT Misc-difference 216
FT /note= "possible Val"
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISR) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13924.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 43; 88pp; Japanese.

CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 87.8%; Score 520; DB 21; Length 239;
Best Local Similarity 87.6%; Pred. No. 1.8e-35;
Matches 99; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMXQSPVLPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGVSGTDFTLRIISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGVSGTDFTLKISRVEADVGVYCMQAXQIPFTFGPGTKVDIKR 133
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Job time : 53.7192 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 17.3846 Seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592

Sequence: 1 EIVLTQSPVLSPLPVTGEPAS.....MOGLQSPETFGGTRVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	532	89.9	113	4	US-09-025-769B-15
2	522	88.2	112	1	US-08-331-398A-49
3	522	88.2	112	2	US-08-331-397B-49
4	522	88.2	112	2	US-08-759-804A-49
5	522	88.2	112	4	US-09-227-693-49
6	510	86.1	114	4	US-09-025-769B-29
7	510	86.1	114	4	US-09-025-769B-45
8	510	86.1	281	4	US-09-025-769B-178
9	505	85.3	112	4	US-09-240-274-30
10	502	84.8	113	1	US-08-082-623-4
11	501	84.6	112	1	US-08-478-039-88
12	501	84.6	112	1	US-08-476-349A-88
13	499	84.3	112	1	US-08-053-171-16
14	484.5	81.8	113	1	US-08-264-093-10
15	484	81.8	112	1	US-08-331-398A-50
16	484	81.8	112	2	US-08-331-397B-50
17	484	81.8	112	2	US-08-759-804A-50
18	484	81.8	112	4	US-09-227-693-50
19	483	81.6	116	1	US-08-482-882-66
20	483	81.6	116	2	US-08-483-389-66
21	483	81.6	116	2	US-08-487-113D-66
22	483	81.6	116	2	US-08-473-503-66
23	483	81.6	116	2	US-08-483-932-66
24	483	81.6	116	2	US-08-720-420A-66
25	483	81.6	116	3	US-08-714-017-66
26	483	81.6	116	3	US-08-475-680-66
27	482	81.4	112	1	US-08-053-171-15

28	482	81.4	112	3	US-08-815-190A-14	Sequence 14, Appl
29	475	80.2	112	4	US-09-000-088-2	Sequence 2, Appli
30	475	80.2	131	1	US-08-129-930B-95	Sequence 95, Appl
31	475	80.2	131	4	US-08-134-346A-50	Sequence 50, Appl
32	475	80.2	131	4	US-08-976-288A-95	Sequence 95, Appl
33	474	80.1	108	1	US-08-488-113B-151	Sequence 151, App
34	474	80.1	108	1	US-08-477-484B-151	Sequence 151, App
35	474	80.1	108	1	US-08-107-669D-15	Sequence 15, Appl
36	474	80.1	108	1	US-08-472-788A-15	Sequence 15, Appl
37	474	80.1	108	2	US-08-477-531B-15	Sequence 15, Appl
38	474	80.1	108	2	US-08-646-360-151	Sequence 151, App
39	474	80.1	108	2	US-08-082-842A-15	Sequence 15, Appl
40	474	80.1	108	4	US-08-839-765-151	Sequence 151, App
41	474	80.1	108	4	US-09-136-389-151	Sequence 151, App
42	474	80.1	108	4	US-09-610-838-151	Sequence 151, App
43	473	79.9	112	1	US-08-478-039-89	Sequence 89, Appl
44	473	79.9	112	1	US-08-476-349A-89	Sequence 89, Appl
45	459	77.5	125	1	US-08-331-398A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-15

Query Match 89.9%; Score 532; DB 4; Length 113;
Best Local Similarity 88.5%; Pred. NO. 4.9e-43;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;


```

; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match      86.1%; Score 510; DB 4; Length 281;
Best Local Similarity 86.7%; Pred. No. 1.5e-40;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRA 60
Db 166 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGNYLDWYLRKPGSQPLLIIYLSNRA 225

QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 226 SGVPRFSGSGGTDFTLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 278

RESULT 9
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      85.3%; Score 505; DB 4; Length 112;
Best Local Similarity 87.3%; Pred. No. 1.6e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRASGV 63
Db 3 LTQSPSLPVTPGEPASISCRSSQSLHSGNFELDWYLRKPGSQPLLIIYSGSHRASGV 62

QY 64 PDRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 63 PDRFSGSGGTDFTLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 112

RESULT 10
US-08-082-623-4
; Sequence 4, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

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; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SD2 MSL 109"
US-08-082-623-4

Query Match      84.8%; Score 502; DB 1; Length 113;
Best Local Similarity 85.0%; Pred. No. 3.1e-40;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRA 60
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGNYLDWYLRKPGSQPLLIIYLSNRA 60

QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 11
US-08-478-039-88
; Sequence 88, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VK2 consensus
US-08-478-039-88

Query Match 84.6%; Score 501; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 3.9e-40;
Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLPVPGEPAISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60
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Qy 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPTGKVDIK 112
Db 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQALQSPYTFGGTKNEIK 112

RESULT 12
US-08-476-349A-88
Sequence 88, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VK2 consensus
US-08-476-349A-88

Query Match 84.6%; Score 501; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 3.9e-40;
Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLPVPGEPAISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSLPLPVPGEPAISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYKVSNR 60
Qy 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPTGKVDIK 112
Db 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQALQSPYTFGGTKNEIK 112

RESULT 13
US-08-053-171-16
Sequence 16, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

RESULT 14
US-08-264-093-10
; Sequence 10, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: NO. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:

ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-1361100S

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 Variable Light
; OTHER INFORMATION: chain (V-L) (Humb3V-L)"
US-08-331-398A-50

Query Match      81.8%   Score 484;   DB 1;   Length 112;
Best Local Similarity 81.2%; Pred. No. 1.5e-38;
Matches 91; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHSHNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
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Db 1 DVLMTQSPPLSLPVTGPGEPAISCRSSQIIIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNR 60
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Qy 61 SGVPDRFSGSVSGTDTLTIRISRVEAEDGVVYVCMQGLQSPFTFGPGTKVDIK 112
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Db 61 SGVPDRFSGSVSGTDTLTIRISRVEAEDGVVYVCMQGLQSPFTFGPGTKVEIK 112
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Job time : 18.3846 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 16.0808 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSPVTPGPEPAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	113	10	US-09-822-698A-1
2	592	100.0	220	10	US-09-822-698A-24
3	592	100.0	381	10	US-09-822-698A-5
4	513	86.7	239	9	US-09-924-340-8
5	513	86.7	239	9	US-09-932-600A-8
6	510	86.1	113	12	US-10-025-687-9
7	505	85.3	112	9	US-09-848-798-30
8	492	83.1	112	10	US-09-850-165-96
9	483	81.6	116	10	US-09-753-436-66
10	481	81.2	157	10	US-09-864-761-48255
11	480	81.1	100	9	US-10-194-975-79
12	480	81.1	100	9	US-10-194-975-80
13	480	81.1	100	10	US-09-822-698A-19
14	480	81.1	100	12	US-10-025-687-24
15	480	81.1	138	10	US-09-748-960-8
16	476.5	80.5	113	10	US-09-840-459-65
17	475.5	80.3	113	10	US-09-840-459-64
18	474	80.1	222	9	US-09-479-614-26
19	474	80.1	242	9	US-09-479-614-20

20	464	78.4	112	10	US-09-850-165-97
21	462.5	78.1	113	10	US-09-840-459-68
22	455	76.9	239	9	US-10-124-905-6
23	455	76.9	239	9	US-09-948-429B-6
24	448	75.7	149	10	US-09-990-205-2
25	447	75.5	111	10	US-09-835-087-2
26	447	75.5	111	10	US-09-809-739-13
27	447	75.5	111	10	US-09-840-459-59
28	446	75.3	140	9	US-09-341-894-4
29	444	75.0	132	12	US-10-006-773-15
30	441	74.5	111	10	US-09-840-459-11
31	440	74.3	112	10	US-09-840-459-55
32	440	74.3	112	10	US-09-840-459-60
33	439	74.2	112	10	US-09-840-459-56
34	438	74.0	112	10	US-09-840-459-58
35	437	73.8	112	10	US-09-840-459-70
36	436.5	73.7	228	9	US-09-909-567B-50
37	436	73.6	112	10	US-09-840-459-62
38	436	73.6	112	10	US-09-840-459-66
39	436	73.6	298	10	US-09-883-758-2
40	435.5	73.6	110	10	US-09-864-761-48276
41	435	73.5	112	10	US-09-840-459-69
42	435	73.5	135	10	US-09-925-301-1527
43	434	73.3	113	10	US-09-971-543-4
44	434	73.3	253	10	US-09-971-543-2
45	433	73.1	114	10	US-09-217-268B-27

ALIGNMENTS

RESULT 1

US-09-822-698A-1
; Sequence 1, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1

Query Match	100.0%;	Score 592;	DB 10;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 1.4e-37;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSPVTPGPEPASISCRSSQLLSHNGYTYLDWYLOKPGQSPQLLIYSGSRA 60		
Db	1	EIVLTQSPVTPGPEPASISCRSSQLLSHNGYTYLDWYLOKPGQSPQLLIYSGSRA 60		
QY	61	SGVPDRFSGSVSGTDTLRLSRVEAEADVGVYCMQGLQSPFTFGPTKVDIKR 113		
Db	61	SGVPDRFSGSVSGTDTLRLSRVEAEADVGVYCMQGLQSPFTFGPTKVDIKR 113		
RESULT 2				
US-09-822-698A-24				
; Sequence 24, Application US/09822698A				
; Patent No. US20020146750A1				
; GENERAL INFORMATION:				

Query Match 85.3%; Score 505; DB 9; Length 112;
Best Local Similarity 87.3%; Pred. No. 3.9e-31;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weunsheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48255
; LENGTH: 157
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001224.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
; OTHER INFORMATION: SWISSPROT HIT: P06309, EVALUAE 8.00e-55
; OTHER INFORMATION: EST_HUMAN HIT: AW406883.1, EVALUAE 3.00e-54
; OS=09-864-761-48255

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	Query Match	81.2%	Score 481;	DB 10;	Length 157;
	Best Local Similarity	90.2%;	Pred. No. 3.1e-29;		
	Matches 92;	Conservative	5;	Mismatches 5;	Indels 0;
	Gaps	0;			
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Db	4	DIVMTQSLPLVPTGEPASTSCRSSQSLLSNGNYTYLDWYLOKPGQSPOLLIIYLSGNSRA	63		
Qy	61	SGVPDRFSSGSGTGFTLIRISVEAEDGVYIYCMQGLQSFT	102		
Db	64	SGVPDRFSSGSGTGFTLIRISVEAEDGVYIYCMQALQTPT	105		


```
RESULT 11
US-10-194-975-79
; Sequence 79, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-79

Query Match      81.1%; Score 480; DB 9; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||:|
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVGTDFTLIRSRVEAEDGVYYCMQGLQSP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYYCMQALQTP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 12
US-10-194-975-80
; Sequence 80, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-80

Query Match      81.1%; Score 480; DB 9; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVGTDFTLIRSRVEAEDGVYYCMQGLQSP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYYCMQALQTP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 13
US-09-822-698A-19
; Sequence 19, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
```

```
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 19
; LENGTH: 100
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region from a DPK 15 germ line
US-09-822-698A-19

Query Match      81.1%; Score 480; DB 10; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVGTDFTLIRSRVEAEDGVYYCMQGLQSP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYYCMQALQTP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 14
US-10-025-687-24
; Sequence 24, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-687-24

Query Match      81.1%; Score 480; DB 12; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVGTDFTLIRSRVEAEDGVYYCMQGLQSP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYYCMQALQTP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 15
US-09-748-960-8
; Sequence 8, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855.2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
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; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Portion of the light chain of LDP-02 with a light
; OTHER INFORMATION: chain signal peptide
; NAME/KEY: SITE
; LOCATION: (20)...(21)
; OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-8

Query Match      81.1%; Score 480; DB 10; Length 138;
Best Local Similarity 81.4%; Pred. No. 3.3e-29;
Matches 92; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY    1  EIVLTQSPLSPVTPGEPASISCRSSGLSHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
      ::::::::::::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     21  DVVMTQSPLSIPVTPGEPASISCRSSGLAKSYGNTYLSWYLQKPGQSPQLLIYGISNRF 80
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY    61  SGVPDRSGSVSGDFTLRLSRVEAEADVGVYCMQGLQSFTFGGGTKVDIKR 113
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     81  SGVPDRSGSVSGDFTLRLSRVEAEADVGVYCMQGLQHTQHPYTFFGGGTKEIKR 133
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Search completed: March 13, 2003, 15:30:30
Job time : 17.0808 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 240.777 Seconds
(without alignments)
302.582 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592

Sequence: 1 EIVLTQSPSLPVTPGPAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
- 18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
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- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
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- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	113	19	US-09-538-913-1
2	592	100.0	113	22	US-09-822-698A-1
3	592	100.0	220	22	US-09-822-698A-24
4	592	100.0	381	19	US-09-538-913-5
5	592	100.0	381	22	US-09-822-698A-5
6	540	91.2	114	21	US-09-791-537-86326

7	534	90.2	262	1	PCT-US01-19110-2081	Sequence 2081, Ap
8	534	90.2	262	22	US-09-880-748-2081	Sequence 2081, Ap
9	533	90.0	136	21	US-09-791-537-71827	Sequence 71827, A
10	533	90.0	137	21	US-09-791-537-56427	Sequence 56427, A
11	532	89.9	113	18	US-09-490-070-15	Sequence 15, Appl
12	531	89.7	114	21	US-09-791-537-86001	Sequence 86001, A
13	529	89.4	116	21	US-09-791-537-43479	Sequence 43479, A
14	529	89.4	117	21	US-09-791-537-48291	Sequence 48291, A
15	529	89.4	118	21	US-09-791-537-129360	Sequence 129360, A
16	529	89.4	135	21	US-09-791-537-12279	Sequence 12279, A
17	529	89.4	135	21	US-09-791-537-123428	Sequence 123428, A
18	528	89.0	112	21	US-09-791-537-21285	Sequence 21285, A
19	527	89.0	114	21	US-09-791-537-137519	Sequence 137519, A
20	527	89.0	117	21	US-09-791-537-107503	Sequence 107503, A
21	526	88.9	113	21	US-09-791-537-59499	Sequence 59499, A
22	524	88.5	112	11	US-08-700-737-8	Sequence 8, Appli
23	524	88.5	112	16	US-09-254-180B-9	Sequence 9, Appli
24	524	88.5	125	24	US-10-010-942B-6	Sequence 6, Appli
25	524	88.5	132	21	US-09-791-537-78289	Sequence 78289, A
26	523.5	88.4	114	18	US-09-430-048-19	Sequence 19, Appl
27	523.5	88.4	131	18	US-09-430-048-25	Sequence 25, Appl
28	523	88.3	118	21	US-09-791-537-54839	Sequence 54839, A
29	522	88.2	112	7	US-08-331-396-49	Sequence 49, Appl
30	522	88.2	112	7	US-08-331-396A-49	Sequence 49, Appl
31	522	88.2	112	7	US-08-331-396C-49	Sequence 49, Appl
32	522	88.2	112	7	US-08-331-396D-49	Sequence 49, Appl
33	522	88.2	112	7	US-08-331-397-49	Sequence 49, Appl
34	522	88.2	112	7	US-08-331-398-49	Sequence 49, Appl
35	522	88.2	112	11	US-08-759-804-49	Sequence 49, Appl
36	522	88.2	112	21	US-09-791-537-21281	Sequence 21281, A
37	522	88.2	112	21	US-09-791-537-110202	Sequence 110202, A
38	522	88.2	125	21	US-09-791-537-26052	Sequence 26052, A
39	521	88.0	112	21	US-09-791-537-34978	Sequence 34978, A
40	521	88.0	113	21	US-09-791-537-64225	Sequence 64225, A
41	520.5	87.9	113	21	US-09-791-537-137518	Sequence 137518, A
42	520	87.8	112	21	US-09-791-537-110195	Sequence 110195, A
43	518.5	87.6	112	18	US-09-430-048-20	Sequence 20, Appl
44	517.5	87.4	248	19	US-09-517-225E-6	Sequence 6, Appli
45	516	87.2	113	21	US-09-791-537-106796	Sequence 106796, A

ALIGNMENTS

RESULT 1
US-09-538-913-1
; Sequence 1, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hooqenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-1

Query Match	100.0%;	Score 592;	DB 19;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 1e-49;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLISGSHRA	60	
Db	1	EIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLISGSHRA	60	
Qy	61	SGVPDRFSGVSGTDFTLRLISRVAEADVGYVMQGLQSPFTFGPTKVDIKR	113	

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 2

US-09-822-698A-1
 ; Sequence 1, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 1
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: light chain variable region of the MUC1-specific
 ; OTHER INFORMATION: binding domain of PH1 Fab antibody
 US-09-822-698A-1

Query Match 100.0%; Score 592; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1e-49;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 3

US-09-822-698A-24
 ; Sequence 24, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 24
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
 US-09-822-698A-24

Query Match 100.0%; Score 592; DB 22; Length 220;
 Best Local Similarity 100.0%; Pred. No. 2.3e-49;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 4

US-09-538-913-5
 ; Sequence 5, Application US/09538913
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Paula
 ; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: seqlist DYX-15
 ; CURRENT APPLICATION NUMBER: US/09/538,913
 ; CURRENT FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 381
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: amino acid
 ; OTHER INFORMATION: sequence for bivPH1-IL-2 immunocytokine fusion
 ; OTHER INFORMATION: protein
 US-09-538-913-5

Query Match 100.0%; Score 592; DB 19; Length 381;
 Best Local Similarity 100.0%; Pred. No. 4.3e-49;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 186

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 187 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 5

US-09-822-698A-5
 ; Sequence 5, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 5
 ; LENGTH: 381
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
 US-09-822-698A-5

Query Match 100.0%; Score 592; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 4.3e-49;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 60

Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLNKPGQSPQLLIYSGSHRA 186

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 187 SGVDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 6


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US-09-791-537-56427
; Sequence 56427, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56427
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-56427

Query Match          90.0%; Score 533; DB 21; Length 137;
Best Local Similarity 89.4%; Pred. No. 7.8e-44;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHEA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 21 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYLSGNRA 80
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVDPFRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVDPFRFSGSGCTDFTLKISRVEADGVVYCMQALQTPFTFGGQTKVEIKR 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-490-070-15
; Sequence 15, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,769
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
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; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070-15

Query Match          89.9%; Score 532; DB 18; Length 113;
Best Local Similarity 88.5%; Pred. No. 7.8e-44;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHEA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYLSGNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVDPFRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVDPFRFSGSGTDFTLKISRVEADGVVYCMQALQTPFTFGGQTKVEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-791-537-86001
; Sequence 86001, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86001
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-86001

Query Match          89.7%; Score 531; DB 21; Length 114;
Best Local Similarity 89.4%; Pred. No. 9.9e-44;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHEA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYLSGNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVDPFRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVDPFRFSGSGTDFTLKISRVEADGVVYCMQALQTPFTFGGQTKVEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-791-537-43479
; Sequence 43479, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43479
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-43479

.. Query Match          89.4%; Score 529; DB 21; Length 116;
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Best Local Similarity 89.4%; Pred. No. 1.6e-43;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 4 DIVMTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYLSNRA 63
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKR 113
Db 64 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQALQTPQTFGQGTKEIKR 116

RESULT 14

US-09-791-537-48291
; Sequence 48291, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48291
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-48291

Query Match 89.4%; Score 529; DB 21; Length 117;
Best Local Similarity 89.4%; Pred. No. 1.6e-43;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYLSNRA 64
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKR 113
Db 65 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQALQTPQTFGQGTKEIKR 117

RESULT 15

US-09-791-537-129360
; Sequence 129360, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129360
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-129360

Query Match 89.4%; Score 529; DB 21; Length 118;
Best Local Similarity 89.4%; Pred. No. 1.6e-43;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHLSNGVYTLDWYLQKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYVYCMQALQTPQTFGQGTKEIKR 113

Search completed: March 13, 2003, 15:28:02
Job time : 242.027 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 41.2885 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592
Sequence: 1 EIVLTQSLPLVPTGEPAS.....MQGLSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	592	100.0	131	1	PCT-US02-34249-2
2	592	100.0	131	1	PCT-US02-34249A-2
3	592	100.0	131	6	US-10-279-833-2
4	534	90.2	113	1	PCT-US03-05128-80
5	534	90.2	262	1	PCT-US02-36496-2081
6	534	90.2	262	6	PCT-US02-36496-2081
7	532	89.9	113	5	US-09-490-153-15
8	531	89.7	112	1	PCT-US02-32613-30
9	531	89.7	112	6	US-10-269-805-30
10	526	88.9	112	1	PCT-US02-32613-18
11	526	88.9	112	1	PCT-US02-32613-26
12	526	88.9	112	1	PCT-US02-38550-33
13	526	88.9	112	6	US-10-269-805-18
14	526	88.9	112	6	US-10-269-805-26
15	526	88.9	112	6	US-10-309-762-33
16	524	88.5	112	5	US-09-254-180C-9
17	522	88.2	112	1	PCT-US02-32613-2
18	522	88.2	112	6	US-10-269-805-2
19	521	88.0	112	1	PCT-US02-38550-32
20	521	88.0	112	6	US-10-309-762-32
21	520	87.8	112	1	PCT-US02-32613-28
22	520	87.8	112	6	US-10-269-805-28
23	519	87.7	112	1	PCT-US02-32613-20
24	519	87.7	112	6	US-10-269-805-20
25	517.5	87.4	222	6	US-10-184-508A-6
26	517.5	87.4	222	6	US-10-186-186-6

27	517.5	87.4	222	6	US-10-186-186A-6
28	517	87.3	112	1	PCT-US02-32613-44
29	517	87.3	112	6	US-10-269-805-44
30	515	87.0	219	1	PCT-US02-33556-104
31	513	86.7	239	5	US-09-392-095B-8
32	513	86.7	239	6	PCT-US02-32613-12
33	512	86.5	112	1	US-10-154-678-8
34	512	86.5	112	6	US-10-269-805-12
35	510	86.1	114	5	US-09-490-153-29
36	510	86.1	114	5	US-09-490-153-45
37	510	86.1	281	5	US-09-490-153-178
38	508	85.8	110	1	PCT-US02-38550-157
39	508	85.8	110	1	PCT-US02-38550-165
40	508	85.8	110	6	US-10-309-762-157
41	508	85.8	110	6	US-10-309-762-165
42	507	85.6	112	1	PCT-US02-38550-34
43	507	85.6	112	5	US-09-936-964A-59
44	507	85.6	112	6	US-10-309-762-34
45	506	85.5	114	1	PCT-US03-00398-322

ALIGNMENTS

RESULT 1
PCT-US02-34249-2
; Sequence 2, Application PC/TUS0234249
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027W01
; CURRENT APPLICATION NUMBER: PCT/US02/34249
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34249-2

Query Match	100.0%;	Score 592;	DB 1;	Length 131;
Best Local Similarity	100.0%;	Pred. No. 2.9e-44;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA	60	
Db	6	EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA	65	
QY	61	SGVPRFSGSVSGTDTLIRSRVEAEDGVYYCMQGLSQSPFTFGPTKVDIKR	113	
Db	66	SGVPRFSGSVSGTDTLIRSRVEAEDGVYYCMQGLSQSPFTFGPTKVDIKR	118	

RESULT 2
PCT-US02-34249A-2
; Sequence 2, Application PC/TUS0234249A
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027W01
; CURRENT APPLICATION NUMBER: PCT/US02/34249A
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131

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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34249A-2

Query Match      100.0%; Score 592; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 6 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 65

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 66 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 118

RESULT 3
US-10-279-633-2
; Sequence 2, Application US/10279633
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-2

Query Match      100.0%; Score 592; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 6 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 65

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 66 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 118

RESULT 4
PCT-US03-05128-80
; Sequence 80, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034W01
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-80

Query Match      90.2%; Score 534; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.8e-39;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

; TYPE: PRT
; ORGANISM: Homo sapiens
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QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 5
PCT-US02-36496-2081
; Sequence 2081, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-2081

Query Match      90.2%; Score 534; DB 1; Length 262;
Best Local Similarity 90.3%; Pred. No. 6.1e-39;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 150 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 209

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 210 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 262

RESULT 6
US-10-293-418-2081
; Sequence 2081, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
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; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: PCT/US02/32613
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32613-18

Query Match      88.9%; Score 526; DB 1; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy 61 SGVPDRFSGSGVTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 SGVPDRFSGSGVTDFTLRISRVEAEDVGVYCMQALQTLPTFGGKVEIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
PCT-US02-32613-26
; Sequence 26, Application PC/TUS0232613
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: PCT/US02/32613
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32613-26

Query Match      88.9%; Score 526; DB 1; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy 61 SGVPDRFSGVSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 SGVPDRFSGSGTDFTLKISRVEAEDVGVYCMQALQTLPTFGGKVEIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 12
PCT-US02-38550-33
; Sequence 33, Application PC/TUS0238550
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: ABGENIX, Jean.
; APPLICANT: GUDAS, Jean
; APPLICANT: FOLTZ, Ian
; APPLICANT: HANDA, Masahisa
; APPLICANT: GALLO, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: PCT/US02/38550
; CURRENT FILING DATE: 2002-12-02
; ORGANISM: Homo sapiens
US-10-269-805-26

Query Match      88.9%; Score 526; DB 6; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy 61 SGVPDRFSGVSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 SGVPDRFSGSGTDFTLKISRVEAEDVGVYCMQALQTLPTFGGKVEIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
US-10-269-805-18
; Sequence 18, Application US/10269805
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-18

Query Match      88.9%; Score 526; DB 6; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
   :||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy 61 SGVPDRFSGVSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 SGVPDRFSGSGTDFTLKISRVEAEDVGVYCMQALQTLPTFGGKVEIK 112
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
US-10-269-805-26
; Sequence 26, Application US/10269805
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-26
```

Search completed: March 13, 2003, 15:29:44
Job time : 42.2885 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 19.5577 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSPVLPVTPGEPAS.....MQGLQSPFTFGPCTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	90.0	136	2 S40357	Ig kappa chain V-J
2	529	89.4	135	2 S40342	Ig kappa chain - h
3	528	89.2	112	2 S58207	Ig light chain V r
4	527	89.0	117	1 K2HUGM	Ig kappa chain pre
5	524	88.5	132	2 S26882	Ig kappa chain V r
6	522	88.2	112	2 S58206	Ig light chain V r
7	522	88.2	125	2 S40356	Ig kappa chain - h
8	507.5	85.7	126	2 S40339	Ig kappa chain - h
9	505	85.3	121	2 S40371	Ig kappa chain - h
10	500	84.5	113	1 K2HUTW	Ig kappa chain V-I
11	494	83.4	131	2 S40372	Ig kappa chain V-I
12	484	81.8	124	2 S03876	Ig kappa chain V-I
13	478.5	80.8	112	1 K2HUNL	Ig kappa chain V-I
14	478	80.7	123	2 S40319	Ig kappa chain V r
15	473.5	80.0	130	2 S40321	Ig kappa chain - h
16	467.5	79.0	115	1 K2HUCM	Ig kappa chain V-I
17	467	78.9	100	2 S24681	Ig kappa chain pre
18	457	77.2	113	2 PL0203	Ig kappa chain - h
19	457	77.2	114	2 S40375	Ig kappa chain - h
20	455	76.9	113	1 K2HUFH	Ig kappa chain V-I
21	452.5	76.4	114	2 S40340	Ig kappa chain V-I
22	449	75.8	131	2 B39276	Ig kappa chain V-J
23	447	75.5	142	2 S22902	Ig light chain pre
24	447	75.5	219	2 S52028	Ig kappa chain V r
25	446	75.3	133	2 S23230	Ig kappa chain - m
26	445.5	75.3	127	2 S40323	Ig kappa chain - h
27	445	75.2	114	2 A32967	Ig kappa chain V-I
28	445	75.2	133	2 S40324	Ig kappa chain V r
29	444	75.0	112	2 A31807	Ig kappa chain V r

30	444	75.0	131	2 B30577	Ig kappa chain pre
31	444	75.0	133	1 K2HURP	Ig kappa chain pre
32	444	75.0	219	2 PC4203	Ig kappa chain (mo
33	443	74.8	112	2 I26317	Ig kappa chain V r
34	443	74.8	118	2 PT0359	Ig kappa chain V r
35	443	74.8	197	2 S29593	Ig kappa chain (WM
36	442.5	74.7	126	2 S40341	Ig kappa chain - h
37	442	74.7	112	2 G26317	Ig kappa chain V r
38	442	74.7	112	2 S38719	Ig light chain V r
39	442	74.7	115	2 S38715	Ig kappa chain V r
40	442	74.7	122	2 S40338	Ig kappa chain - h
41	441	74.5	112	2 A26317	Ig kappa chain V r
42	441	74.5	112	2 F27887	Ig kappa chain V r
43	441	74.5	112	2 F26317	Ig kappa chain V r
44	441	74.5	113	2 B41940	Ig light chain V r
45	441	74.5	126	2 S40312	Ig kappa chain - h

ALIGNMENTS

RESULT 1
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 533; DB 2; Length 136;
Best Local Similarity 89.4%; Pred. No. 6.7e-42;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY	1	EIVLTQSPVLPVTPGEPASISCRSSQLLHNSGYTLWDYLOKPGQSPQLIYSGSHRA	60
Db	21	DIIVTQSPVLPVTPGEPASISCRSSQLLHNSGYTLWDYLOKPGQSPQLIYLCGNRA	80
QY	61	SGVPDRFSGSVSGTDFTLRLSRVEADGVYCYCMQGLQSPFTFGPCTKVDIKR	113
Db	81	SGVPDRFSGSVSGTDFTLRLSRVEADGVYCYCMQALQTPWTFPGQTRVEIKR	133

RESULT 2
S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 529; DB 2; Length 135;

```
Best Local Similarity 89.4%; Pred. No. 1.5e-41;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 14 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLGSNRA 73
QY 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 74 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQALQTPRTFGGQTKVEIKR 126

RESULT 3
S58207
Ig kappa chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58207
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 528; DB 2; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.6e-41;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQALQTPWTFGGQTKVEIK 112

RESULT 4
K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506; PMID:6325927
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted

Query Match 89.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 2e-41;
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```
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 5 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLGSNRA 64
QY 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 65 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQTPQTFTGGQTKVEIKR 117

RESULT 5
S26882
Ig kappa chain V region (V607) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882; MUID:90370099; PMID:2118596
A:Accession: S26882
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 524; DB 2; Length 132;
Best Local Similarity 89.3%; Pred. No. 4.3e-41;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLGSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIK 112
Db 81 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQALQTPQTFTGGQTKVEIK 132

RESULT 6
S58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58206
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitlin
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable regi
A:Reference number: S58206
A:Accession: S58206
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:g929641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 522; DB 2; Length 112;
Best Local Similarity 88.4%; Pred. No. 5.5e-41;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIK 112
```


Db 61 SGVPRFSGSGTDTFLKISRVEADVGVYCMQALQTLTFGGTKVEIK 112
|||||

RESULT 7

S40356

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40356

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40356

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72466; NID:q441400; PIDN:CAA51134.1; PID:q441401

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-104/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.2%; Score 522; DB 2; Length 125;

Matches 100; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1

1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60

Db 10 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYLSNRA 69

QY 61

SGVPRFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

Db 70 SGVPRFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVEIKR 122

RESULT 8

S40339

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40339

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40339

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-126 <KLE>

A:Cross-references: EMBL:X72449; NID:q441366; PIDN:CAA51117.1; PID:q441367

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-110/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 507.5; DB 2; Length 126;

Matches 98; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1

1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60

Db 16 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYLSNRA 75

QY 61

SGVPRFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 112

Db 76 SGVPRFSGSGTDTFLKISRVEADVGVYCMQALQ-PWTFGGTKVEIK 126

RESULT 9

S40371

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40371

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40371

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-121 <KLE>

A:Cross-references: EMBL:X72481; NID:q441430; PIDN:CAA511149.1; PID:q441431

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:13-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.3%; Score 505; DB 2; Length 121;

Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4

LTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRAGV 63

Db 1 MTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYLSKRAGV 60

QY 64

PDREFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 PDREFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVEIKR 110

RESULT 10

K2HUTW

Ig kappa chain V-II region (Tew) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A90370; A92764; A01888

R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.

Biochemistry 12, 3763-3780, 1973

A>Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary au

A:Reference number: A90370; MUID:74148480; PMID:4596149

A:Contents: Bence Jones protein Tew

A:Accession: A90370

A:Molecule type: protein

A:Residues: 1-113 <PUT>

A>Note: This protein was isolated from the urine of a patient with plasma cell dyscra

A>Note: The C region of this chain has the inv (1,2) marker

R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glenner, G.G.

J. Clin. Invest. 52, 1276-1281, 1973

A>Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient

A:Reference number: A92764; MUID:73166638; PMID:4700495

A:Contents: amyloid protein Tew

A:Accession: A92764

A:Molecule type: protein

A:Residues: 1-27 <TER>

A>Note: the major amyloid protein appears to be identical with the Bence Jones protei

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: amyloid; heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 84.5%; Score 500; DB 1; Length 113;

Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1

EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60

Db 1 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYALSRA 60

QY 61

SGVPRFSGSGTDTFLKISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

|||||

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYCMZALQAPITFGQGTRLLEIKR 113

RESULT 11

S40372

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40372

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40372

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 494; DB 2; Length 131;

Best Local Similarity 83.8%; Pred. No. 2.4e-38;

Matches 93; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGHNYLDWYLOKPGQSPQLLIYLGSTRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQGLQSPFTFGPGTKVDI 111

Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQPLQTPYTFGQGTKLEI 131

RESULT 12

S03876

Ig kappa chain V-II region (Inc) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S03876

R:Ferrl, G.; Stoppin, M.; Iadarola, P.; Bellotti, V.; Merlini, G.

Biochim. Biophys. Acta 995, 103-108, 1989

A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.

A:Reference number: S03876; MUID:89194238; PMID:2495028

A:Accession: S03876

A:Molecule type: protein

A:Residues: 1-124 <FER>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 484; DB 2; Length 124;

Best Local Similarity 82.3%; Pred. No. 1.9e-37;

Matches 93; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 1 DIVLTQSPVLPVTPGEPASISCRSSQSLHNSGDNLDWYLOKPGQSPQIVILGNSRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVPDRFSGSGGTDFTLLISVGAEDGYYVCMQALQTPWTFGQGTKVGIKR 113

RESULT 13

K2HUMI

Ig kappa chain V-II region (MI) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A01887

R:Dreyer, W.J.; Gray, W.R.; Hood, L.

Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967

A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts

A:Reference number: A01887

A:Accession: A01887

A:Molecule type: protein

A:Residues: 1-112 <DRE>

A:Note: the C region of this chain has the Inv (3) marker

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 80.8%; Score 478.5; DB 1; Length 112;

Best Local Similarity 78.8%; Pred. No. 5.3e-37;

Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 1 DIVLTQSPVLPVTPGEPASISCRSSQSLHNSBG-BYLDWYLZKPGSPZLLIYLGNSRA 59

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQGLQSPFTFGPGTKVDIKR 113

Db 60 SGVPDRFSGSGGTDFTLKISRVAZBVGYYVCMQALQTPITFGGTVNVEIKR 112

RESULT 14

S40319

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40319

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40319

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 478; DB 2; Length 123;

Best Local Similarity 90.0%; Pred. No. 6.5e-37;

Matches 90; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 11 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYLDWYLOKPGQSPQLLIYLGNSRA 70

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQGLQSP 100

Db 71 SGVPDRFSGSGGTDFTLKISRVEAEDGYYVCMQALQTP 110

RESULT 15

S40321

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40321

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40321
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-130 <KLE>
 A:Cross-references: EMBL:X72431
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:31-111/Domain: immunoglobulin homology <IMM>

Query Match	80.0%	Score 473.5;	DB 2;	Length 130;
Best Local Similarity	80.7%	Pred. No. 1.8e-36;		
Matches	92;	Conservative 13;	Mismatches 8;	Indels 1; Gaps 1;

Qy	1	EIVLTQSPVLPVTPGEPASISCRSSQSLHS-NGYTYLDWYLOKPGQSPOLLIYSGSHR	59
Db	16	DIWMTQTPLSVPVTPGEPASISCRSSQSLDSDGNTYLDWYLOKPGQSPOLLIYTLISYR	75

Qy	60	ASGVDPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKR	113
Db	76	ASGVDPDRFSGSGGTAFTLKISRVEAEDVGLYCMQRIEFPYTFGQGTKLEIKR	129

Search completed: March 13, 2003, 15:17:49
 Job time : 19.5577 secs

ID	KV2C_HUMAN	STANDARD;	PRT;	112 AA.
AC	P01616;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region MIL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE.			
RA	Dreyer W.J., Gray W.R., Hood L.E.;			
RT	"The genetic, molecular, and cellular basis of antibody formation:			
RT	some facts and a unifying hypothesis."			
RT	Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).			
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
CC	P1R; A01887; K2HUML.			
DR	HSP; P80362; IWLTL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART; SM00406; IgV; 1.			
KW	Immunoglobulin V region; Bence-Jones protein.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 38			
FT	DOMAIN 39 53			
FT	DOMAIN 54 60			
FT	DOMAIN 61 92			
FT	DOMAIN 93 101			
FT	DOMAIN 102 111			
FT	DISULFID 23 92			
FT	NON_TER 112 112			
SQ	SEQUENCE 112 AA; 12055 MW; F5B2E2FA7ABE481 CRC64;			
Query Match 80.8%; Score 478.5; DB 1; Length 112;				
Best Local Similarity 78.8%; Pred. No. 1.9e-41;				
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps				
QY	1 EIVLTOSPLSLVPTGEGPASTICSRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60			
DB	1 DIVLTOSPLSLVPTGEGPASTICSRSSQNLLZSBG-BYLDWYLKPGZSPZLLIYLSNRA 112			
QY	61 SGVDFRFGSGGFTFLRISRVAEDGVVYVYCMQGLSPFTFGPGTKVDIKR 113			
DB	60 SGVFNRFSGSGGTFTLKISRVAZBVGIVYCMQALQTPLEFGGTNVEIKR 112			
RESULT 4				
KV2A_HUMAN	STANDARD;	PRT;	115 AA.	
AC	P01614;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region Cum.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE.			
RA	MEDLINE=68242259; PubMed=5586923;			
RT	Hiltschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-			
RT	type).";			
RT	Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).			
RN	[2]			
RP	REVIEWS TO 50; 52; 96 AND 97.			
RP	MEDLINE=70063440; PubMed=4188189;			
RA	Hiltschmann N.;			
RT	"Molecular basis of antibody formation.";			

```
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 79.0%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 2.5e-40;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHLS-NGYTYLDWYLOKPGQSPOLLIVSGSHR 59
DB 2 DIVMTQSPISLPVTPGEPASISCRSSQSLDSDGNTYLNWYLOKPGQSPOLLIVTLYSYR 61

QY 60 ASGVPDRFSGSVSGTDFTLIRISRVEADVGVVYCMQGLQSPFTFGPTKVDIKR 113
DB 62 ASGVPDRFSGSVSGTDFTLKISRVAEDVGVIYCMQRLIEIPYTFGGTKLEIRR 115

RESULT 5
KV2B_HUMAN
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR: A01886; K2HURF.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46D996BE CRC64;

Query Match 76.9%; Score 455; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 4.4e-39;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPOLLIVSGSHR 60
DB 1 DIVMTQSPISLPVTLGLGASIQCRSSQSLVYRGGTYLEWYLOKPGQSPOLLIVLSYRD 60
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QY 61 SGVPDRFSGSVSGTDFTLIRISRVEADVGVVYCMQGLQSPFTFGPTKVDIKR 113
DB 61 SGVPDRFSGSVSGTDFTLKISRVAEDVGVIYCMQATZSPYTFGGTKLAIKR 113

RESULT 6
KV2F_HUMAN
ID KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; P80362; IWLH.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 75.0%; Score 444; DB 1; Length 133;
Best Local Similarity 75.2%; Pred. No. 6.7e-38;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPOLLIVSGSHR 60
DB 21 DIVMTQSPISLPVTLGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIVKVSND 80

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEADVGVVYCMQGLQSPFTFGPTKVDIKR 113
DB 81 SGVPDRFSGSVSGTDFTLKISRVAEDVGVIYCMQTHSWTFGGTKVIEIKR 133

RESULT 7
KV2E_MOUSE
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
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DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Hybridoma; PubMed=6441768;
RX MEDLINE=85128968;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Ig_V.
DR Fram; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 73.0%; Score 432; DB 1; Length 113;
Best Local Similarity 75.2%; Pred. No. 9e-37;
Matches 85; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLVPVTPGEPASISCRSSQLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
Db 1 DIVMTQVFPVLTGTSASISCRSSKSLHNSGYTYLYWYLOKPGQSPOLLIYQMSNLA 60

Qy 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGVVYCAHNLELPTFGGFKLEIKR 113

RESULT 8
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
DR PIR; A01914; KVM526.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Iq_MHC.

Qy 1 EIVLTQSLPLVPVTPGEPASISCRSSQLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
Db 1 DIVMTQVFPVLTGTSASISCRSSKSLHNSGYTYLYWYLOKPGQSPOLLIYQMSNLA 60

Qy 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGVVYCAHNLELPTFGGFKLEIKR 113

RESULT 8
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
DR PIR; A01914; KVM526.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Iq_MHC.
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DR InterPro; IPR003596; Ig_V.
DR Fram; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE9A9A4C3A CRC64;

Query Match 72.5%; Score 429; DB 1; Length 113;
Best Local Similarity 72.6%; Pred. No. 1.8e-36;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLVPVTPGEPASISCRSSQLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
Db 1 DVVMTQTLPLSPVSLGDAQSISCRSSQLVHSNGTYLWYLOKAGQSPKLIYKVSNRF 60

Qy 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSGVSGDTFTLRISRVEAEDGLIYFCSTHTVPTFGGFKLEIKR 113

RESULT 9
KV2F_MOUSE STANDARD; PRT; 113 AA.
ID KV2F_MOUSE
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Ig_V.
DR Fram; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 7.2e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunohistochemistry 15:303-305(1978).
CC -1- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC PTR: A01907; K2DGGM.
DR HSP; P01607; JREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 25 49
FT DOMAIN 30 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 66.6%; Score 394.5; DB 1; Length 108;
Best Local Similarity 69.0%; Pred. No. 5e-33;
Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps

QY 1 EIVLTQSPLESLPTVPEPASISCRSSQSLHNSGYIYLOWYLOKPGQSPQLIYSGSHRA 60
Db 1 DIVMTQPTLSLSPGPASISCRSSQSLN-----DYLAWYLQKAGSPRLLPEDQSRA 55
QY 61 SGVPDRFSGSVSGTDTFLRISRVAEADVGVYVCMQGLQSPETFGPTGKVDIKR 113
Db 56 SGVPDRFSGSVSGTDTFLRIGRVEADAGIYCMQRSFYPIYFGQGRLEVR 108

RESULT 12
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 13-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PTR: A01910; KVM651.
DR HSP; P80362; LWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 1 23
SQ SEQUENCE 1. 23

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FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match
Best Local Similarity 66.6%; Score 394; DB 1; Length 113;
Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 1 DIVITODELSKPVTSGESVSISCRSSKSLYKDGKTYLWNFLQGGPQQSPRLIYLMSTRA 60

QY 61 SGVDPFRFSGSGVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVDRFSGSGSGDTFTLEISRVAEDGVYVYCOQLVEYPLTFGAGTKLELKR 113

RESULT 13
KV2A_MOUSE STANDARD; PRT; 112 AA.
ID P01626;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -I- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CC CHAIN HAS ALSO BEEN DETERMINED.
DR PTR: A01908; KVM516.
DR HSSP: P80362; IWTLL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58BDFD6404B9726 CRC64;

Query Match
Best Local Similarity 65.4%; Score 387; DB 1; Length 112;
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 1 DIVITODELSKPVTSGESVSISCRSSKSLYKDGKTYLWNFLQGGPQQSPRLIYLMSTRA 60

QY 61 SGVDPFRFSGSGVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKR 112
Db 61 SGVDRFSGSGSGDTFTLEISRVAEDGVYVYCOQLVEYPLTFGAGTKLELKR 112
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Db 61 SGVDRFSGSGSGRTDFTLEISRVAEDGVYVYCOQLVEYPLTFGAGTKLELKR 112

RESULT 14
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID P18135;
DR 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO022; K3HUHA.
DR HSSP: P80362; IWTLL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match
Best Local Similarity 62.5%; Score 370; DB 1; Length 129;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSS----YLAWYQKPGQAPRLIYGAASSRA 76

QY 61 SGVDPFRFSGSGVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKR 113
Db 77 TGIPDRFSGSGSGDTFTLTISRLEPEDFAVYVYCOQYGTSPRTFGGQTKVEIKR 129

RESULT 15
KV3M_HUMAN STANDARD; PRT; 129 AA.
ID P18136;
DR 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO021; K3HUHI.
DR HSP: P80362; 1WTL.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_LV.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 62.3%; Score 369; DB 1; Length 129;
Best Local Similarity 65.5%; Pred. No. 2.2e-30;
Matches 74; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPVLSLPTGQEPASISCRSSQSLHLSNGYTYLDWYLRKPGSQPOLLIYSGSHRA 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSS---YLAWYQQKPGQAPRLLIYGASSRA 76

QY 61 SGVPDRFGSGVSGTDFTLRISRVEAEDEVGYVYCMQGLQSPFTFGTKVDIKR 113
DB 77 TGIPTDFSGSGSDTFTLTISRLEPDXDFAVYVYCOYQYSSPWTFGQTKVEIKR 129

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Search completed: March 13, 2003, 15:15:13
Job time : 12.3 secs

Result No.	Query No.	Score	Query		Length	DB	ID	Description
			Match	%				
1	1	457	77.2	238	11	Q99M37	Q99m37 mus musculus	
2	2	444	75.0	239	11	Q8VC55	Q8vc55 mus musculus	
3	3	438	74.0	238	11	Q8VC16	Q8vc16 mus musculus	
4	4	436	73.6	239	4	Q8VCDO	Q8vcdo homo sapien	
5	5	428.5	72.4	114	4	Q9UL80	Q9ul80 homo sapien	
6	6	406	68.6	104	11	Q9JL82	Q9jl82 mus musculus	
7	7	373	63.0	109	4	Q9UL78	Q9ul78 homo sapien	
8	8	369	62.3	109	4	Q9UL86	Q9ul86 homo sapien	
9	9	351.5	59.4	108	4	Q9UL83	Q9ul83 homo sapien	
10	10	340.5	57.5	111	11	Q920E9	Q920e9 mus musculus	
11	11	325.5	55.0	107	11	Q9E8Z9	Q9ez9 mus musculus	
12	12	322	54.4	107	4	Q9UL81	Q9ul81 homo sapien	
13	13	322	54.4	109	4	Q9UL85	Q9ul85 homo sapien	
14	14	316.5	53.5	108	4	Q9UL77	Q9ul77 homo sapien	
15	15	313	52.9	106	5	Q9UL10	Q9u410 schistosoma	
16	16	309.5	52.3	108	4	Q9UL79	Q9ul79 homo sapien	

QY 61 SGVPDRFSGSGTDFTLRLSRVEADGVGYCMOGLQSPFTFGPTKVDIKR 113
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
DB 80 SGVPDRFSGSGTDFTLRLSRVEADLGVYCFQSGSHVPTFGSGTKLEIKR 132
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

RESULT 2
Q8VC55 PRELIMINARY; PRT; 239 AA.
ID Q8VC55
AC Q8VC55; 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CAC25C337 CRC64;

Query Match 75.0%; Score 444; DB 11; Length 239;
Best Local Similarity 74.3%; Pred. No. 4.9e-42;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 21 DVLVTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYVSNRF 80
SEQUENCE 239 AA; 26234 MW; FACE3A3B03871D CRC64;

QY 61 SGVPDRFSGSGTDFTLRLSRVEADGVGYCMOGLQSPFTFGPTKVDIKR 113
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
DB 81 SGVPDRFSGSGTDFTLRLSRVEADLGVYCFQSGSHVPTFGSGTKLEIKR 133
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

RESULT 3
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16
AC Q8VC16; 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 74.0%; Score 438; DB 11; Length 238;
Best Local Similarity 74.3%; Pred. No. 2.3e-41;
Matches 84; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 20 DVLVTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYVSNRF 79
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

QY 61 SGVPDRFSGSGTDFTLRLSRVEADGVGYCMOGLQSPFTFGPTKVDIKR 113
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
DB 80 SGVPDRFSGSGTDFTLRLSRVEADLGVYCFQSGSHVPTFGSGTKLEIKR 132
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
ID Q8TCD0
AC Q8TCD0; 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACE3A3B03871D CRC64;

Query Match 73.6%; Score 436; DB 4; Length 239;
Best Local Similarity 72.6%; Pred. No. 3.9e-41;
Matches 82; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 21 DVLVTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGTYLDWYLOKPGQSPQLLIYVSNRF 80
SEQUENCE 239 AA; 26234 MW; FACE3A3B03871D CRC64;

QY 61 SGVPDRFSGSGTDFTLRLSRVEADGVGYCMOGLQSPFTFGPTKVDIKR 113
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
DB 81 SGVPDRFSGSGTDFTLRLSRVEADGVYCFQSGSHVPTFGSGTKLEIKR 133
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

RESULT 5
Q9UL80 PRELIMINARY; PRT; 114 AA.
ID Q9UL80
AC Q9UL80; 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";

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RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035034; AAD56270.1; -.
DR HSSP: P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 72.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 11e-40;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPLVPTGEPASISCRSSQSLHNSGYTYLDWYLRKPGSQPOLLIYSGSHRA 60
Db 1 DVVMTQSPISLPLVTLRQASISCRSSQSPVYSDGNTYLNWFQQRPGSPRLIYKVSNRD 60

QY 61 SGVPDRFSGSGTDFTLIRISRVAEADVGVYCMQGLQ-SPFTFGPCTKVDIKR 113
Db 61 SGVPDRFSGSGTDFTLIKISRVAEADVGVYCMQGTHTWPPWTFGGGTKEIKR 114

RESULT 6
QYJL82 PRELIMINARY; PRT; 104 AA.
AC QYJL82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20448942; PubMed=10992488;
RC STRAIN=BALE/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206024; AAF69322.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 104
FT NON_TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 68.6%; Score 406; DB 11; Length 104;
Best Local Similarity 75.0%; Pred. No. 3.3e-38;
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 9 LSLPVTGEPASISCRSSQSLHNSGYTYLDWYLRKPGSQPOLLIYSGSHRASGVDPDRFS 68
Db 1 LSLPVSIGQASISCRSSQSLVHTNGNTYLHWYLRKPGSQPKLLIYKVSNRFSGVDPDRFS 60

QY 69 GSVGSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPCTKVDIK 112
Db 61 GSGSGTDFTLIKISRVAEADLVYFCSQTHVPTFGGTKEIK 104

RESULT 7
QYJL78 PRELIMINARY; PRT; 109 AA.
AC QYJL78;

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR HSSP: P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 63.0%; Score 373; DB 4; Length 109;
Best Local Similarity 66.4%; Pred. No. 1.9e-34;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPISLPLVPTGEPASISCRSSQSLHNSGYTYLDWYLRKPGSQPOLLIYSGSHRA 60
Db 1 EIVLTQSPGLSLSPGERATLSCASQSVSSS---YLAWYQQKPGQAPRLIYGASSRA 56

QY 61 SGVPDRFSGSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPCTKVDIKR 113
Db 57 TGIPDRFSGSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGGTKEIKR 109

RESULT 8
QYJL86 PRELIMINARY; PRT; 109 AA.
AC QYJL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 62.3%; Score 369; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 5.3e-34;

```



```
RESULT 12
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 54.4%; Score 322; DB 4; Length 107;
Best Local Similarity 59.3%; Pred. No. 1.1e-28;
Matches 67; Conservative 15; Mismatches 25; Indels 6; Gaps 3;

QY 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db :|:||||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1 DIQMTQSPSSLSASVGDRVTITCRASQI--SN---YLNWYQKQKRAPNLLIYASLSQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db ||||| ||||| ||||| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
56 SGVPSRFSGSGGTDFLTISLQAEAFATYYCQSYSTSWTFCGTKVEIKR 107

RESULT 13
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035029; AAD56265.1; -.
DR HSSP: P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 54.4%; Score 322; DB 4; Length 109;
Best Local Similarity 58.8%; Pred. No. 1.1e-28;
Matches 67; Conservative 18; Mismatches 23; Indels 6; Gaps 3;

QY 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db ||||| ||||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1 EIVMTQSPATLSVSPGERATISCVASQS-SSN----LAWYQKQKQAPRLLIYGASTRA 55

QY 61 SGVPDRFSGSVSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db :|:| ||||| ||||| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
56 TGIPARFSGSGGTDFLTISLQAEAFATYYCQSYNSWPLTFGGTKVEIKR 109

RESULT 14
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; RAD56273.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 53.5%; Score 316.5; DB 4; Length 108;
Best Local Similarity 54.9%; Pred. No. 4.5e-28;
Matches 62; Conservative 18; Mismatches 28; Indels 5; Gaps 1;

QY 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db :|:| ||||| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1 DIQMTQSPSSLSASVGDRVTITCRASQI-----SSYLNWYQKQKRAPNLLIYASLSQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db ||||| ||||| ||||| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
56 SGVPSRFSGSGGTDFLTISLQAEAFATYYCQSYSTSWTFCGTKVEIKR 108

RESULT 15
Q9UL10
ID Q9UL10 PRELIMINARY; PRT; 106 AA.
AC Q9UL10;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
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Search completed: March 13, 2003, 15:16:56
Job time : 41.8538 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time, 55.3808 Seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-3
Perfect score: 644
Sequence: 1 QVQIVSGGGLVPGGSLRL.....GGWDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	644	100.0	121	AAE12706	Human PH1 Fab anti
2	644	100.0	381	AAE12707	Human biyPHJ-IL-2
3	644	100.0	451	AAE12715	Human recombinant
4	548	85.1	121	AAE07029	Human heavy chain
5	543.5	84.4	120	AAW27553	Human Ab heavy chain
6	543.5	84.4	281	AAW27560	Consensus single c
7	541.5	84.1	116	AAE07017	Human heavy chain
8	540.5	83.9	246	ABP45964	Human BlyS binding
9	539	83.7	240	AAU79563	Monoclonal scfv an
10	537.5	83.5	131	AAW13520	Anti-melanoma anti

11	537.5	83.5	239	23	ABP45911	Human BlyS binding
12	537	83.4	117	22	AAE12061	Human anti-tissue
13	537	83.4	313	22	AAU14320	Human novel protei
14	536.5	83.3	240	20	AAU02472	A single chain ant
15	535	83.1	117	18	AAW13532	Anti-melanoma anti
16	533	82.8	119	22	AAU02512	Anti-adiocyte mon
17	532	82.8	246	21	AAV58235	Internalising anti
18	532	82.6	227	22	AAE75051	TRO005 Humab Happa
19	531.5	82.5	118	23	AAU83803	MS-GPC-6 heavy cha
20	531.5	82.5	118	23	ABE57561	HLA-DR-specific pr
21	531.5	82.5	120	22	AAE07022	Human heavy chain
22	530.5	82.4	116	23	AAO21548	Antibody screening
23	529.5	82.2	246	23	ABP45969	Human BlyS binding
24	529	82.1	240	21	AAV15124	Anti-human CTLA-4
25	529	82.1	240	21	AAV15125	Anti-murine CTLA-4
26	528.5	82.1	268	23	AAU97197	Human anti-EGFR si
27	527.5	81.9	122	20	AAW78432	Antibody heavy cha
28	527.5	81.9	122	23	ABE97975	Heavy chain variab
29	527.5	81.9	252	23	ABP45626	Human BlyS binding
30	527	81.8	117	23	ABE05053	Fibronectin isofor
31	527	81.8	121	23	ABE57571	HLA-DR-specific pr
32	527	81.8	245	22	AAE67620	Human leukocyte an
33	526.5	81.8	248	23	ABP44910	Human BlyS binding
34	526.5	81.8	248	23	ABP45445	Human BlyS binding
35	526.5	81.8	250	23	ABP45409	Human BlyS binding
36	525.5	81.6	251	23	ABP45729	Human BlyS binding
37	525	81.5	120	15	AAE54803	SPA-reactive VH re
38	524.5	81.4	116	18	AAW13529	Anti-melanoma anti
39	524.5	81.4	247	23	ABP45912	Human BlyS binding
40	524	81.4	120	15	AAE54802	SPA-reactive VH re
41	524	81.4	120	15	AAE54804	SPA-reactive VH re
42	524	81.4	120	15	AAE54805	SPA-reactive VH re
43	524	81.4	120	15	AAE54806	SPA-reactive VH re
44	524	81.4	123	22	AAE07019	Human heavy chain
45	523.5	81.3	293	22	AAE65715	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX
AC AAE12706;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody variable heavy chain region (VH).
XX
KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
OS Homo sapiens.
XX
FH Key
FH Region
FT Location/Qualifiers
FT 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
FT /note= "VH domain"
FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

	/note= "Framework region 4"
WT	
XX	WO200175110-A2.
PN	
XX	11-OCT-2001.
PD	
XX	30-MAR-2001; 2001WO-US10589.
Pf	
XX	30-MAR-2000; 2000US-0538913.
PR	(DYAX-) DYAX CORP.
XX	
PA	Hoogenboom HRJM, Henderikx MPG;
PI	
XX	WPI; 2001-626437/72.
DR	N-PSDB; AAD20731.
XX	
PT	Novel isolated tumor-associated antigen mucin-1-specific binding member
PT	for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT	its portion for binding to an epitope of the protein core of mucin-1 -
XX	
PS	Claim 2; Page 94-95; 126pp; English.
PS	
XX	The invention relates to an isolated tumour-associated antigen mucin-1
CC	(MUC-1)-specific binding member comprising an antigen binding domain
CC	region having an antibody variable light (VL) or heavy (VH) region,
CC	or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC	binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC	The binding of MUC1-specific binding member to MUC1 is detected by a
CC	detection method selected from enzyme-linked immunosorbent assay,
CC	magnetic resonance imaging, scintillation counting, and x-ray film.
CC	MUC1-specific binding member is useful for treating cancer, preferably
CC	adenocarcinoma, in an individual, where the cancer is present in tissue
CC	of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC	binding member is useful for diagnosing and imaging MUC1-expressing
CC	cancer cells and tissues, for purifying or isolating non-glycosylated,
CC	underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC	containing molecules, and for therapeutically or prophylactically
CC	treating cancer. The present sequence is anti-MUC1 human PH1 Fab
CC	antibody VH region.
XX	
SQ	Sequence 121 AA;
	Query Match 100.0%; Score 644; DB 22; Length 121;
	Best Local Similarity 100.0%; Pred. No. 3.2e-50;
	Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 QVOLVGSGGLVPGGSLRLSCAASGFFRSNMGWRQAPGKGLEWVSIGSGGSTYY 60
Dd	1 QVOLVGSGGLVPGGSLRLSCAASGFFRSNMGWRQAPGKGLEWVSIGSGGSTYY 60
QY	61 ADSVKGRFTISRDNKSNTLYLQMNSLRRAEDTAVYYCAKHTGGGVWDPTIDYWGQGTLTVS 120
Dd	61 ADSVKGRFTISRDNKSNTLYLQMNSLRRAEDTAVYYCAKHTGGGVWDPTIDYWGQGTLTVS 120
QY	121 S 121
Dd	121 S 121
RESULT 2	
AAE12707	
ID	AAE12707 standard; Protein; 381 AA.
XX	
AC	AAE12707;
XX	
DT	04-JAN-2002 (first entry)
XX	
DE	Human bivPH1-IL-2 immunocytokine protein.
XX	
KW	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX	breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX	

QS	Homo sapiens.
PX	
PN	WO200175110-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US10589.
XX	
PP	30-MAR-2000; 2000US-0538913.
XX	
PA	{DYAX-} DYAX CORP.
PI	
PL	Hoogenboom HRJM, Henderikx MPG;
DR	WPI; 2001-626437/72.
DR	N-PSDB; AAD20732.
XX	
XX	Novel isolated tumor-associated antigen mucin-1-specific binding member
PT	for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT	its portion for binding to an epitope of the protein core of mucin-1 -
XX	
PS	Claim 9; Page 95-97; 126pp; English.
XX	
CC	The invention relates to an isolated tumour-associated antigen mucin-1
CC	(MUC-1)-specific binding member comprising an antigen binding domain
CC	region having an antibody variable light (VL) or heavy (VH) region,
CC	or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC	binding member is useful for diagnosing cancer, preferably adenocarcino-
CC	mucins. The binding of MUC1-specific binding member to MUC1 is detected by a
CC	detection method selected from enzyme-linked immunosorbent assay,
CC	magnetic resonance imaging, scintillation counting, and X-ray film.
CC	MUC1-specific binding member is useful for treating cancer, preferably
CC	adenocarcinoma, in an individual, where the cancer is present in tissue
CC	of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC	binding member is useful for diagnosing and imaging MUC1-expressing
CC	cancer cells and tissues, for purifying or isolating non-glycosylated,
CC	underglycosylated or cancer-associated forms of MUC1 or MUC1 ectopod,
CC	containing molecules, and for therapeutically or prophylactically
CC	treating cancer. The present sequence is human bivPH1-IL-2
CC	immunocytokine protein. bivPH1 is mucin specific binding portion.
XX	
SQ	Sequence 381 AA;
	Query Match 100.0%; Score 644; DB 22; Length 381;
	Best Local Similarity 100.0%; Pred. No. 1.le-49;
	Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 QVOLVGGLVQPGGSLRLSCAASGFTFRSANGWRQAPGKLEWVSIGSGGSTYY 60
Db	1 QVOLVGGLVQPGGSLRLSCAASGFTFRSANGWRQAPGKLEWVSIGSGGSTYY 60
Qy	61 ADSVKGRFTISRDNSKNTLYQMNSLRADTVAVYCAKHGTGGGVDPIDYWGGTLVTWS 120
Db	61 ADSVKGRFTISRDNSKNTLYQMNSLRADTVAVYCAKHGTGGGVDPIDYWGGTLVTWS 120
Qy	121 \$ 121
Db	121 \$ 121
RESULT 3	
AAE12715	
ID	AAE12715 standard; Protein; 451 AA.
XX	
AC	AAE12715;
XX	
DT	04-JAN-2002 (first entry)
XX	
DE	Human recombinant immunoglobulin (Ig) heavy chain region.
XX	
KW	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XN	heavy chain region; cancer; breast; ovary; lung; bladder;
KW	cytostatic; therapy; immunoglobulin; Ig.

XX OS Homo sapiens.
XX KW WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR 30-MAR-2000; 2000US-0538913.
XX PA (DYAX-) DYAX CORP.
XX PI Hooenboom HRJM, Henderikx MPG;
XX DR WPI; 2001-626437/72.
XX DR N-PSDB; AAD20745.
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX Claim 12; Page 106-108; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human recombinant immunoglobulin
CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX Sequence 451 AA;
Query Match 100.0%; Score 644; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSGSGGSTYY 60
DB 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSGSGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVMDPDIYWGQGLTVTS 120
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVMDPDIYWGQGLTVTS 120
QY 121 S 121
DB 121 S 121
RESULT 4
AAE07029
ID AAE07029 standard; Protein; 121 AA.
XX AAE07029;
XX 16-OCT-2001 (first entry)
XX Human heavy chain variable (VH) region, VH clone 41.
XX Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;

KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
KW AIDS; inflammatory glomerulopathy; vascular intervention; LD9 antibody;
KW neointimal hyperplasia; VH; heavy chain variable region.
XX Homo sapiens.
XX Location/Qualifiers
XX Key 31..35
XX Region /label= CDR1
XX /note= "Complementarity determining region 1"
XX Region 50..66
XX /label= CDR2
XX /note= "Complementarity determining region 2"
XX Region 99..110
XX /label= CDR3
XX /note= "Complementarity determining region 3"
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US03537.
XX 03-FEB-2000; 2000US-0497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-489888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor
XX 2-mediated disorder in a patient, comprises a binding specificity for
XX CCR2, and a non-human antigen binding region and human immunoglobulin
XX .
XX Disclosure; Page 174-175; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR-2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angioplasty and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is human heavy chain variable (VH) region,
XX VH clone 41.
XX Sequence 121 AA;
Query Match 85.1%; Score 548; DB 22; Length 121;
Best Local Similarity 87.6%; Pred. No. 1.2e-41;
Matches 106; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSGSGGSTYY 60

Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTTSSYAMSVWRQAPGKLEWVSAISGSGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLVTVS	120
Db	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDISWGDLEGLDYWGQGLTLVTVS	120
Qy	121	S	121
Db	121	S	121
RESULT 5			
AAW27553			
ID	AAW27553 standard; Protein; 120 AA.		
XX	AC		
XX	AAW27553;		
XX	DT	23-JAN-1998 (first entry)	
XX	DE	Human Ab heavy chain variable region VH3 consensus.	
XX	KW	Human; antibody; preparation; library; VH3; variable region;	
XX	KW	heavy chain; consensus.	
XX	OS	Homo sapiens.	
XX	PN	W09708320-A1.	
XX	PD	06-MAR-1997.	
XX	PF	19-AUG-1996; 96WO-EP03647.	
XX	PR	18-AUG-1995; 95EP-0113021.	
XX	PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
XX	PI	Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;	
XX	DR	WPI; 1997-179277/16.	
XX	DR	N-PSDB; AAT87951.	
XX	CC	Preparation of human derived antibody gene library - using synthetic	
XX	CC	consensus sequences, and signal consensus antibody gene as universal	
XX	CC	framework for highly diverse antibody libraries	
XX	PS	Example 1; Fig 5D; 436pp; English.	
XX	CC	The present sequence is the human antibody heavy chain	
XX	CC	variable region synthetic sequence VH3, used in the preparation of	
XX	CC	a human derived antibody gene library.	
XX	SQ	Sequence 120 AA;	
Query Match 84.4%; Score 543.5; DB 18; Length 120;			
Best Local Similarity 87.6%; Pred. No. 3e-41;			
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;			
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSAISGSGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSVWRQAPGKLEWVSAISGSGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLVTVS	120
Db	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARWGGDGFY-AMDYWGQGLTLVTVS	119
Qy	121	S	121
Db	120	S	120
RESULT 6			
AAW27560			
ID	AAW27560 standard; Protein; 281 AA.		
XX	AC	AAW27560;	
XX	DT	23-JAN-1998 (first entry)	
XX	DE	Consensus single chain fragment VH3-V-kappa-2.	
XX	KW	Human; antibody; preparation; library; VH3; variable region;	
XX	KW	light chain; heavy chain; V-kappa-2; single chain; consensus.	
XX	OS	Homo sapiens.	
XX	OS	Synthetic.	
XX	PH	Key	
XX	FT	Peptide	
XX	FT	/label= sig_peptide	
XX	FT	22..281	
XX	FT	/label= mat_peptide	
XX	PN	W09708320-A1.	
XX	PD	06-MAR-1997.	
XX	PF	19-AUG-1996; 96WO-EP03647.	
XX	PR	18-AUG-1995; 95EP-0113021.	
XX	PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
XX	PI	Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;	
XX	DR	WPI; 1997-179277/16.	
XX	DR	N-PSDB; AAT87958.	
XX	CC	Preparation of human derived antibody gene library - using synthetic	
XX	CC	consensus sequences, and signal consensus antibody gene as universal	
XX	CC	framework for highly diverse antibody libraries	
XX	PS	Example 2; Fig 8; 436pp; English.	
XX	CC	The present sequence is the consensus single chain fragment	
XX	CC	VH3-V-kappa-2, which comprises the human antibody	
XX	CC	heavy and light chain variable region consensus sequences VH3 and	
XX	CC	V-kappa-2, was used in the preparation of a human derived antibody	
XX	CC	gene library.	
XX	SQ	Sequence 281 AA;	
Query Match 84.4%; Score 543.5; DB 18; Length 281;			
Best Local Similarity 87.6%; Pred. No. 7.5e-41;			
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;			
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSAISGSGSTYY	60
Db	26	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSVWRQAPGKLEWVSAISGSGSTYY	85
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLVTVS	120
Db	86	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARWGGDGFY-AMDYWGQGLTLVTVS	144
Qy	121	S	121
Db	145	S	145
RESULT 7			
AAE07017			
ID	AAE07017 standard; Protein; 116 AA.		
XX	AC	AAE07017;	
XX	DT	16-OCT-2001 (first entry)	

XX DE Human heavy chain variable (VH) region, 034514.

XX KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; LD9 antibody; neonatal hyperplasia; VH; heavy chain variable region.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT Region 99..105

FT /label= CDR3

FT /note= "Complementarity determining region 3"

XX WO200157226-A1.

XX PN 09-AUG-2001.

XX PD 02-FEB-2001; 2001WO-US03537.

XX PF 03-FEB-2000; 2000US-0497625.

XX PR (MILL-) MILLENNIUM PHARM INC.

XX PA Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T; WPI; 2001-488888/53.

XX DR Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin -

XX PS Disclosure; Page 169-170; 183pp; English.

XX CC The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neonatal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is human heavy chain variable (VH) region, 034514.

XX CC Sequence 116 AA;

Query Match 84.1%; Score 541.5; DB 22; Length 116;

Best Local Similarity 88.4%; Pred. No. 4.4e-41;

Matches 107; Conservative 2; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWYRQAPGKGLWVSGISGGSTYY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWYRQAPGKGLWVSAISGGSTYY 60

QY 61 ADSVKGRTFISRDNSKNTLYLQMNSLRAEDTAVYCAKHTGGVYMDPIDYWGQGLTVTS 120

Db 61 ADSVKGRTFISRDNSKNTLYLQMNSLRAEDTAVYCAKDKSG-W-----YWGQGLTVTS 115

QY 121 S 121

Db 116 S 116

RESULT 8

ABP45964

ID ABP45964 standard; Protein; 246 AA.

XX AC ABP45964;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1975.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US19110.

XX PR 16-JUN-2000; 2000US-212210P.

XX PR 17-OCT-2000; 2000US-240816P.

XX PR 16-MAR-2001; 2001US-276248P.

XX PR 21-MAR-2001; 2001US-277379P.

XX PR 25-MAY-2001; 2001US-293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -

XX PS Claim 1; Page 2757-2758; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43950-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 246 AA;
 Query Match 83.9%; Score 540.5; DB 23; Length 246;
 Best Local Similarity 89.3%; Pred. No. 1.2e-40;
 Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSGISGGSTYY 60
 DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 120
 DB 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 119
 QY 121 S 121
 DB 120 S 120
 RESULT 9
 AAU79563
 ID AAU79563 standard; Protein; 240 AA.
 XX
 AC AAU79563;
 DT 03-SEP-2002 (first entry)
 DE Monoclonal scFv antibody, ME-4C, binding Fibronectin ED-B domain.
 XX
 KW Antibody; single chain antibody variable region fragment; scFv; ME-4C;
 KW human; Fibronectin; ED-B; antiangiogenic; CDR3;
 KW complementarity determining region 3; heavy chain; VH; DP-47;
 KW light chain; VL; DPL-16; 7B89; angiogenesis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 220..229
 FT /note= "CDR3 if the scFv light chain"
 XX
 XX WO200246455-A2.
 XX 13-JUN-2002.
 XX
 XX 06-DEC-2001; 2001WO-EPL4330.
 XX
 XX 06-DEC-2000; 2000IT-FI00247.
 XX (PHIL-) PHILGEN SRL.
 XX Giovannoni L;
 XX
 XX WPI; 2002-452759/48.
 XX N-PSDB; ABK86789.
 XX
 PT Novel process for selecting anti-angiogenesis antibody fragments -
 XX
 PS Claim 5; Page 16-17; 18pp; English.
 CC The invention discloses a process for selecting anti-angiogenesis
 CC antibody fragments, in which, starting from a highly complex system
 CC containing billions of different binding specificities, several cycles of
 CC filter selection of colonies and of amplification of positive clones are
 CC carried out. The method is an improvement on existing antibody selection
 CC methods by allowing the selection from a large repertoire of antibody
 CC fragments expressed in bacteria. It can also avoid the use of phage
 CC display, identifying directly, the clones expressing the antibody
 CC fragments in soluble form. The invention discloses, in particular, a
 CC monoclonal antibody fragment scFv, ME-4C, produced according to the

CC process, with the CDR3 sequences of the heavy chain VH (DP-47) and the
 CC light chain VL (DPL-16) characterised. The monoclonal antibody was
 CC isolated by the recognition of epitopes from a decapeptide library of the
 CC recombinant protein, 7B89, containing the domains 7, 8 and 9, and more
 CC particularly, ED-B (not defined), of human Fibronectin. The identified
 CC monoclonal antibody fragment scFv ME-4C can act as a reagent in the
 CC determination of angiogenesis in tissue samples in vivo and/or in vitro.
 CC The protein sequence presented is the monoclonal scFv antibody, ME-4C,
 CC binding to the human Fibronectin ED-B domain. The antibody was isolated
 CC from the ETH-2000 library.
 XX
 SQ Sequence 240 AA;
 Query Match 83.7%; Score 539; DB 23; Length 240;
 Best Local Similarity 87.5%; Pred. No. 1.6e-40;
 Matches 105; Conservative 2; Mismatches 9; Indels 4; Gaps 1;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSGISGGSTYY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSSYAMSVWRQAPGKGLVWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 120
 DB 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 116
 RESULT 10
 AAU13520
 ID AAU13520 standard; protein; 131 AA.
 XX
 AC AAU13520;
 DT 28-OCT-1997 (first entry)
 DE Anti-melanoma antibody heavy chain clone V13.
 XX Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
 KW cancer; tumourigenesis; anticancer vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 FT Region 99..105
 FT /label= CDR3
 XX
 XX WO9702479-A2.
 XX
 XX 23-JAN-1997.
 XX
 XX 28-JUN-1996; 96WO-IB01032.
 XX
 XX 30-JUN-1995; 95US-0497647.
 XX (UYVA) UNIV YALE.
 XX Cai X, Garen A;
 XX
 XX WPI; 1997-109061/10.
 XX
 PT Prodn. of human monoclonal anti-tumour antibodies - by screening a
 PT fusion phage library produced using peripheral blood lymphocytes
 PT from a cancer patient
 XX
 PS Claim 19; Page 58; 82pp; English.
 CC A process for isolating and synthesising human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phage library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BlyS. The antibodies bind to BlyS and so may be used to detect and quantitate the presence of BlyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BlyS. They may also be administered to treat diseases associated with aberrant BlyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX

AA
PN
WO200170984-A2.

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PD 27-SEP-2001.
XX
XX 08-MAR-2001; 2001WO-US07501.
XX
XX 16-MAR-2000; 2000US-189775P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kirchofer DK, Lowe DG, Presta LG;
XX
XX WPI; 2001-616406/71.
XX
XX Identifying anti-tissue factor antibodies for treating thrombotic
XX disorders, comprises epitope mapping of anti-TF antibodies and
XX selecting antibodies that bind to C-terminal macromolecular
XX substrate-binding region of TF -
XX
XX Disclosure; Fig 8; 75pp; English.
XX
XX The invention relates to a method for identifying anti-tissue factor
XX (anti-TF) antibodies with enhanced anticoagulant potency. The method
XX comprises subjecting a number of anti-TF antibodies to epitope mapping,
XX and selecting the antibodies that bind to an epitope comprising at least
XX a part of the C-terminal macromolecular substrate-binding region of
XX tissue factor (TF). The method is useful for identifying anti-TF
XX antibodies which are useful for blocking a TF-FVIIa associated process
XX or event and for treating a TF-FVIIa related disease or disorder
XX e.g. thrombotic or coagulopathic disorder including deep venous
XX thrombosis, arterial thrombosis, stroke, tumour, metastasis,
XX thrombolysis, arteriosclerosis and restenosis following angioplasty,
XX acute and chronic indications such as inflammation, septic shock,
XX septicemia, hypotension, adult respiratory distress syndrome (ARDS) and
XX disseminated intravascular coagulopathy (DIC). The present sequence is
XX human anti-tissue factor subgroup III variable heavy chain (VH) domain.
XX
XX Sequence 117 AA;

Query Match 83.4%; Score 537; DB 22; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.1e-40;
Matches 105; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIVISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDPIDTWGGTILTVTS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGGGG----SDYWGQGTILTVTS 116

QY 121 S 121
   |
Db 117 S 117

RESULT 13
AAU14320
XX AAU14320 standard; Protein; 313 AA.
XX
XX AAU14320;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human novel protein #191.
XX
XX Human; novel protein; Antianemic; osteopathic; antiinflammatory;
XX immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antischmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.
XX
XX Homo sapiens.
OS

XX WO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22625.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 630-631; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX polypeptides. Polynucleotides of the invention are used as probes and
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicite an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma,
XX graft-versus-host disease, eczema, haemophilia, thrombosis,
XX anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence represents a protein of the invention.
XX
XX Sequence 313 AA;

Query Match 83.4%; Score 537; DB 22; Length 313;
Best Local Similarity 83.5%; Pred. No. 3.2e-40;
Matches 106; Conservative 4; Mismatches 11; Indels 6; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGGSTYY 120

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDP-----IDYWGQG 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKSHPGYDYDSSGYSYFDYWGQG 180

QY 115 TLTVTS 121
   :|||||:
Db 181 TLTVTS 187

RESULT 14
AAU02472
XX AAU02472 standard; Protein; 240 AA.
XX
XX AAU02472;
XX
XX 15-JUL-1999 (first entry)
DT

```


GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 18.6154 seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....GGVMDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	543.5	84.4	120	4	US-09-025-769B-38
2	543.5	84.4	120	4	US-09-025-769B-63
3	543.5	84.4	281	4	US-09-025-769B-178
4	537.5	83.5	131	4	US-08-983-607-28
5	535	83.1	117	4	US-08-983-607-46
6	527	81.8	120	2	US-08-428-197-20
7	527	81.8	120	5	PCT-US93-10555-20
8	527	81.8	125	5	US-08-428-197-1
9	527	81.8	125	5	PCT-US93-10555-1
10	525	81.5	120	2	US-08-428-197-22
11	525	81.5	120	5	PCT-US93-10555-22
12	524.5	81.4	116	4	US-08-983-607-36
13	524.5	81.4	122	2	US-07-934-373C-21
14	524.5	81.4	122	3	US-08-437-642B-21
15	524.5	81.4	122	4	US-08-146-206C-21
16	524.5	81.4	122	5	PCT-US93-07832-21
17	524	81.4	120	2	US-08-428-197-24
18	524	81.4	120	2	US-08-428-197-26
19	524	81.4	120	2	US-08-428-197-28
20	524	81.4	120	5	PCT-US93-10555-24
21	524	81.4	120	5	PCT-US93-10555-26
22	524	81.4	120	5	PCT-US93-10555-28
23	523	81.2	113	3	US-08-974-899-6
24	520.5	80.8	140	4	US-08-983-607-32
25	520	80.7	117	4	US-09-025-769B-24
26	517	80.3	125	1	US-08-478-039-99
27	517	80.3	125	1	US-08-476-349A-99

28 514 79.8 120 2 US-08-428-197-40 Sequence 40, Appl
29 514 79.8 120 5 PCT-US93-10555-40 Sequence 40, Appl
30 512.5 79.6 263 4 US-09-069-821-3 Sequence 3, Appl
31 512.5 79.6 283 4 US-09-420-592A-6 Sequence 6, Appl
32 511 79.3 119 1 US-07-988-925-11 Sequence 11, Appl
33 511 79.3 119 2 US-08-362-780-11 Sequence 11, Appl
34 511 79.3 120 2 US-08-428-197-30 Sequence 30, Appl
35 511 79.3 120 2 US-08-428-197-32 Sequence 32, Appl
36 511 79.3 120 5 PCT-US93-10555-30 Sequence 30, Appl
37 511 79.3 120 5 PCT-US93-10555-32 Sequence 32, Appl
38 510.5 79.3 123 2 US-08-428-197-38 Sequence 38, Appl
39 510.5 79.3 123 5 PCT-US93-10555-38 Sequence 38, Appl
40 508 78.9 120 2 US-08-428-197-34 Sequence 34, Appl
41 508 78.9 120 5 PCT-US93-10555-34 Sequence 34, Appl
42 508 78.9 123 2 US-08-665-202-30 Sequence 30, Appl
43 505.5 78.5 116 2 US-08-428-197-2 Sequence 2, Appl
44 505.5 78.5 116 5 PCT-US93-10555-2 Sequence 2, Appl
45 505.5 78.5 118 2 US-08-958-201-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-38
; Sequence 38, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/025,769B
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-38

Query Match 84.4%; Score 543.5; DB 4; Length 120;
Best Local Similarity 87.6%; Pred. No. 2.5e-46;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 119
QY 121 S 121
Db 120 S 120
RESULT 2
US-09-025-769B-63
; Sequence 63, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-63
Query Match 84.4%; Score 543.5; DB 4; Length 120;
Best Local Similarity 87.6%; Pred. No. 2.5e-46;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 119
QY 121 S 121

Db 120 S 120
RESULT 3
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178
Query Match 84.4%; Score 543.5; DB 4; Length 281;
Best Local Similarity 87.6%; Pred. No. 6.5e-46;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
Db 26 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 85
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 86 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 144
QY 121 S 121
Db 145 S 145

RESULT 4
US-08-983-607-28
; Sequence 28, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESS: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fUSE5 fusion phage construct
CLONE: V13
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-28

Query Match 83.5%; Score 537.5; DB 4; Length 131;
Best Local Similarity 89.3%; Pred. No. 1.1e-45;
Matches 108; Conservative 1; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:|||||
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
:|||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVWDPIDYWGOGTLTVTS 120
:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVWDPIDYWGOGTLTVTS 115
:|||||
QY 121 S 121
: |
Db 116 S 116
: |

RESULT 5
US-08-983-607-46
; Sequence 46, Application US/08983607
; Patent No. 6140470

GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESS: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: C55
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-46

Query Match 83.1%; Score 535; DB 4; Length 117;
Best Local Similarity 88.4%; Pred. No. 1.6e-45;
Matches 107; Conservative 2; Mismatches 8; Indels 4; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:|||||
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
:|||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVWDPIDYWGOGTLTVTS 120
:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGVWDPIDYWGOGTLTVTS 116
:|||||
QY 121 S 121
: |
Db 117 S 117
: |

RESULT 6

```

US-08-428-197-20
; Sequence 20, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-197-20
Query Match 81.8%; Score 527; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44;
Matches 101; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
;
QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVKLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKLEWVSDISASGSTYY 60
;
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDPDIYWGQGLTVTS 120
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RESULT 7
PCT-US93-10555-20
; Sequence 20, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-197-20
Query Match 81.8%; Score 527; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44;
Matches 101; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
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QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
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Db 1 QVKLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKLEWVSDISASGSTYY 60
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QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDPDIYWGQGLTVTS 120
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RESULT 7
PCT-US93-10555-20
; Sequence 20, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-197-20
Query Match 81.8%; Score 527; DB 5; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44;
Matches 101; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
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; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-10555-20
Query Match 81.8%; Score 527; DB 5; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44;
Matches 101; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
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QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
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RESULT 8
US-08-428-197-1
; Sequence 1, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:

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Query Match 81.8%; Score 527; DB 5; Length 125;
Best Local Similarity 83.2%; Pred. No. 1.1e-44;
Matches 104; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

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D6			
QY	117	VTVSS	121
D6			
D6	121	VTVSS	125

RESULT 10
US-08-428-197-22
; Sequence 22, Application US/08428197
; Patent No. 5891438

TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Spensley Horn Jubas & Lubitz
 STREET: 1880 Century Park East - Suite 500
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90067

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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: PCT/US93/10555
4 FILING DATE: 29-OCT-1993
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Howells, Stacy L.
7 REGISTRATION NUMBER: 34,842
8 REFERENCE/DOCKET NUMBER: FD-2630
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (619) 455-5100
11 TELEFAX: (619) 455-5110
12 INFORMATION FOR SEQ ID NO: 22:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 120 amino acids
15 TYPE: amino acid
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 US-08-428-197-22

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Query Match 81.5%; Score 525; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 1.6e-44;
Matches 101; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

us-09-822-698a-3.rai

[illegible]

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; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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; US-07-934-373C-21
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Best Local Similarity 85.2%; Pred. No. 1.8e-44;
Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

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QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-HTGGGVWDPIDYWGOGTLTV 119
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Db 121 SS 122

RESULT 14
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; Sequence 21, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
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; US-08-437-642B-21
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Best Local Similarity 85.2%; Pred. No. 1.8e-44;
Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

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Db 121 SS 122

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; Sequence 21, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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; US-08-146-206C-21
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; Query Match 81.4%; Score 524.5; DB 4; Length 122;
; Best Local Similarity 85.2%; Pred. No. 1.8e-44;
; Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

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Title: US-09-822-698A-3

Perfect score: 644

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	644	100.0	451	10	US-09-822-698A-26
4	548	85.1	121	10	US-09-840-459-92
5	543.5	84.4	120	12	US-10-025-687-4
6	541.5	84.1	116	10	US-09-840-459-80
7	536.5	83.3	240	9	US-09-968-561A-2
8	536.5	83.3	240	10	US-09-192-854-2
9	531.5	82.5	118	9	US-10-001-934-39
10	531.5	82.5	120	10	US-09-840-459-85
11	528.5	82.1	268	10	US-09-976-118-1
12	524	81.4	123	10	US-09-840-459-82
13	523.5	81.3	288	10	US-09-818-247-22
14	523	81.2	113	10	US-09-056-160B-11
15	523	81.2	119	10	US-09-811-123-3
16	522	81.1	249	12	US-10-039-785-53
17	521	80.9	125	10	US-09-840-459-76
18	519	80.6	125	10	US-09-840-459-84
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23	515.5	80.0	124	10	US-09-840-459-89	Sequence 89, Appl
24	514.5	79.9	124	10	US-09-840-459-81	Sequence 81, Appl
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27	512.5	79.6	283	9	US-09-985-442-6	Sequence 6, Appl
28	512.5	79.6	283	10	US-09-983-580-6	Sequence 6, Appl
29	511	79.3	449	10	US-09-736-371B-21	Sequence 21, Appl
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31	499.5	77.6	443	10	US-09-917-410-4	Sequence 4, Appl
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39	484.5	75.2	120	10	US-09-229-200A-22	Sequence 22, Appl
40	484	75.2	127	10	US-09-811-737-1	Sequence 1, Appl
41	484	75.2	255	10	US-09-423-800-56	Sequence 15, Appl
42	482.5	74.9	118	9	US-09-423-800-56	Sequence 56, Appl
43	482.5	74.9	137	9	US-09-423-800-77	Sequence 77, Appl
44	479.5	74.5	120	10	US-09-229-200A-24	Sequence 24, Appl
45	478.5	74.3	120	10	US-09-229-200A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match	100.08;	Score 644;	DB 10;	Length 121;
Best Local Similarity	100.08;	Pred. No. 3.8e-46;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY	60	
Db	1	QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY	60	
QY	61	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTVS	120	
Db	61	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTVS	120	
QY	121	S 121		
Db	121	S 121		

RESULT 2

	Query Match	100.0%	Score 644:	DB 10:	Length 451;
	Best Local Similarity	100.0%;	Prod. No. 1.4e-45;		
	Matches 121;	Conservative	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVQLVQSGGGLVPQGSRLRLSCAASGFTFRSNAMGVNRQAPKGLIEWVSGISGGSGSTYY	60		
Db	1	QVQLVQSGGGLVPQGSRLRLSCAASGFTFRSNAMGVNRQAPKGLIEWVSGISGGSGSTYY	60		
Qy	61	ADSVKGRFTISRDNSKNTLYIQMNSLRAREDYAVYCAKHTGGVWVDPIDYWGQGLPLTVTS	120		
Db	61	ADSVKGRFTISRDNSKNTLYIQMNSLRAREDYAVYCAKHTGGVWVDPIDYWGQGLPLTVTS	120		

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RESULT 5
US-10-025-687-4
; Sequence 4, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region

```


Qy	121	S	121
Db	116	S	116

RESULT 9

```

US-10-001-934-39
; Sequence 39, Application US/10001934
; Publication NO. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/
; TITLE OF INVENTION: KILLING OF CELL
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/0
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-39

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Query Match	Score	DB	Length
Best Local Similarity	82.5%	531.5	118
Matches 106;	87.6%	pred. No. 5,7e-37	
Conservative	4	Mismatches	8
Indels	33	Gaps	2

Qy	1	QVQLVDSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVRQAPGKLEWVSISCSGGSTYY	60
		: :	
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGGSTYY	60
Qy	61	ADSVKGRTTISRDNKNTLYLQMNSLRADTAIVYCAKHTGGGVNDPIDYWGGOTLVTVS	120
		: :	
Db	61	ADSVKGRTTISRDNKNTLYLQMNSLRADTAIVYCAR--GYGRYS-DLWGOGTLVTVS	117
Qy	121 S 121		
	I		
Db	118 S 118		

RESULT 10

```

US-09-840-459-85
: Sequence 85, Application US/09840459
: Patent No. US20020150576A1
: GENERAL INFORMATION:
: APPLICANT: LaRosa, Gregory J.
: APPLICANT: Horvath, Christopher
: APPLICANT: Newman, Walter
: APPLICANT: Jones, S. Tarran
: APPLICANT: O'Brien, Stobhan H.
: APPLICANT: O'Keefe, Theresa
: TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: 1855.1052-012
: CURRENT APPLICATION NUMBER: US/09/840,459
: CURRENT FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: PCT/US01/03537
: PRIOR FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: 09/497,625
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: 09/359,193
: PRIOR FILING DATE: 1999-07-22
: PRIOR APPLICATION NUMBER: 09/421,781
: PRIOR FILING DATE: 1998-07-23
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 85
: LENGTH: 120
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-840-459-85

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[illegible]

RESULT 17

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US-09-976-118-1
; Sequence 1, Application US/09976118
; Patent No. US20020058033A1
; GENERAL INFORMATION:
; APPLICANT: Raisch, Kevin Paul
; APPLICANT: Curiel, David T.
; APPLICANT: Bonner, James Allen
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFV
; OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

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Query Match	82.1%	Score 528.5;	DB 10;	Length 268;
Best Local Similarity	83.1%	Pred. NO. 2.3e-36;		
Matches 103;	Conservative	6;	Mismatches 12;	Indels 3;
Gaps	1;			

Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVVRQAPGKGLEWKSISGSGGSTYY	60
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Db	1	EVQLVESGGGLVQPGGSLRLSCASGFTFSYAMHWVRQAPGKGLLEYVAISNNGGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKHTGGGVW---DPIDYWGQGTLLV	117
		: : : : : : : : : :	
Db	61	ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCVKDVGGSSWYADYFDYWGQGTLLV	120
Qy	118	TVSS 121	
Db	121	TVSS 124	

RESULT 12

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US-09-840-459-82
: Sequence 82, Application US/09840459
: Patent No. US20020150576A1.
: GENERAL INFORMATION:
: APPLICANT: LaRosa, Gregory J.
: APPLICANT: Hewath, Christopher
: APPLICANT: Newman, Walter
: APPLICANT: Jones, S. Farran
: APPLICANT: O'Brien, Stobhan H.
: APPLICANT: O'Keefe, Theresa
: TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR

```


Db	23	QVQLVQSGGGLVQPGGSLRLSCAASGFTFS	SYAMSVWRQAPGKGLEWVSAISGSGSTYY	82
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV	YCAKHTGGGVNDPDIYWGQGLT	118
Db	83	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV	YCARSTFVNSGYF--QHWGQGLT	139
Qy	119	VSS	121	
Db	140	VSS	142	
RESULT 14				
US-09-056-160B-11				
; Sequence 11, Application US/09056160B				
; Patent No. US20020032315A1				
; GENERAL INFORMATION:				
; APPLICANT: Baca, Manuel				
; APPLICANT: Wells, James A.				
; APPLICANT: Presta, Leonard G.				
; APPLICANT: Lowman, Henry B.				
; APPLICANT: Chen, Yvonne M.				
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES				
; NUMBER OF SEQUENCES: 131				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Genentech, Inc.				
; STREET: 1 DNA Way				
; CITY: South San Francisco				
; STATE: California				
; COUNTRY: USA				
; ZIP: 94080				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk				
; COMPUTER: IBM PC compatible				
; OPERATING SYSTEM: PC-DOS/MS-DOS				
; SOFTWARE: WinPatIn (Genentech)				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/09/056,160B				
; FILING DATE: 06-Apr-1998				
; CLASSIFICATION: 424				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: 60/054,856				
; FILING DATE: 06-AUG-1997				
; ATTORNEY/AGENT INFORMATION:				
; NAME: Hasak, Janet E.				
; REGISTRATION NUMBER: 28,616				
; REFERENCE/DOCKET NUMBER: P1093R2				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: 650/225-1896				
; TELEFAX: 650/952-9881				
; INFORMATION FOR SEQ ID NO: 11:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 113 amino acids				
; TYPE: Amino Acid				
; TOPOLOGY: Linear				
; US-09-056-160B-11				
Query Match 81.2%; Score 523; DB 10; Length 113;				
Best Local Similarity 85.1%; Pred. No. 2.7e-36;				
Matches 103; Conservative 3; Mismatches 7; Indels 8; Gaps				
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFS	RNAMGWVRQAPGKGLEWVSGISGSGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS	SYAMSVWRQAPGKGLEWVSVISGSGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV	YCAKHTGGGVNDPDIYWGQGLT	120
Db	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV	YCAR-----GFDYWGQGLT	112
Qy	121	S	121	
Db	113	S	113	

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RESULT 15
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

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Query Match	81.2%;	Score 523;	DB 10;	Length 119;
Best Local Similarity	85.1%;	Pred. No. 2.8e-36;		
Matches 103;	Conservative 5;	Mismatches 11;	Indels 2;	Gaps 1;
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		: :		
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVAVISGGGSYY	60	
		: :		
Qy	61	ADSVKGRFTISRDNKNTLYIQMNSLRAEDTAVYVYCAKHTGGGVNDPIDDYWGQGTLTIVS	120	
Db	61	ADSVKGRFTISRDNKNTLYIQMNSLRAEDTAVYVYCARGRVG--YSLDYWGQGTLTIVS	118	
Qy	121	S 121		
		I		
Db	119	S 119		

Search completed: March 13, 2003, 15:30:31
Job time : 18.2192 secs

GenCore version 5.1.4.p5.4578
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 257.823 Seconds
 (without alignments)
 302.582 Million cell updates/sec

Title: US-09-822-698A-3
 Perfect score: 644
 Sequence: 1 QVQLVQSGGGLVPGGSLRL.....GGVWDPIYWGQGLTVTVSS 121

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
 Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_Main: *
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 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep: *
 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep: *
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 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep: *
 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep: *

Pred. NO. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	121	19	US-09-538-913-3
2	644	100.0	121	22	US-09-822-698A-3
3	644	100.0	381	19	US-09-538-913-5
4	644	100.0	381	22	US-09-822-698A-5
5	644	100.0	451	22	US-09-822-698A-26
6	548	85.1	121	1	PCT-US01-03537-92

7	548	85.1	121	18	US-09-497-625-92	Sequence 92, Appl
8	548	85.1	121	18	US-09-497-625A-92	Sequence 92, Appl
9	548	85.1	121	22	US-09-840-459-92	Sequence 92, Appl
10	548	85.1	129	21	US-09-791-537-116631	Sequence 116631,
11	545.5	84.7	229	21	US-09-791-537-128087	Sequence 128087,
12	544.5	84.5	222	1	PCT-US02-12801-152	Sequence 152, App
13	543.5	84.4	120	1	PCT-US02-12202-4	Sequence 4, Appli
14	543.5	84.4	120	18	US-09-490-070-38	Sequence 38, Appl
15	543.5	84.4	120	18	US-09-490-070-63	Sequence 63, Appl
16	543.5	84.4	120	24	US-10-025-687-4	Sequence 4, Appli
17	543.5	84.4	120	25	US-10-125-687-4	Sequence 4, Appli
18	543.5	84.4	281	18	US-09-490-070-178	Sequence 178, App
19	543	84.3	119	21	US-09-791-537-31899	Sequence 31899, A
20	542.5	84.2	124	24	US-10-040-244-16	Sequence 16, Appl
21	542	84.2	119	21	US-09-791-537-79748	Sequence 79748, A
22	542	84.2	145	21	US-09-791-537-19722	Sequence 19722, A
23	541.5	84.1	116	1	PCT-US01-03537-80	Sequence 80, Appl
24	541.5	84.1	116	18	US-09-497-625A-80	Sequence 80, Appl
25	541.5	84.1	116	21	US-09-791-537-110614	Sequence 110614,
26	541.5	84.1	116	21	US-09-840-459-80	Sequence 80, Appl
27	541.5	84.1	116	22	US-09-791-537-106410	Sequence 106410,
28	541	84.0	123	21	US-09-791-537-106410	Sequence 171, App
29	541	84.0	221	1	PCT-US02-12801-171	Sequence 171, App
30	541	84.0	224	23	US-09-972-656-68	Sequence 68, Appl
31	540.5	83.9	128	21	US-09-791-537-55187	Sequence 55187, A
32	540.5	83.9	246	1	PCT-US01-19110-1975	Sequence 1975, Ap
33	540.5	83.9	246	22	US-09-880-748-1975	Sequence 1975, Ap
34	538.5	83.6	120	21	US-09-791-537-102538	Sequence 102538,
35	538.5	83.6	238	21	US-09-791-537-78365	Sequence 78365, A
36	537.5	83.5	131	8	US-08-497-647E-28	Sequence 28, Appl
37	537.5	83.5	239	1	PCT-US01-19110-1922	Sequence 1922, Ap
38	537.5	83.5	239	22	US-09-880-748-1922	Sequence 1922, Ap
39	536.5	83.3	122	21	US-09-791-537-124246	Sequence 124246,
40	536.5	83.3	130	21	US-09-791-537-116038	Sequence 116038,
41	536.5	83.3	240	15	US-09-192-854-2	Sequence 2, Appli
42	536.5	83.3	240	19	US-09-511-939-2	Sequence 2, Appli
43	536.5	83.3	240	23	US-09-968-561A-2	Sequence 2, Appli
44	535.5	83.2	120	21	US-09-791-537-87873	Sequence 87873, A
45	535.5	83.2	122	21	US-09-791-537-102572	Sequence 102572,

ALIGNMENTS

RESULT 1
 US-09-538-913-3
 ; Sequence 3, Application US/09538913
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Paula
 ; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: seqlist DYX-15
 ; CURRENT APPLICATION NUMBER: US/09/538,913
 ; CURRENT FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-538-913-3

Query Match 100.0%; Score 644; DB 19; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e-60;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QVQLVQSGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
 Db 1 QVQLVQSGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
 Qy 61 ADVSKGRTTISRDNKNTLYLQNMNRAEDTAVYCAKHTGGGVWDPIYWGQGLTVTVS 120

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Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Qy 121 S 121
|
Db 121 S 121

RESULT 2
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHI Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 644; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
|
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match 100.0%; Score 644; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPHI-IL-2
US-09-822-698A-5

Query Match 100.0%; Score 644; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
|
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
```

RESULT 7
US-09-497-625-92
; Sequence 92, Application US/09497625
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter

Query Match 85.1%; Score 548; DB 18; Length 121;
Best Local Similarity 87.6%; Pred. NO. 3.9e-50;
Matches 106; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVOLVSGGGLVPGGSLRUSCAASGFTRFSNMGWVRAPAGKLEWVSIGSGGSTYY 60
: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRUSCAASGFTRFSYMSWVRAPAGKLEWVSIGSGGSTYY 60

QY 61 ADSVKGRFTISRDNISKNNTLYLQNSLRFAEDTAVYICAKHTGGGVDPIDYWGCGTLVTYS 120

Search completed: March 13, 2003, 15:28:03
Job time : 259.073 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 44.2115 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....GGWDPIDYWGQGLTVTVSS 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	543.5	84.4	120	5	US-09-490-153-38
2	543.5	84.4	120	5	US-09-490-153-63
3	543.5	84.4	281	5	US-09-490-153-178
4	541	84.0	224	1	PCT-US02-33536-68
5	540.5	83.9	246	1	PCT-US02-36496-1975
6	540.5	83.9	246	6	US-10-293-418-1975
7	537.5	83.5	239	1	PCT-US02-36496-1922
8	537.5	83.5	239	6	US-10-293-418-1922
9	536.5	83.3	240	5	US-09-968-744A-2
10	535	83.1	244	1	PCT-US02-40597-45
11	535	83.1	244	6	US-10-322-673-45
12	534.5	83.0	223	1	PCT-US02-33556-86
13	532	82.6	243	1	PCT-US02-40597-55
14	532	82.6	243	6	US-10-322-673-55
15	531.5	82.5	122	6	US-10-180-648-13
16	531.5	82.5	467	6	US-10-180-648-2
17	530	82.3	123	1	PCT-US02-32613-59
18	530	82.3	123	6	US-10-269-805-59
19	528.5	82.2	246	1	PCT-US02-36496-1980
20	528.5	82.2	246	6	US-10-293-418-1980
21	528.5	82.1	246	1	PCT-US02-26246A-80
22	527.5	81.9	248	1	PCT-US02-26246A-78
23	527.5	81.9	252	1	PCT-US02-36496-1637
24	527.5	81.9	252	6	US-10-293-418-1637
25	526.5	81.8	248	1	PCT-US02-36496-921
26	526.5	81.8	248	1	PCT-US02-36496-1456

27	526.5	81.8	248	6	US-10-293-418-921	Sequence 921, Appl
28	526.5	81.8	248	6	US-10-293-418-1456	Sequence 1456, Ap
29	526.5	81.8	250	1	PCT-US02-36496-1420	Sequence 1420, Ap
30	526.5	81.8	250	6	US-10-293-418-1420	Sequence 1420, Ap
31	526	81.7	119	1	PCT-US02-38540-18	Sequence 18, Appl
32	526	81.7	119	6	US-10-309-764-18	Sequence 18, Appl
33	526	81.7	138	1	PCT-US02-38540-87	Sequence 87, Appl
34	526	81.7	138	6	US-10-309-764-87	Sequence 87, Appl
35	525.5	81.6	251	1	PCT-US02-36496-1740	Sequence 1740, Ap
36	525.5	81.6	251	6	US-10-293-418-1740	Sequence 1740, Ap
37	525	81.5	123	1	PCT-US02-32613-23	Sequence 23, Appl
38	525	81.5	123	6	US-10-269-805-23	Sequence 23, Appl
39	524.5	81.4	247	1	PCT-US02-36496-1923	Sequence 1923, Ap
40	524.5	81.4	247	6	US-10-293-418-1923	Sequence 1923, Ap
41	524.5	81.4	253	1	PCT-US02-26246A-76	Sequence 76, Appl
42	523	81.2	113	4	US-08-975-329B-6	Sequence 6, Appli
43	523	81.2	113	6	US-10-234-671-11	Sequence 11, Appl
44	523	81.2	119	6	US-10-268-501-6	Sequence 6, Appli
45	521.5	81.0	124	6	US-10-031-722-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-490-153-38

; Sequence 38, Application US/09490153

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,153

; FILING DATE: 24-Jan-2000

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 120 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-490-153-38

Query Match 84.4%; Score 543.5; DB 5; Length 120;
 Best Local Similarity 87.6%; Pred. No. 1e-38;
 Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSSYAMSWVRQAPGKGLVWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVMDPIDYWGQGTLLVTVS 120
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARWGGDGFY-AMDYWGQGTLLVTVS 119

QY 121 S 121
 DB 120 S 120

RESULT 2
 US-09-490-153-63
 : Sequence 63, Application US/09490153
 : GENERAL INFORMATION:
 : APPLICANT: Knappik, Achim
 : Pack, Peter
 : Ilag, Vic
 : Ge, Liming
 : Moroney, Simon
 : Plueckthun, Andreas
 : TITLE OF INVENTION: Protein/(Poly)peptide libraries
 : NUMBER OF SEQUENCES: 373
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 : STREET: 1251 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10021
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/490.153
 : FILING DATE: 24-Jan-2000
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/09/025.769B
 : FILING DATE: 18-FEB-1998
 : APPLICATION NUMBER: EP 95 11 3021.0
 : FILING DATE: 18-AUG-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: James F. Haley, Jr., Esq.
 : REGISTRATION NUMBER: 27,794
 : REFERENCE/DOCKET NUMBER: MORPHO/5
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212)596-9000
 : TELEFAX: (212)596-9090
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 120 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : SEQUENCE DESCRIPTION: SEQ ID NO: 63:
 US-09-490-153-63

Query Match 84.4%; Score 543.5; DB 5; Length 120;
 Best Local Similarity 87.6%; Pred. No. 1e-38;
 Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSSYAMSWVRQAPGKGLVWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVMDPIDYWGQGTLLVTVS 120
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARWGGDGFY-AMDYWGQGTLLVTVS 119

QY 121 S 121
 DB 120 S 120

RESULT 3
 US-09-490-153-178
 : Sequence 178, Application US/09490153
 : GENERAL INFORMATION:
 : APPLICANT: Knappik, Achim
 : Pack, Peter
 : Ilag, Vic
 : Ge, Liming
 : Moroney, Simon
 : Plueckthun, Andreas
 : TITLE OF INVENTION: Protein/(Poly)peptide libraries
 : NUMBER OF SEQUENCES: 373
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 : STREET: 1251 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10021
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/490.153
 : FILING DATE: 24-Jan-2000
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/09/025.769B
 : FILING DATE: 18-FEB-1998
 : APPLICATION NUMBER: EP 95 11 3021.0
 : FILING DATE: 18-AUG-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: James F. Haley, Jr., Esq.
 : REGISTRATION NUMBER: 27,794
 : REFERENCE/DOCKET NUMBER: MORPHO/5
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212)596-9000
 : TELEFAX: (212)596-9090
 : INFORMATION FOR SEQ ID NO: 178:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 281 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : SEQUENCE DESCRIPTION: SEQ ID NO: 178:
 US-09-490-153-178

Query Match 84.4%; Score 543.5; DB 5; Length 281;
 Best Local Similarity 87.6%; Pred. No. 2.3e-38;
 Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
 DB 26 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSSYAMSWVRQAPGKGLVWVSAISGGSTYY 85

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVMDPIDYWGQGTLLVTVS 120
 DB 86 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARWGGDGFY-AMDYWGQGTLLVTVS 144

QY 121 S 121
 DB 145 S 145

RESULT 4
PCT-US02-33556-68
; Sequence 68, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Angen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent version 3.0
; SEQ ID NO 68
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-68

Query Match 84.0%; Score 541; DB 1; Length 224;
Best Local Similarity 87.6%; Pred. No. 3e-38;
Matches 106; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKDRVGYSSLDYWGQGLTVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 5
PCT-US02-36496-1975
; Sequence 1975, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1975
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1975

Query Match 83.9%; Score 540.5; DB 1; Length 246;
Best Local Similarity 89.3%; Pred. No. 3.6e-38;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKEFFGYV-LTDYWGRTLVTVS 119
QY 121 S 121
Db 120 S 120

RESULT 6
US-10-293-418-1975
; Sequence 1975, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1975
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1975

Query Match 83.9%; Score 540.5; DB 6; Length 246;
Best Local Similarity 89.3%; Pred. No. 3.6e-38;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKEFFGYV-LTDYWGRTLVTVS 119
QY 121 S 121
Db 120 S 120

RESULT 7
PCT-US02-36496-1922
; Sequence 1922, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1922
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1922

Query Match 83.5%; Score 537.5; DB 1; Length 239;
Best Local Similarity 86.0%; Pred. No. 6.2e-38;
Matches 104; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 8

US-10-293-418-1922
 ; Sequence 1922, Application US/10293418
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 9

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 10

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 11

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 12

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 13

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

RESULT 14

US-09-968-744A-2
 ; Sequence 2, Application US/09968744A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomlinson, Ian M
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
 ; FILE REFERENCE: 8039/1073
 ; CURRENT APPLICATION NUMBER: US/09/968,744A
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: GB 9722131.1

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
 Db 1 EVOLVETGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----WRGVDYWGRTLVTVS 115

QY 121 S 121

Db 116 S 116

```
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGGTGLTVTS 120
|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKVRPGRSGYFDYWGRGTLTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 11
US-10-322-673-45
; Sequence 45, Application US/10322673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 45
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM029B01 scFv
US-10-322-673-45

Query Match 83.1%; Score 535; DB 6; Length 244;
Best Local Similarity 87.6%; Pred. No. le-37;
Matches 106; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGGTGLTVTS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKVRPGRSGYFDYWGRGTLTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 12
PCT-US02-33556-86
; Sequence 86, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
PCT-US02-33556-86

Query Match 83.0%; Score 534.5; DB 1; Length 223;
Best Local Similarity 87.5%; Pred. No. le-37;
Matches 105; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 2 VOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYYA 61
|||||
Db 2 VOLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGSTYYA 61
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGGTGLTVTS 121
|||||
Db 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-TSNAGGPIDYWGGNLTVTSS 120

RESULT 13
PCT-US02-40597-55
; Sequence 55, Application PC/TUS0240597
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40597
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 55
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM075A01 scFv
PCT-US02-40597-55

Query Match 82.6%; Score 532; DB 1; Length 243;
Best Local Similarity 85.1%; Pred. No. 1.8e-37;
Matches 103; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGGTGLTVTS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCVK----GAW--LDYWGRTWTVTSS 114
QY 121 S 121
Db 115 S 115

RESULT 14
US-10-322-673-55
; Sequence 55, Application US/10322673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
```

; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 55
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM075A01 scFv
US-10-322-673-55

Query Match 82.5%; Score 532; DB 6; Length 243;
Best Local Similarity 85.1%; Pred. No. 1.8e-37;
Matches 103; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:||||:|||||
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGGSTYY 60
:||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKHTGGGVDPIDYWGQGLTVTVS 120
:||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCVK----GAW--LDYWGRTMTVTVS 114
:||||:|||||

Qy 121 S 121
|
Db 115 S 115
|

RESULT 15
US-10-180-648-13
; Sequence 13, Application US/10180648
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPGL
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-13

Query Match 82.5%; Score 531.5; DB 6; Length 122;
Best Local Similarity 85.5%; Pred. No. 1e-37;
Matches 106; Conservative 4; Mismatches 9; Indels 5; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:||||:|||||
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSGITGGSTYY 60
:||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKHTGGGV---WDPIDYWGQGLTV 117
:||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKDPGTTVIMSW--FDPWGQGLTV 118
:||||:|||||

Qy 118 TVSS 121
*.

Db 119 TVSS 122
||||
Search completed: March 13, 2003, 15:29:45
Job time : 45.2115 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 20.9423 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698a-3

Perfect score: 644

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....GGVWDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	84.3	119	2 S31107	Ig heavy chain - h
2	542	84.2	119	2 C36005	Ig heavy chain v r
3	535.5	83.2	120	2 S48798	Ig heavy chain v r
4	534	82.9	140	2 S31686	Ig heavy chain v r
5	531	82.5	119	2 S31108	Ig heavy chain - h
6	528	82.0	119	2 D36005	Ig heavy chain v r
7	528	82.0	121	2 I55673	Ig heavy chain - h
8	527	81.8	127	2 S38489	Ig heavy chain - h
9	527	81.8	140	2 S31588	Ig heavy chain v r
10	526	81.7	134	2 S31699	Ig heavy chain v r
11	522	81.1	123	2 S31114	Ig heavy chain - h
12	522	81.1	138	2 S31666	Ig heavy chain v r
13	519	80.6	160	2 S05271	Ig heavy chain pre
14	518.5	80.5	124	2 S20782	Ig heavy chain v r
15	518	80.4	120	2 S36278	Ig heavy chain v r
16	509.5	79.1	112	2 PH1647	Ig heavy chain v r
17	508.5	79.0	116	2 S31110	Ig heavy chain - h
18	503	78.1	109	2 PH1649	Ig heavy chain v r
19	501	77.8	121	2 S19666	Ig heavy chain v r
20	501	77.8	140	2 C30532	Ig heavy chain pre
21	498	77.3	121	2 G36005	Ig heavy chain v r
22	495.5	76.9	108	2 PH1648	Ig heavy chain v r
23	494	76.7	134	2 S31679	Ig heavy chain v r
24	492.5	76.5	122	2 S20772	Ig heavy chain v r
25	492	76.4	121	2 S31113	Ig heavy chain - h
26	492	76.4	143	2 S23624	Ig heavy chain v r
27	490	76.1	135	2 S31598	Ig heavy chain v r
28	489.5	76.0	120	2 S44111	Ig heavy chain v-D
29	489.5	76.0	151	2 A60943	Ig heavy chain pre

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30      489      75.9      125      2 S30531      Ig heavy chain v r
31      488.5      75.9      114      2 S46390      Ig heavy chain v r
32      488.5      75.9      140      2 S70442      Ig heavy chain pre
33      486.5      75.5      118      2 S31105      Ig heavy chain (su
34      485.5      75.4      114      2 S31120      Ig heavy chain - h
35      482      74.8      119      2 F36005      Ig heavy chain v r
36      481.5      74.8      128      2 S26790      Ig heavy chain v r
37      481.5      74.8      118      2 S31595      Ig heavy chain v r
38      481      74.7      128      2 S31121      Ig heavy chain - h
39      481      74.7      120      2 S36273      Ig heavy chain v r
40      480.5      74.6      114      2 S46391      Ig heavy chain v r
41      480.5      74.6      120      2 S31112      Ig heavy chain - h
42      480.5      74.6      147      2 I37780      Ig variable region
43      480      74.5      117      2 S78486      Ig heavy chain v r
44      480      74.5      132      2 S31603      Ig heavy chain v r
45      479.5      74.5      122      2 E36005      Ig heavy chain v r

```

ALIGNMENTS

RESULT 1

S31107

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C:Accession: S31107

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third com

A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31107

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-119 <RAA>

A:Cross-references: EMBL:X62955

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 543; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 2e-40;

Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSNAMGVVRQAPGKLEWVSGISGSGSTIY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVVRQAPGKLEWVSAISGSGSTIY 60

QY 61 ADSVKGRFTISDRNSKNTLYLQMSLRADETAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120

Db 61 ADSVKGRFTISDRNSKNTLYLQMSLRADETAVYYCAKDPGASY--FDYWGQGLTVTVS 118

QY 121 S 121

Db 119 S 119

RESULT 2

C36005

Ig heavy chain V region (30pl) - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996

C:Accession: C36005

R:Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable g

A:Reference number: A36005; MUID:90349571; PMID:2117273

A:Accession: C36005

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SCH>

A:Cross-references: GB:M18513

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 542; DB 2; Length 119;
Best Local Similarity 87.6%; Pred. No. 2.4e-40;
Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSGISGGSTYY 60
:||||:|||||
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSAISGGSTYY 60
:||||:|||||
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
:||||:|||||
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 118
:||||:|||||

QY 121 S 121
|
DB 119 S 119

RESULT 3
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S48798
R:Maamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48798
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAH>
A:Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.9%; Pred. No. 9e-40;
Matches 106; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSGISGGSTYY 60
:||||:|||||
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSAISGGSTYY 60
:||||:|||||
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTV 119
:||||:|||||
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDR--GFWSGYKDYWGQGLTVTV 118
:||||:|||||

QY 120 SS 121
||
DB 119 SS 120

RESULT 4
S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31686
R:Guisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31686
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CU1>
A:Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 534; DB 2; Length 140;
Best Local Similarity 86.0%; Pred. No. 1.4e-39;
Matches 104; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSGISGGSTYY 60
:||||:|||||
DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSAISGGSTYY 79
:||||:|||||
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
:||||:|||||
DB 80 SDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 139
:||||:|||||

QY 121 S 121
|
DB 140 S 140

RESULT 5
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 531; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.2e-39;
Matches 106; Conservative 3; Mismatches 7; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSGISGGSTYY 60
:||||:|||||
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSAISGGSTYY 60
:||||:|||||
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKH---TGGGVWDPIDYWGQGLTV 117
:||||:|||||
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRRLTG----TFDYWGQGLTV 115
:||||:|||||

QY 118 TVSS 121
|||
DB 116 TVSS 119

RESULT 6
D36005
Ig heavy chain V region (M43) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: D36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: D36005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34024
C:Genetics:

A:Gene: GDB:IGH@; IGHDIY1

A:Cross-references: GDB:118731; OMIM:146910

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 528; DB 2; Length 119;

Best Local Similarity 86.0%; Pred. No. 4e-39;

Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGTSGSGGTY 60

Db 1 EVQLLEGGGGLVOPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLEWVAISGSGGTY 60

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTVTS 120

Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTVTS 118

Qy 121 S 121

Db 119 S 119

RESULT 7

Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: 155673

R:Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panka, D.J.; Zhang, Q.X.

J. Exp. Med. 178, 1903-1911, 1993

A:Title: Human rheumatoid factor cross-idiotypes. IV. Studies on WA Xid-positive Igm with

tinct from the 17.109 and G6 Xids.

A:Reference number: 155673; MUID:94065558; PMID:8245772

A:Accession: 155673

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: GB:M87268; NID:g186197; PIDN:AAC37536.1; PID:g186198

C:Genetics:

A:Gene: GDB:IGHM

A:Cross-references: GDB:120086; OMIM:147020

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 528; DB 2; Length 121;

Best Local Similarity 83.1%; Pred. No. 4.1e-39;

Matches 103; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGTSGSGGTY 60

Db 1 EVQLLEGGGGLVOPGGSLRLSCAASGFTFSTYGMVWRQAPGKGLEWVAISGSGGTY 60

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTV 117

Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAAPRHAGS---PPDYWGQGLTV 117

Qy 118 TVSS 121

Db 118 TVSS 121

RESULT 8

S38489

Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38489

R:Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finner, R.; Gorick, B.D.; Voak, D.; Thorpe, S

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from a p

A:Reference number: S38488

A:Accession: S38489

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-127 <MAR>

C:Cross-references: EMBL:723028; NID:g414025; PIDN:CAA80563.1; PID:g414026

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 527; DB 2; Length 127;

Best Local Similarity 82.0%; Pred. No. 5.2e-39;

Matches 105; Conservative 3; Mismatches 10; Indels 10; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGTSGSGGTY 60

Db 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLEWVAISGSGGTY 60

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTV 111

Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTV 119

Qy 112 QGGLTVTV 119

Db 120 QGGLTVTV 127

RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31588

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from

A:Reference number: S31585

A:Accession: S31588

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

C:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 527; DB 2; Length 140;

Best Local Similarity 85.1%; Pred. No. 5.8e-39;

Matches 103; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGTSGSGGTY 60

Db 20 EVQLLEGGGGLVOPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLEWVAISGSGGTY 79

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTVTS 120

Db 80 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVNDPIDYWGQGLTVTS 139

Qy 121 S 121

Db 140 S 140

RESULT 10

S31699

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31699

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

A:Reference number: S31585

A:Accession: S31666
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <GUI>
A:Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 526; DB 2; Length 134;
Best Local Similarity 83.5%; Pred. No. 6.7e-39;
Matches 101; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 20 EVQLLESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKHTGGVWDPIIDYWGQGTLYTVS 120
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 120
Db 80 SDSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAR-----WRDLDYWGQGTLYTVS 133
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 133

QY 121 S 121
|
Db 134 S 134

RESULT 11
S31114
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31114
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31114
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <RAA>
A:Cross-references: EMBL:X62963
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 522; DB 2; Length 123;
Best Local Similarity 84.7%; Pred. No. 1.4e-38;
Matches 105; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLLESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKHTGGVWDPIIDYWGQGTLY 117
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 117
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKASLYLRFLW-LFDYWGQGTLY 119
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 119

QY 118 TVSS 121
|
Db 120 TVSS 123

RESULT 12
S31666
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31666
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585

A:Accession: S31666
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <GUI>
A:Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 522; DB 2; Length 138;
Best Local Similarity 86.0%; Pred. No. 1.5e-38;
Matches 104; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
Db 20 EVQLLESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKHTGGVWDPIIDYWGQGTLYTVS 120
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 120
Db 80 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAK-ARTGYW-YFDLNGRGTLYTVS 137
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 137

QY 121 S 121
|
Db 138 S 138

RESULT 13
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C:Accession: S05271; S04602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: EMBL:X14584
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 519; DB 2; Length 160;
Best Local Similarity 82.4%; Pred. No. 3.3e-38;
Matches 103; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
Db 20 EVQLLESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKHTGGV----WDPIDYWGQGTLY 116
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 116
Db 80 ADSVKGRFTISRDNKNTLYQMNSLRADTAAYYCAKAVVRGVISYYMGDMVGQGT 139
:||||:||||| PGGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 139

QY 117 TVSS 121
|
Db 140 TVSS 144

RESULT 14
S20782
Ig heavy chain V region - human

```
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S20782
R:Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of the IgA and IgG rearranged VH repertoire of human cord blood
A:Reference number: S20765
A:Accession: S20782
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <MOR>
A:Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      80.5%; Score 518.5; DB 2; Length 124;
Best Local Similarity 83.9%; Pred. No. 2.e-38;
Matches 104; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCGKLEWVSGISGGSTYY 60
Db 1 EVQLLESGGGLVPGGSLRLSCAASGFTFSYAMNVRQAPCGEGLEWVSTISGGSTYY 60

Qy 61 ADSVKGRFTISRNSKNTLYLQNSLRAREDVAVYCAKH--TGGGYWDPIDYWGQGLV 117
Db 61 ADSVKGRFTISRNSKNTLYLQNSLRAREDVAVYCAKERTAFGVVPIPHFDYWGQGLV 120

Qy 118 TVSS 121
Db 121 TVSS 124

RESULT 15
S36278
Ig heavy chain V region (clone alpha-THY-23) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36278
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; M0ID:93178448; PMID:7679990
A:Accession: S36278
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-120 <GRI>
A:Cross-references: EMBL:Z18830; NID:g33114; PIDN:CAA79282.1; PID:g939894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 518; DB 2; Length 120;
Best Local Similarity 85.8%; Pred. No. 3e-38;
Matches 103; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCGKLEWVSGISGGSTYY 60
Db 1 QVQLQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCGKLEWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRNSKNTLYLQNSLRAREDVAVYCAKH--TGGGYWDPIDYWGQGLTVTS 120
Db 61 ADSVKGRFTISRNSKNTLYLQNSLRAREDVAVYCAKSMIVVARYFDYWGQGLTVTS 120

Search completed: March 13, 2003, 15:17:50
Job time : 21.9423 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 12.1 Seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698A-3
Perfect score: 644
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....GGWDPIDYWGQGITLVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	471	73.1	117	1 HV3C_HUMAN	P01764 homo sapien
2	466.5	72.4	114	1 HV3B_HUMAN	P01763 homo sapien
3	456.5	70.9	122	1 HV3A_HUMAN	P01762 homo sapien
4	450.5	70.0	122	1 HV3A_HUMAN	P01781 homo sapien
5	449.5	69.8	116	1 HV3J_HUMAN	P01771 homo sapien
6	447	69.4	121	1 HV3J_HUMAN	P19181 carassius a
7	438.5	68.1	116	1 HV05_CARAU	P01769 homo sapien
8	437.5	67.9	122	1 HV3H_HUMAN	P01769 homo sapien
9	437.5	67.9	126	1 HV3K_HUMAN	P01772 homo sapien
10	435.5	67.6	136	1 HV16_MOUSE	P01783 mus musculu
11	435	67.5	115	1 HV3D_HUMAN	P01765 homo sapien
12	432	67.1	117	1 HV02_CANFA	P01785 canis fami
13	428	66.5	119	1 HV3I_HUMAN	P01770 homo sapien
14	427	66.3	115	1 HV3F_HUMAN	P01767 homo sapien
15	422.5	65.6	120	1 HV3U_HUMAN	P01782 homo sapien
16	419.5	65.1	119	1 HV3M_HUMAN	P01774 homo sapien
17	419	65.1	120	1 HV3E_HUMAN	P01766 homo sapien
18	417.5	64.8	119	1 HV3N_HUMAN	P01775 homo sapien
19	414	64.3	119	1 HV3L_HUMAN	P01773 homo sapien
20	400.5	62.2	114	1 HV01_CANFA	P01784 canis fami
21	398	61.8	117	1 HV54_MOUSE	P18525 mus musculu
22	397.5	61.7	117	1 HV3O_HUMAN	P01776 homo sapien
23	396.5	61.6	97	1 HV56_MOUSE	P18527 mus musculu
24	396	61.5	117	1 HV55_MOUSE	P18526 mus musculu
25	395.5	61.4	119	1 HV3P_HUMAN	P01777 homo sapien
26	395.5	61.4	122	1 HV20_MOUSE	P01789 mus musculu
27	395	61.3	115	1 HV32_MOUSE	P01801 mus musculu
28	394.5	61.3	122	1 HV21_MOUSE	P01790 mus musculu
29	394	61.2	116	1 HV3Q_HUMAN	P01778 homo sapien
30	393.5	61.1	111	1 HV35_MOUSE	P01804 mus musculu
31	393	61.0	113	1 HV30_MOUSE	P01799 mus musculu
32	390	60.6	142	1 HV01_RAT	P01805 rattus norv
33	389	60.4	116	1 HV3R_HUMAN	P01779 homo sapien

34	388	60.2	113	1 HV27_MOUSE	P01796 mus musculu
35	387.5	60.2	119	1 HV37_MOUSE	P01807 mus musculu
36	386.5	60.0	119	1 HV40_MOUSE	P01810 mus musculu
37	384.5	59.7	119	1 HV38_MOUSE	P01808 mus musculu
38	384	59.6	113	1 HV31_MOUSE	P01800 mus musculu
39	384	59.6	115	1 HV33_MOUSE	P01802 mus musculu
40	383	59.5	123	1 HV18_MOUSE	P01787 mus musculu
41	382	59.3	113	1 HV28_MOUSE	P01797 mus musculu
42	382	59.3	123	1 HV19_MOUSE	P01788 mus musculu
43	380	59.0	98	1 HV57_MOUSE	P18528 mus musculu
44	380	59.0	123	1 HV25_MOUSE	P01794 mus musculu
45	379	58.9	123	1 HV23_MOUSE	P01792 mus musculu

ALIGNMENTS

RESULT 1					
HV3C_HUMAN					
ID	HV3C_HUMAN	STANDARD;	PRT;	117 AA.	
AC	P01764;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V-III region VH26 precursor.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
..	RN				
..	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81101090; PubMed=6450418;				
RA	Matthysens G., Rabbitts T.H.;				
RT	"Structure and multiplicity of genes for the human immunoglobulin				
RT	heavy chain variable region.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).				
CC	-----				
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CC	-----				
DR	EMBL; J00236; AAA53516.1; -				
DR	EMBL; M35415; AAA58735.1; -				
DR	PIR; A02047; H3HU26.				
DR	HSP; P01772; 2FB4.				
DR	Genew; HGNC:5545; IGHV@.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL 1 19				
ET	CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.				
FT	NON_TER 117 117				
SO	SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;				
Query Match					
Best Local Similarity 73.1%; Score 471; DB 1; Length 117;					
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;					
Qy	1	QVQLVQSGGGLVPGGSLRLSCAASGFTPRSNAMGWVRQAPGKGLWVSGISGGSGSTYY	60		
Db	20	EVQLLEGGGGLVPGGSLRLSCAASGFTFSYAMSWSVRQAPGKGLWVSAISGGSGSTYY	79		
Qy	61	ADSVKGRFTISRNKNTLYLQMNSLRAEDTAVYYCAK	98		
Db	80	GDSVKGRFTISRNKNTLYLQMNSLRAEDTAVYYCAK	117		

```
RESULT 2
HV3B_HUMAN          STANDARD;          PRT;   114 AA.
ID   HV3B_HUMAN
AC   P01763;
DT   21-JUL-1986 (Rel. 01, Created)
DR   InterPro: IPR003006; Iq_MHC.
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DR   Pfam: PF00047; Iq; 1.
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DR   SMART; SM00406; Iq; 1.
DE   Ig heavy chain V-III region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC   AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC   WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR: A02046; M3HUWE.
DR   HSSP; P01772; 2FB4.
DR   InterPro: IPR003006; Iq_MHC.
DR   InterPro: IPR003596; Iq_v.
DR   Pfam: PF00047; Iq; 1.
DR   SMART; SM00406; Iq; 1.
KW   Immunoglobulin v region.
FT   MOD_RES   1
FT   NON_TER   114
FT   SEQUENCE  114 AA; 12256 MW; D88294FB418A07B7 CRC64;
SQ
Query Match      72.4%; Score 466.5; DB 1; Length 114;
Best Local Similarity 76.0%; Pred. No. 2.1e-39;
Matches 92; Conservative 11; Mismatches 11; Indels 7; Gaps 2;

Oy  1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSTYY 60
Db  1 QVQLVDSGGGLVEPGGSLRLSCSASGFTFSANDMHWVRQAPGKGLWLSFISGSGSIYY 60

Oy  61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db  61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 113

Oy  121 S 121
Db  114 S 114

RESULT 3
HV3G_HUMAN          STANDARD;          PRT;   122 AA.
ID   HV3G_HUMAN
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DR   InterPro: IPR003006; Iq_MHC.
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DR   Pfam: PF00047; Iq; 1.
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DR   SMART; SM00406; Iq; 1.
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC   PATIENT WITH MACROGLOBULINEMIA.
DR   PIR: A02051; M3HUAM.
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DR   HSSP; P01772; 2FB4.
DR   InterPro: IPR003006; Iq_MHC.
DR   InterPro: IPR003596; Iq_v.
DR   Pfam: PF00047; Iq; 1.
DR   SMART; SM00406; Iq; 1.
KW   Immunoglobulin v region.
FT   MOD_RES   1
FT   NON_TER   122
FT   SEQUENCE  122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
SQ
Query Match      70.9%; Score 456.5; DB 1; Length 122;
Best Local Similarity 73.0%; Pred. No. 2.2e-38;
Matches 89; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Oy  1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSTYY 60
Db  1 QVELVESGGGVVZPGSLRLSCAASGFTFSNVMHWVRQPPGKGLWVAVISYGBBKYY 60

Oy  61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWDPIDYWGQGLTVTV 119
Db  61 ABSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GLVWVAVISYGBBKYY 120

Oy  120 SS 121
Db  121 SS 122

RESULT 4
HV3A_HUMAN          STANDARD;          PRT;   122 AA.
ID   HV3A_HUMAN
AC   P01762;
DT   21-JUL-1986 (Rel. 01, Created)
DR   InterPro: IPR003006; Iq_MHC.
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DR   Pfam: PF00047; Iq; 1.
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN TRO).
RX   MEDLINE=76023781; PubMed=809331;
RA   Kratzin H., Altevoigt P., Ruban E., Kortt A., Starosck K.,
RA   Hilschmann N.;
RT   "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.);
RT   II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT   structure of the complete IgA-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC   -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
DR   PIR: A02045; ALHUTR.
DR   HSSP; P01772; 2FB4.
DR   InterPro: IPR003006; Iq_MHC.
DR   InterPro: IPR003596; Iq_v.
DR   Pfam: PF00047; Iq; 1.
DR   SMART; SM00406; Iq; 1.
KW   Immunoglobulin v region.
FT   MOD_RES   1
FT   NON_TER   122
FT   SEQUENCE  122 AA; 13472 MW; 2E21A1DA04D80F9 CRC64;
SQ
Query Match      70.0%; Score 450.5; DB 1; Length 122;
Best Local Similarity 68.3%; Pred. No. 8.7e-38;
Matches 84; Conservative 16; Mismatches 20; Indels 3; Gaps 2;

Oy  1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
Db  1 QVQLVQSGGGLVQPGGSLRLSCVASFDFYMSIRZTPGKGLZMWVSYIGSGSTLYY 60

Oy  61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGGVWD--PIDYWGQGLTVTV 118
Db  61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGGVWD--TBBFBWSTFSLBYWVGZGLVTV 119

Oy  119 VSS 121
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Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
MEDLINE-75124033; PubMed-420800;

```
Best Local Similarity 87.8%; Pred. No. 1.3e-36;
Matches 86; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMVMWVRQPGKLEWVSVIY-SGGSTYY 78
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK 98
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 79 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAR 116
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
HV3K_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A02052; M3HUGA.
DR HSP: P01772; 2PB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 745EB6959E84100A CRC64;

Query Match 67.9%; Score 437.5; DB 1; Length 122;
Best Local Similarity 68.9%; Pred. No. 1.7e-36;
Matches 84; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVZLVZSGGAVZPGRSLRLSCAASGFSFYAMHWVRQAPGKGLZWLVSISYEGBBZY 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK-TGGGVWDPIDYWGQGLTV 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 AASVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK-TGGGVWDPIDYWGQGLTV 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 120 SS 121
||
Db 121 SS 122

RESULT 9
HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
DR PIR: A02055; G1HUKL.
DR PDB: 2PB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 15
FT STRAND 14 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 67.9%; Score 437.5; DB 1; Length 126;
Best Local Similarity 69.8%; Pred. No. 1.7e-36;
Matches 88; Conservative 10; Mismatches 23; Indels 5; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVQLVESGGGVQPGKSLRLSCSSSGFISSYAMVVRQAPGKLEWVAIIWDDGSDQHY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGGVWDPI-----DYWGQGT 115
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGGVWDPI-----DYWGQGT 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 116 LVTVSS 121
|||||
Db 121 PVTVSS 126
|||||

RESULT 10
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```


OX		NCBI_TaxID=9606;	
RP	[1]		
RN		SEQUENCE.	
RA	Wang A.-C., Wang I.Y., Fudenberg H.H.;		
RT	"Immunoglobulin structure and genetics. Identity between variable		
RL	regions of a mu and a gamma2 chain.";		
J. Biol. Chem. 252:7192-7199(1977).			
-I-	MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS		
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL			
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO			
IDENTICAL.			
PIR; A02048; H3HUTL.			
HSSP; P01772; 2FB4.			
InterPro; IPR003006; Ig_MHC.			
Interfam; IPR003596; Ig_v.			
Pfam; PF00047; Ig; 1.			
SMART; SM00406; IGV; 1.			
Immunoglobulin V region.			
NON_TER	115	115	
FT			
SEQUENCE	115 AA; 12356 MW; 4DCC67D179F62326 CRC64;		
Query Match	67.5%; Score 435; DB 1; Length 115;		
Best Local Similarity	71.1%; Pred.No. 2.8e-36;		
Matches	86; Conservative 10; Mismatches 19; Indels 6; Gaps		
Qy	1 OVLVQSGLGGLVQPGSLRLSCAASGTFTPSNAGMWVRQAPCGKLEWVGSGSGSTYY	60	
	: :		
Db	1 EVOLLSEGGGLVQPGGSURLSCAASGTFFTSYVMRWQRAPCGKLZWMGAIZGLSVSZSY	60	
	: :		
Qy	61 ADSVKGRFTISRDSKNLTLYQMNSLRADTAIVYCAKHGTGGVWDPTDYWGQGTLVTVS	120	
	: :		
Db	61 ABSVKGRFTISRDSKNT---NNLSRADTAIVYCAKGVSAAY-FBYWGZCTLVTVS	114	
	: :		
Qy	121 \$ 121		
Db	115 \$ 115		
RESULT 12			
HW02_CANFA			
ID	HW02_CANFA	STANDARD;	PRT; 117 AA.
AC	F01785;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig heavy chain v region MOO.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_Taxid=9615;		
OX	[1]		
REMEDLINE=77242268; PubMed=407924;			
Waterman R.L., Capra J.D.;			
"Primary structure of the variable regions of two canine			
immunoglobulin heavy chains.";			
Biochemistry 16:3160-3168(1977).			
[2]			
SEQUENCE OF 113-117.			
REMEDLINE=80077682; PubMed=117299;			
McCumber L.J., Capra J.D.;			
"The complete amino-acid sequence of a canine mu chain.";			
Mol. Immunol. 16:563-570(1979).			
-I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.			
PIR; A02068; MHDMO.			
HSSP; P01772; 2FB4.			
InterPro; IPR003006; Ig_MHC.			
Interfam; IPR003596; Ig_v.			
Pfam; PF00047; Ig; 1.			
SMART; SM00406; IGV; 1.			
Immunoglobulin V region.			
NON_TER	117	117	
FT			


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RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A.; Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region
RT deletion.";
RL Biochemistry 18:4054-4067(1979).
CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC DISULFIDE BONDS.
DR PIR: A02065; G1H0DB.
DR HSSP: P01772; 2F8A.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
KW Immunoglobulin V region.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 65.6%; Score 422.5; DB 1; Length 120;
Best Local Similarity 69.1%; Pred. No. 5e-35;
Matches 85; Conservative 10; Mismatches 23; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFSRNAMGWVRQAPFGKGLEWVSGISGGGTTY 60
DB :||||:||||| ||||| ||||| | | ||| ||||| ||||| | :||| |
QY 1 EVQLVESGGDLVQPGRSLRLSCAASGFTFHEYNMHWLRQPGKGPFWSTITWNGGSVLY 60
DB :||||| ||||| : ||||| | ||||| ||||| | : | |||||
QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGGYWDP--IDYWGQGTLYT 118
DB :||||| ||||| : ||||| | ||||| ||||| | : | |||||
QY 61 ADSVKGRFAISRDNACKTLYLQNLIRPEDTAFYYCAK--GYIWNNGWFDWNGQGTLYT 117
DB :|||
QY 119 VSS 121
DB 118 VSS 120

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Search completed: March 13, 2003, 15:15:13
Job time : 12.1 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	524	81.4	597	4	Q6B89	Q6B89 homo sapien
2	504	78.7	121	4	Q9UL71	Q9UL71 homo sapien
3	487.5	73.7	573	4	Q8WU38	Q8WU38 homo sapien
4	486.5	73.5	613	4	Q8WUK1	Q8WUK1 homo sapien
5	483	75.0	113	4	Q9UL90	Q9UL90 homo sapien
6	480	74.5	116	4	Q9UL93	Q9UL93 homo sapien
7	479.5	74.5	112	4	Q9UL72	Q9UL72 homo sapien
8	471.5	73.2	118	4	Q9HC1	Q9HC1 homo sapien
9	470.5	73.1	118	4	Q9UL91	Q9UL91 homo sapien
10	466.5	72.4	471	4	Q8TC77	Q8TC77 homo sapien
11	458.5	71.2	147	4	Q9Y509	Q9Y509 homo sapien
12	452.5	70.3	122	4	Q9UL84	Q9UL84 homo sapien
13	451.5	70.1	487	11	Q99RA4	Q99ka4 mus musculus
14	449.5	69.8	494	4	Q96K68	Q96K68 homo sapien
15	444	68.9	119	11	Q92OE7	Q92oe7 mus musculus
16	434.5	67.5	473	11	Q91Z05	Q91z05 mus musculus

```
RESULT 2
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCEFA5D50736 CRC64;

Query Match 78.7%; Score 507; DB 4; Length 121;
Best Local Similarity 81.0%; Pred. No. 2.7e-42;
Matches 98; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
Db 121 S 121

RESULT 3
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 63.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.

Qy 121 S 121
Db 121 S 121

Query Match 75.5%; Score 486.5; DB 4; Length 613;
Best Local Similarity 80.2%; Pred. No. 2.3e-39;
Matches 97; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLVESGGGVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 138
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
Db 139 S 139

RESULT 5
Q9UL90
```

```
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 75.7%; Score 487.5; DB 4; Length 573;
Best Local Similarity 78.2%; Pred. No. 1.7e-39;
Matches 97; Conservative 8; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLV 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLV 139
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 118 TVSS 121
Db 140 TVSS 143

RESULT 4
Q8WU1 PRELIMINARY; PRT; 613 AA.
AC Q8WU1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 75.5%; Score 486.5; DB 4; Length 613;
Best Local Similarity 80.2%; Pred. No. 2.3e-39;
Matches 97; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLVESGGGVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKHTGGVNDPIDYWGQGTFLTVS 138
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
Db 139 S 139

RESULT 5
Q9UL90
```

```
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 75.0%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 5.6e-40;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLWFAFTRYDGSNYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 112
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 S 121
Db 113 S 113

RESULT 6
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 75.0%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 5.6e-40;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLWFAFTRYDGSNYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 112
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 S 121
Db 113 S 113

RESULT 6
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
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FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match 74.5%; Score 480; DB 4; Length 116;
Best Local Similarity 80.8%; Pred. No. 1.1e-39;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Qy 2 VOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYYA 61
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 VOLVESGGGVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKGLWVAVISYDGSNKYYA 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 DSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVSS 121
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 DSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVSS 116
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 7
Q9UL72
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.5%; Score 479.5; DB 4; Length 118;
Best Local Similarity 81.0%; Pred. No. 1.3e-39;
Matches 98; Conservative 6; Mismatches 14; Indels 3; Gaps 2;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNMVVRQAPGKGLSVS-VTVSGSSYY 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTVTVS 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 S 121
Db 118 S 118

RESULT 8
Q9HCC1
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
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OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : Isolation from a
RL human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_Like; 1.
FT NON_TER 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 73.2%; Score 471.5; DB 4; Length 112;
Best Local Similarity 76.9%; Pred. No. 7.4e-39;
Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNMGWVRQAPGKGLWVSGISGGSTYY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVLVESGGVVRPGGSLRLSCAASGFTFDYGMWSVRQAPGKGLWVSGINWGGSTGY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWMDPIDYWGQGLTV 117
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
1 QVQLVQSGGGLVQPGGSLRLSRAEDTAIVYCAKHTG---GGVWDPIDYWGQGLTV 118

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTG---GGVWDPIDYWGQGLTV 118
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
1 QVQLVQSGGGLVQPGGSLRLSRAEDTAIVYCAKHTG---GGVWDPIDYWGQGLTV 118

RESULT 9
QY9191 ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 73.1%; Score 470.5; DB 4; Length 118;
Best Local Similarity 77.5%; Pred. No. 1e-38;
Matches 93; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNMGWVRQAPGKGLWVSGISGGSTYY 60

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Db 1 EVLVESGGGLVQPGGSLRLSRAEDTAIVYCAKHTGGVWMDPIDYWGQGLTV 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWMDPIDYWGQGLTV 120
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWMDPIDYWGQGLTV 117

RESULT 10
Q8TC77 ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 72.4%; Score 466.5; DB 4; Length 471;
Best Local Similarity 75.6%; Pred. No. 1.5e-37;
Matches 93; Conservative 9; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSRAEDTAIVYCAKHTG---GGVWDPIDYWGQGLTV 118
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
20 EVLVESGGGLVQPGGSLRLSRAEDTAIVYCAKHTG---GGVWDPIDYWGQGLTV 119

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTG---GGVWDPIDYWGQGLTV 118
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTG---GGVWDPIDYWGQGLTV 138

QY 119 VSS 121
Db 139 VSS 141

RESULT 11
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VH3 protein (Fragment).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR HSSP; S80860; AAD14339.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.

```



```
FT NON_TER 1 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 71.2%; Score 458.5; DB 4; Length 147;
Best Local Similarity 72.7%; Pred. No. 2e-37;
Matches 93; Conservative 7; Mismatches 19; Indels 9; Gaps 2;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGSGSTYY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVHLVESGGGVQPGKSLRLSCAASGFTFTYGMSSWVRQAPGKGLDWALLISYDGSQYY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAAYVYCAKHTGGVWDP-----IDYWGQ 113
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AGSVKGRFTISRNSKNTLYLQWNSLRADTAAYVYCAK--DGNVFDSDVGYVYAGIDYWGQ 118
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 114 GTLVTVSS 121
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 GTLVTVSS 126
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 70.3%; Score 452.5; DB 4; Length 122;
Best Local Similarity 74.8%; Pred. No. 6.1e-37;
Matches 91; Conservative 8; Mismatches 22; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGSGSTYY 60
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVQPGKSLRLSCAASRFTESNYGMHWVRQAPGKGLEWVAISNDGSKFY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAAYVYCAKHTGGG--VWDPIDYWGQGLTVV 119
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTIFRDNKSNMMDLQWNSLRADTAAYVYCAKDERGLRVGTVFDYWGQGLTVV 120
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 120 SS 121
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SS 122
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 70.1%; Score 451.5; DB 11; Length 487;
Best Local Similarity 69.4%; Pred. No. 4.6e-36;
Matches 86; Conservative 14; Mismatches 21; Indels 3; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGSGSTYY 60
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTSSYAMSWVRQTPTEKRLWVAITSDGGSYYY 79
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAAYVYCAKHTGG--GYWDPIDYWGQGLTV 117
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 PDNVKGRFTISRNANKNLYLQWNSLRADTAAYVYCAKMGSGSPGYGSRFDYWGQGTIT 139
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 118 TVSS 121
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 TVSS 143
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ14473 fis, clone MAMMAJ001080, highly similar to Homo
DE sapiens SNC73 protein (SNC73) mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Niomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027379; BAB55072.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5ABE4C0E CRC64;
  Query Match          69.8%; Score 449.5; DB 4; Length 494;
  Best Local Similarity 72.1%; Pred. No. 7.3e-36;
  Matches 88; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

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Db :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
20 EVLVESGGDLVKPGSLRLSCAASGLSFSTYAMNVRQAPGKGLEWVSSISRSYIYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT--GGGVWDPIDYWGQGLTVTV 119
Db :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
80 RDSVKGRFTISRDNKNTLYLQMNLSRLVDDTAVYYCARDSCNGAICYGFSFGQGLTVTV 139
QY 120 SS 121
Db :|:|
140 SS 141

RESULT 15
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iace A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
  in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307937; AAL09421.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR NON_TER 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

  Query Match          68.9%; Score 444; DB 11; Length 119;
  Best Local Similarity 71.3%; Pred. No. 4e-36;
  Matches 87; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

QY 1 QVOLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
Db :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
1 EVLVESGGDLVKPGSLRLSCAASGFTFSYGSWSVRQTPDKRLEWVATISSGSYTY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGYMD-PIDYWGQGLTVTV 119
Db :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
61 PDSVKGRFTISRDNKNTLYLQMNLSLKSDTAMYYCARH---GDYDVGFAWGGQGLTVTV 117
QY 120 SS 121
Db :|:|
118 SA 119

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Search completed: March 13, 2003, 15:16:58
 Job time : 45.7462 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:33:09 ; Search time 11.3077 Seconds
(without alignments)
57.066 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110

Perfect score: 14

Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications.AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	121	10	US-09-822-698A-3
2	14	100.0	381	10	US-09-822-698A-5
3	14	100.0	451	10	US-09-822-698A-26
4	13	92.9	14	10	US-09-822-698A-75
5	13	92.9	14	10	US-09-822-698A-97
6	13	92.9	14	10	US-09-822-698A-105
7	12	85.7	14	10	US-09-822-698A-30
8	12	85.7	14	10	US-09-822-698A-31
9	12	85.7	14	10	US-09-822-698A-76
10	12	85.7	14	10	US-09-822-698A-79
11	12	85.7	14	10	US-09-822-698A-83
12	12	85.7	14	10	US-09-822-698A-86
13	12	85.7	14	10	US-09-822-698A-89
14	12	85.7	14	10	US-09-822-698A-90
15	12	85.7	14	10	US-09-822-698A-94
16	12	85.7	14	10	US-09-822-698A-96
17	12	85.7	14	10	US-09-822-698A-100
18	12	85.7	14	10	US-09-822-698A-102
19	12	85.7	14	10	US-09-822-698A-109

20	11	78.6	14	10	US-09-822-698A-78	Sequence 78, Appl
21	11	78.6	14	10	US-09-822-698A-81	Sequence 81, Appl
22	11	78.6	14	10	US-09-822-698A-82	Sequence 82, Appl
23	11	78.6	14	10	US-09-822-698A-88	Sequence 88, Appl
24	11	78.6	14	10	US-09-822-698A-91	Sequence 91, Appl
25	11	78.6	14	10	US-09-822-698A-92	Sequence 92, Appl
26	11	78.6	14	10	US-09-822-698A-93	Sequence 93, Appl
27	11	78.6	14	10	US-09-822-698A-98	Sequence 98, Appl
28	11	78.6	14	10	US-09-822-698A-99	Sequence 99, Appl
29	11	78.6	14	10	US-09-822-698A-101	Sequence 101, Appl
30	11	78.6	14	10	US-09-822-698A-103	Sequence 103, Appl
31	11	78.6	16	10	US-09-822-698A-65	Sequence 65, Appl
32	10	71.4	14	10	US-09-822-698A-32	Sequence 32, Appl
33	10	71.4	14	10	US-09-822-698A-77	Sequence 77, Appl
34	10	71.4	14	10	US-09-822-698A-84	Sequence 84, Appl
35	10	71.4	14	10	US-09-822-698A-107	Sequence 107, Appl
36	10	71.4	16	10	US-09-822-698A-67	Sequence 67, Appl
37	9	64.3	14	10	US-09-822-698A-80	Sequence 80, Appl
38	9	64.3	14	10	US-09-822-698A-104	Sequence 104, Appl
39	8	57.1	14	10	US-09-822-698A-106	Sequence 106, Appl
40	8	57.1	14	10	US-09-822-698A-108	Sequence 108, Appl
41	7	50.0	16	10	US-09-822-698A-41	Sequence 41, Appl
42	7	50.0	16	10	US-09-822-698A-43	Sequence 43, Appl
43	7	50.0	16	10	US-09-822-698A-45	Sequence 45, Appl
44	7	50.0	16	10	US-09-822-698A-47	Sequence 47, Appl
45	7	50.0	16	10	US-09-822-698A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-09-822-698A-3

; Sequence 3, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 3

; LENGTH: 121

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: heavy chain variable region of the MUC1-specific binding domain of the PHI Fab antibody

US-09-822-698A-3

Query Match 100.0% Score 14; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14

|||||

Db 97 AKHTGGGVWDPIDY 110

RESULT 2

US-09-822-698A-5

; Sequence 5, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match          92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVDPID 13
   |||||
Db 1 AKHTGGGVDPID 13

RESULT 5
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match          92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVDPID 13
   |||||
Db 1 AKHTGGGVDPID 13

RESULT 6
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match          92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
US-09-822-698A-5

Query Match          100.0%; Score 14; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVDPID 14
   |||||
Db 97 AKHTGGGVDPID 110

RESULT 3
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match          100.0%; Score 14; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVDPID 14
   |||||
Db 97 AKHTGGGVDPID 110

RESULT 4
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
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QY 2 KHTGGGVWDPI 14
| | | | | | | | | | | | | | | |
Db 2 KHTGGGVWDPI 14

RESULT 7

US-09-822-698A-30
; Sequence 30, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 8

US-09-822-698A-31
; Sequence 31, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPI 12

RESULT 9

US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1

; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 10

US-09-822-698A-79
; Sequence 79, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 11

US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 12
US-09-822-698A-86
; Sequence 86, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-86

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 13
US-09-822-698A-89
; Sequence 89, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 89
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-89

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 14
US-09-822-698A-90
; Sequence 90, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 90
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-90

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
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Db 1 AKHTGGGVWDPI 12

RESULT 15
US-09-822-698A-94
; Sequence 94, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 94
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-94

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AKHTGGGVWDPI 12

Search completed: March 13, 2003, 15:40:23
Job time : 11.3077 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:31:49 ; Search time 151.846 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 14

Sequence: 1 AKHTGGGVWDPIDY 14

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	14	100.0	121	22	US-09-822-698A-3
3	14	100.0	381	19	US-09-538-913-5
4	14	100.0	381	22	US-09-822-698A-5
5	14	100.0	451	22	US-09-822-698A-26
6	13	92.9	14	22	US-09-822-698A-75

7	13	92.9	14	22	US-09-822-698A-97	Sequence 97, Appl
8	13	92.9	14	22	US-09-822-698A-105	Sequence 105, App
9	12	85.7	14	22	US-09-822-698A-30	Sequence 30, Appl
10	12	85.7	14	22	US-09-822-698A-31	Sequence 31, Appl
11	12	85.7	14	22	US-09-822-698A-76	Sequence 76, Appl
12	12	85.7	14	22	US-09-822-698A-79	Sequence 79, Appl
13	12	85.7	14	22	US-09-822-698A-83	Sequence 83, Appl
14	12	85.7	14	22	US-09-822-698A-86	Sequence 86, Appl
15	12	85.7	14	22	US-09-822-698A-89	Sequence 89, Appl
16	12	85.7	14	22	US-09-822-698A-90	Sequence 90, Appl
17	12	85.7	14	22	US-09-822-698A-94	Sequence 94, Appl
18	12	85.7	14	22	US-09-822-698A-96	Sequence 96, Appl
19	12	85.7	14	22	US-09-822-698A-100	Sequence 100, App
20	12	85.7	14	22	US-09-822-698A-102	Sequence 102, App
21	12	85.7	14	22	US-09-822-698A-109	Sequence 109, App
22	11	78.6	14	22	US-09-822-698A-78	Sequence 78, Appl
23	11	78.6	14	22	US-09-822-698A-81	Sequence 81, Appl
24	11	78.6	14	22	US-09-822-698A-82	Sequence 82, Appl
25	11	78.6	14	22	US-09-822-698A-88	Sequence 88, Appl
26	11	78.6	14	22	US-09-822-698A-91	Sequence 91, Appl
27	11	78.6	14	22	US-09-822-698A-92	Sequence 92, Appl
28	11	78.6	14	22	US-09-822-698A-93	Sequence 93, Appl
29	11	78.6	14	22	US-09-822-698A-98	Sequence 98, Appl
30	11	78.6	14	22	US-09-822-698A-99	Sequence 99, Appl
31	11	78.6	14	22	US-09-822-698A-101	Sequence 101, App
32	11	78.6	14	22	US-09-822-698A-103	Sequence 103, App
33	11	78.6	16	22	US-09-822-698A-65	Sequence 65, Appl
34	10	71.4	14	22	US-09-822-698A-32	Sequence 32, Appl
35	10	71.4	14	22	US-09-822-698A-77	Sequence 77, Appl
36	10	71.4	14	22	US-09-822-698A-84	Sequence 84, Appl
37	10	71.4	14	22	US-09-822-698A-107	Sequence 107, App
38	10	71.4	16	22	US-09-822-698A-67	Sequence 67, Appl
39	9	64.3	14	22	US-09-822-698A-80	Sequence 80, Appl
40	9	64.3	14	22	US-09-822-698A-104	Sequence 104, App
41	8	57.1	14	22	US-09-822-698A-106	Sequence 106, App
42	8	57.1	14	22	US-09-822-698A-108	Sequence 108, App
43	7	50.0	16	22	US-09-822-698A-41	Sequence 41, Appl
44	7	50.0	16	22	US-09-822-698A-43	Sequence 43, Appl
45	7	50.0	16	22	US-09-822-698A-45	Sequence 45, Appl

ALIGNMENTS

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RESULT 1
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hooogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

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Query Match 100.0%; Score 14; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

DB 97 AKHTGGGVWDPIDY 110

RESULT 2

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US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHL Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 14; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPTDY 14
   |||||
Db 97 AKHTGGVWDPTDY 110

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 14; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPTDY 14
   |||||
Db 97 AKHTGGVWDPTDY 110

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 14; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPTDY 14
   |||||
Db 97 AKHTGGVWDPTDY 110

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PHL-IgG1
US-09-822-698A-26

Query Match      100.0%; Score 14; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPTDY 14
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Db 97 AKHTGGVWDPTDY 110

RESULT 6
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75
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Query Match 92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPID 13
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Db 1 AKHTGGGWDPID 13

RESULT 7
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match 92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPID 13
|||||
Db 1 AKHTGGGWDPID 13

RESULT 8
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGGWDPIDY 14
|||||
Db 2 KHTGGGWDPIDY 14

RESULT 9

US-09-822-698A-30
; Sequence 30, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match 85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 12
|||||
Db 1 AKHTGGGWDPI 12

RESULT 10
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match 85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 12
|||||
Db 1 AKHTGGGWDPI 12

RESULT 11
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPI 12
   |||||
Db 1 AKHTGGVWDPI 12

RESULT 12
US-09-822-698A-79
; Sequence 79, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPI 12
   |||||
Db 1 AKHTGGVWDPI 12

RESULT 13
US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPI 12
   |||||
Db 1 AKHTGGVWDPI 12

RESULT 14
US-09-822-698A-86
; Sequence 86, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-86

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPI 12
   |||||
Db 1 AKHTGGVWDPI 12

RESULT 15
US-09-822-698A-89
; Sequence 89, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 89
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-89

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPI 12
   |||||
Db 1 AKHTGGVWDPI 12

Search completed: March 13, 2003, 15:39:00
Job time : 151.846 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:32:14 ; Search time 24.2308 Seconds
(without alignments)
75.113 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 596842 seqs, 130003698 residues

Word size : 0

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/PC/T_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	6	42.9	55	1 PCT-US02-32727-11588
2	6	42.9	55	Sequence 11588, A
3	6	42.9	55	US-09-978-825-28218
4	6	42.9	93	1 PCT-US02-32727-9150
5	6	42.9	93	Sequence 9150, Ap
6	6	42.9	93	US-09-978-825-9150
7	6	42.9	330	6 US-10-057-498-9150
8	6	42.9	330	Sequence 9150, Ap
9	6	42.9	435	5 US-09-724-676-78529
10	6	42.9	474	6 US-09-724-676A-78529
11	6	42.9	512	5 US-10-369-493-11831
12	6	42.9	512	US-09-724-676-78531
13	6	42.9	526	5 US-09-724-676A-78532
14	6	42.9	526	US-09-724-676A-78532
15	6	42.9	701	6 US-10-282-122A-62129
16	6	42.9	1583	5 PCT-US02-32727-15149
17	6	42.9	1583	Sequence 15149, A
18	6	42.9	1583	US-09-978-825-15149
19	5	35.7	38	6 US-10-057-498-15149
20	5	35.7	51	5 US-10-156-761-15030
21	5	35.7	51	US-09-724-676-87689
22	5	35.7	56	1 PCT-US02-32727-26391
23	5	35.7	56	Sequence 26391, A
24	5	35.7	56	US-09-978-825-26391
25	5	35.7	58	6 US-10-057-498-26391
26	5	35.7	58	Sequence 553, App

27	5	35.7	66	1	PCT-US02-32727-28218	Sequence 28218, A
28	5	35.7	66	5	US-09-978-825-28218	Sequence 28218, A
29	5	35.7	66	6	US-10-057-498-28218	Sequence 28218, A
30	5	35.7	67	1	PCT-US02-32727-9117	Sequence 9117, Ap
31	5	35.7	67	5	US-09-978-825-9117	Sequence 9117, Ap
32	5	35.7	67	6	US-10-057-498-9117	Sequence 9117, Ap
33	5	35.7	68	1	PCT-US02-32727-28689	Sequence 28689, A
34	5	35.7	68	5	US-09-978-825-28689	Sequence 28689, A
35	5	35.7	68	6	US-10-057-498-28689	Sequence 28689, A
36	5	35.7	77	5	US-09-724-676-87695	Sequence 87695, A
37	5	35.7	77	5	US-09-724-676A-87695	Sequence 87695, A
38	5	35.7	78	1	PCT-US02-32727-21401	Sequence 21401, A
39	5	35.7	78	5	US-09-978-825-21401	Sequence 21401, A
40	5	35.7	78	6	US-10-057-498-21401	Sequence 21401, A
41	5	35.7	84	5	US-09-724-676-87694	Sequence 87694, A
42	5	35.7	84	5	US-09-724-676A-87694	Sequence 87694, A
43	5	35.7	93	1	PCT-US02-32727-16769	Sequence 16769, A
44	5	35.7	93	5	US-09-978-825-16769	Sequence 16769, A
45	5	35.7	93	6	US-10-057-498-16769	Sequence 16769, A

ALIGNMENTS

RESULT 1

PCT-US02-32727-11588

; Sequence 11588, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Siqing

; APPLICANT: Jen, Shytan

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 11588

; LENGTH: 55

; TYPE: PRT

; ORGANISM: Propionl acnes

PCT-US02-32727-11588

Query Match

Best Local Similarity 42.9%; Score 6; DB 1; Length 55;

Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8

Db 37 HTGGGV 42

RESULT 2

US-09-978-825-11588

; Sequence 11588, Application US/09978825

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Siqing

```

; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-11588

Query Match 42.9%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
Db 37 HTGGGV 42

RESULT 3
US-10-057-498-11588
; Sequence 11588, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-11588

Query Match 42.9%; Score 6; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
Db 37 HTGGGV 42

RESULT 4
PCT-US02-32727-9150
; Sequence 9150, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-9150

Query Match 42.9%; Score 6; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
Db 10 GGGVWD 15

RESULT 5
US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-9150

Query Match 42.9%; Score 6; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
Db 10 GGGVWD 15

RESULT 6
US-10-057-498-9150
; Sequence 9150, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-9150

Query Match 42.9%; Score 6; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
Db 10 GGGVWD 15
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US-10-057-498-9150

Query Match 42.9%; Score 6; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
| | | | |
DB 10 GGGVWD 15

RESULT 7

US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 42.9%; Score 6; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VWDPID 13
| | | | |
DB 103 VWDPID 108

RESULT 8

US-09-724-676-78529
; Sequence 78529, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78529
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78529

Query Match 42.9%; Score 6; DB 5; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
| | | | |
DB 396 KHTGGG 401

RESULT 9

US-09-724-676A-78529
; Sequence 78529, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78529
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78529

Query Match 42.9%; Score 6; DB 5; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
| | | | |
DB 396 KHTGGG 401

RESULT 10

US-10-369-493-11831
; Sequence 11831, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11831
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-11831

Query Match 42.9%; Score 6; DB 6; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGG 6
| | | | |
DB 32 AKHTGG 37

RESULT 11

US-09-724-676-78531
; Sequence 78531, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78531
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78531

Query Match 42.9%; Score 6; DB 5; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 KHTGGG 7
Db      473 KHTGGG 478

RESULT 12
US-09-724-676A-78531
; Sequence 78531, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78531
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78531

Query Match      42.9%; Score 6; DB 5; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KHTGGG 7
Db      473 KHTGGG 478

US-09-724-676A-78532
; Sequence 78532, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78532
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78532

Query Match      42.9%; Score 6; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KHTGGG 7
Db      487 KHTGGG 492

RESULT 13
US-09-724-676-78532
; Sequence 78532, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78532
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78532

Query Match      42.9%; Score 6; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KHTGGG 7
Db      487 KHTGGG 492

RESULT 14
US-09-724-676A-78532
; Sequence 78532, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78532
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78532

Query Match      42.9%; Score 6; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HTGGGV 8
Db      75 HTGGGV 80

US-09-724-676A-78532
; Sequence 62129, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62129
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62129

Query Match      42.9%; Score 6; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HTGGGV 8
Db      75 HTGGGV 80

Search completed: March 13, 2003, 15:39:54
Job time : 25.2308 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:29:54 ; Search time 14.5385 Seconds
(without alignments)
92.574 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR.73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	42.9	114	2 T08411	hypothetical prote
2	6	42.9	193	2 C82683	disulfide oxidore
3	6	42.9	436	2 H84121	NADH oxidase (nox)
4	6	42.9	511	2 A54676	antiquitin - human
5	6	42.9	1123	2 S20497	phytochrome A - po
6	5	35.7	10	2 H60787	sperm-activating p
7	5	35.7	10	2 D60788	sperm-activating p
8	5	35.7	10	2 B60787	sperm-activating p
9	5	35.7	10	2 A60788	sperm-activating p
10	5	35.7	10	2 C60589	sperm-activating p
11	5	35.7	10	2 D60588	sperm-activating p
12	5	35.7	71	2 T26663	hypothetical prote
13	5	35.7	72	2 T48971	hypothetical prote
14	5	35.7	75	2 A69147	hypothetical prote
15	5	35.7	101	2 S22454	ribosomal protein
16	5	35.7	107	2 S58218	hypothetical prote
17	5	35.7	113	2 S25575	ig heavy chain v r
18	5	35.7	119	2 T08142	thioredoxin h homo
19	5	35.7	119	2 D83723	hypothetical prote
20	5	35.7	119	2 T48745	hypothetical prote
21	5	35.7	120	2 C53482	transcription regu
22	5	35.7	130	1 S52339	ribosomal protein
23	5	35.7	130	1 JC2234	ribosomal protein
24	5	35.7	130	2 T18510	hypothetical prote
25	5	35.7	133	2 C97301	uncharacterized co
26	5	35.7	144	2 F64094	ribosomal protein
27	5	35.7	145	1 A35932	angiogenin precurs
28	5	35.7	145	2 D70938	hypothetical prote
29	5	35.7	150	2 AH3482	exsf protein limpo

30	5	35.7	155	2 C86206	hypothetical prote
31	5	35.7	158	2 C95159	shikimate kinase (
32	5	35.7	158	2 C98025	shikimate kinase (
33	5	35.7	160	2 G69376	conserved hypothet
34	5	35.7	163	2 A70847	hypothetical prote
35	5	35.7	168	2 D82310	CinA-related prote
36	5	35.7	169	2 A40522	plasma (EC 3.4.21
37	5	35.7	170	2 H87704	thiol-disulfide in
38	5	35.7	175	2 A71680	cytochrome C (cycM
39	5	35.7	175	2 A97742	cytochrome c (limp
40	5	35.7	181	1 I41314	K88 fimbrial prote
41	5	35.7	185	2 F95008	acetyltransferase,
42	5	35.7	188	2 B95365	probable oxidoredu
43	5	35.7	189	1 S74659	shikimate kinase (
44	5	35.7	189	2 D69128	conserved hypothet
45	5	35.7	189	2 A87254	hypothetical prote

ALIGNMENTS

RESULT 1

T08411

hypothetical protein F18B3.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T08411

R:Querier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Sala-

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16409

A:Accession: T08411

A:Molecule type: DNA

A:Residues: 1-114 <QUE>

A:CROSS-references: EMBL:AL049862; GSPDB:GN000061; ATSP:F18B3.180

A:Experimental source: cultivar Columbia; BAC clone F18B3

C:Genetics:

A:Gene: ATSP:F18B3.180

A:Map position: 3

C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 42.9%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDP 11
|||||

Db 99 GGWDP 104

RESULT 2

C82683

disulfide oxidoreductase XF1436 [Imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: C82683

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82683

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-193 <SIM>

A:CROSS-references: GB:AF003973; GB:AF003849; NID:g9106438; PIDN:AAF84245.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer

as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
A:Genetics:
A:Gene: XF1436

Query Match 42.9%; Score 6; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDPI 11
|||||
DB 68 GGWDPI 73

RESULT 3
H84121
NADH oxidase (nox) BH3776 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84121
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H84121
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <SOT>
A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07495.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3776
C:Superfamily: NADH peroxidase; dihydrolipoamide dehydrogenase homology

Query Match 42.9%; Score 6; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GGWDPI 12
|||||
DB 424 GGWDPI 429

RESULT 4
A54676
antiqutin - human
N:Alternate names: 26g turgor protein homolog
C:Species: Homo sapiens (man)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jan-2000
C:Accession: A54676
R:Lee, P.; Kuhl, W.; Gelbart, T.; Kamimura, T.; West, C.; Beutler, E.
Genomics 21, 371-378, 1994
A:Title: Homology between a human protein and a protein of the green garden pea.
A:Reference number: A54676; MUID:94375061; PMID:8088832
A:Accession: A54676
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <LEE>
A:Cross-references: GB:S74728; NID:g797409; PIDN:AAB31966.1; PID:g797410
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
F:59-322/Domain: aldehyde dehydrogenase homology <ALD>

Query Match 42.9%; Score 6; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
|||||

Db 472 KHTGGG 477

RESULT 5
S20497
phytochrome A - potato
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 30-Apr-1999
C:Accession: S20497
R:Heyer, A.; Gatz, C.
Plant Mol. Biol. 18, 535-544, 1992
A:Title: Isolation and characterization of a cDNA-clone coding for potato type A phyt
A:Reference number: S20497; MUID:92163018; PMID:1536928
A:Accession: S20497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1123 <HEY>
C:Genetics:
A:Gene: phyA
C:Superfamily: phytochrome; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
F:67-382/Domain: phytochrome homology <PHYT>
F:323/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 42.9%; Score 6; DB 2; Length 1123;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
|||||
DB 1058 HTGGGV 1063

RESULT 6
H60787
sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: H60787
R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, pseudocen
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: H60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all
at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
DB 5 TGGGV 9

RESULT 7
D60788
sperm-activating peptide (Thr-5 speract) - sea urchin (Pseudocentrotus depressus)
C:Species: Pseudocentrotus depressus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: D60788
R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: D60788
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all

at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 8

B60787
sperm-activating peptide (Thr-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
C:Species: Hemicentrotus pulcherrimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: B60787

R:Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A:Reference number: A60787; MUID:88242184; PMID:3378407
C:Accession: B60787

A:Molecule type: protein

A:Residues: 1-10 <SU2>

C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.

C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 9

A60788
sperm-activating peptide (Thr-5 speract) - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: A60788

R:Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988

A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A:Reference number: A60787; MUID:88242184; PMID:3378407

A:Accession: A60788

A:Molecule type: protein

A:Residues: 1-10 <SU2>

C:Comment: This oligopeptide from egg jelly is one of several from this species. Unlike
of the repeats in the known precursor (see PIR:A34543).

C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 10

C60589
sperm-activating peptide (Thr-5 SAP-I) - Echinometa mathaei
C:Species: Echinometa mathaei
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: C60589

R:Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
Comp. Biochem. Physiol. B 94, 739-751, 1989

A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinometa mathaei and Heterocentrotus mammillatus.
A:Reference number: A60527

A:Accession: C60589

A:Molecule type: protein

A:Residues: 1-10 <VOS>

C:Note: An identical peptide was isolated from Echinometa mathaei type A and type B
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 11

D60588
sperm-activating peptide (Thr-5 SAP-I) - sea urchin (Strongylocentrotus nudus)
N:Alternate names: speract homolog
C:Species: Strongylocentrotus nudus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: D60588

R:Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yama
Comp. Biochem. Physiol. B 94, 739-751, 1989

A:Title: A halogenated amino acid-containing sperm activating peptide and its related
otus nudus, Echinometa mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527

A:Accession: D60588

A:Molecule type: protein

A:Residues: 1-10 <VOS>

C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 12

T26663
hypotheical protein Y38E10A.m - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26663

R:Wallis, J.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20252

A:Accession: T26663

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-71 <WIL>

A:Cross-references: EMBL:AL110484; NID:el542205; PIDN:CA544404.1; CESP:Y38E10A.m

A:Experimental source: clone Y38E10A

C:Genetics:

A:Gene: CESP:Y38E10A.m

Query Match 35.7%; Score 5; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 32 TGGGV 36

RESULT 13

T48971
hypotheical protein Fl4D17.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T48971
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25008
A:Accession: T48971
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <J0R>
A:Cross-references: EMBL:AL353992; GSPDB:GN00061; ATSP:F14D17.20
A:Experimental source: cultivar Columbia; BAC clone F14D17
C:Genetics:
A:Gene: ATSP:F14D17.20
A:Map position: 3
A:Introns: 42/3

Query Match 35.7%; Score 5; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVW 9
|||||
Db 66 GGGVW 70

RESULT 14
A69147
hypothetical protein MTH364 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69147
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69147
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-75 <MTH>
A:Cross-references: GB:AE000822; GB:AE000666; MID:g2621420; PIDN:AAB84870.1; PID:g262142
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH364
A:Start codon: TTG

Query Match 35.7%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 23 TGGGV 27

RESULT 15
S22454
ribosomal protein L2 REP - wood tobacco mitochondrion (fragment)
C:Species: mitochondrion Nicotiana sylvestris (wood tobacco)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 21-Jul-2000
C:Accession: S22454
R:Vitart, V.; de Paeppe, R.; Mathieu, C.; Chetrit, P.; Vedel, F.
Mol. Gen. Genet. 233, 193-200, 1992
A:Title: Amplification of substoichiometric recombinant mitochondrial DNA sequences in a
A:Reference number: S22454; MUID:92293115; PMID:1376403
A:Accession: S22454
A:Molecule type: DNA
A:Residues: 1-101 <VIT>
A:Cross-references: EMBL:X66519; MID:g396185; PIDN:CAA47138.1; PID:g396186
C:Genetics:
A:Genome: mitochondrion

C:Superfamily: Escherichia coli ribosomal protein L2
C:Keywords: mitochondrion

Query Match 35.7%; Score 5; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 73 TGGGV 77

Search completed: March 13, 2003, 15:33:40
Job time : 16.5385 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:18:49 ; Search time 7.53846 Seconds
(without alignments)
77.027 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6	42.9	511	1 DHAX_HUMAN	P49419 homo sapien
2	6	42.9	1123	1 PHYA_SOLTU	P30733 solanum tub
3	6	42.9	1124	1 PHYI_TOBAC	P33530 nicotiana t
4	5	35.7	68	1 YYY4_HUMAN	Q9ui36 homo sapien
5	5	35.7	114	1 PT11_STYPL	P28203 styela plic
6	5	35.7	119	1 THH2_BRANA	Q39362 brassica na
7	5	35.7	129	1 RS1A_HUMAN	P39027 homo sapien
8	5	35.7	129	1 RS1A_ICTPU	Q90yq8 ictalurus p
9	5	35.7	144	1 RL15_HAEIN	P44353 haemophilus
10	5	35.7	145	1 ANGI_MOUSE	P21570 mus musculu
11	5	35.7	169	1 PLMN_RAT	Q01177 rattus norv
12	5	35.7	181	1 FMKA_ECOLI	P04738 escherichia
13	5	35.7	184	1 VP50_BFAPS	Q9t1p8 bacterioph
14	5	35.7	189	1 AROK_SYNY3	P72796 synecocyst
15	5	35.7	197	1 VG23_BPMO2	Q38362 mycobacteri
16	5	35.7	197	1 VG23_BPML5	Q05229 mycobacteri
17	5	35.7	201	1 CLPP_AQUAE	Q07357 aquifex aeo
18	5	35.7	207	1 CLPP_YEREN	Q60107 yersinia en
19	5	35.7	208	1 CLPP_XYLFA	Q9pe41 xyella fas
20	5	35.7	223	1 RLA_MYCBO	Q06045 mycobacteri
21	5	35.7	223	1 RLA_MYCTU	P95050 mycobacteri
22	5	35.7	229	1 H1S4_PYRAE	Q8zy14 pyrobaculum
23	5	35.7	238	1 MOTB_TREPA	Q07887 treponema p
24	5	35.7	240	1 HLXV_ACTPL	P23619 actinobacil
25	5	35.7	241	1 PYRE_TRETH	P36076 thermus the
26	5	35.7	245	1 PFLA_HAEIN	P33751 haemophilus
27	5	35.7	245	1 T2M4_METJA	Q58723 methanococc
28	5	35.7	261	1 YY00_MYCLE	Q49741 mycobacteri
29	5	35.7	262	1 RS2_THEMEA	Q9wzml thermotoga
30	5	35.7	265	1 H1S4_XYLFA	Q9pbc9 xyella fas
31	5	35.7	270	1 L181_CHLEU	Q03965 chlamydomon
32	5	35.7	270	1 URED_SYNY3	P73047 synecocyst
33	5	35.7	285	1 NADC_MYCTU	O06594 mycobacteri

34	5	35.7	294	1 TOXR_VIBCH	P15795 vibrio chol
35	5	35.7	296	1 SAPR_STRPU	P11761 strongyloce
36	5	35.7	297	1 EZV3_CHLRE	Q08356 chlamydomon
37	5	35.7	303	1 Y722_SYNY3	P72667 synecocyst
38	5	35.7	304	1 LST_HAEIN	Q48211 haemophilus
39	5	35.7	319	1 AES_ECOLI	P23872 escherichia
40	5	35.7	325	1 YC83_MYCTU	Q10611 mycobacteri
41	5	35.7	333	1 EBP2_SCHPO	O13802 schizosacch
42	5	35.7	337	1 TAT_HTLV2	P03410 human t-cel
43	5	35.7	343	1 SLAM_MOUSE	Q9cgm4 mus musculu
44	5	35.7	344	1 JUNE_MOUSE	P09450 mus musculu
45	5	35.7	344	1 JUNE_RAT	P24898 rattus norv

ALIGNMENTS

RESULT 1
DHAX_HUMAN
ID DHAX_HUMAN STANDARD; PRT; 511 AA.
AC P49419;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiquitin (EC 1.2.1.1).
GN ALDH7A1 OR ATQ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
.. OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, Liver, and Placenta;
RX MEDLINE=94375061; PubMed=8088832;
RA Lee P., Kuhl W., Gelbart T., Kamimura T., West C., Beutler E.;
RT "Homology between a human protein and a protein of the green garden pea.";
RL Genomics 21:371-378(1994).
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC STRONGEST, TO PEA 26G.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

CC EMBL; S74728; AAB31966.1; -.
DR HSSP; P51977; IBOX.
DR Genew; HGNC:877; ALDH7A1.
DR MIM; 107323; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00171; aldedh; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR KW Oxidoreductase; NAD.
FT NP_BIND 246 251 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 268 268 BY SIMILARITY.
FT ACT_SITE 302 302 BY SIMILARITY.
SQ SEQUENCE 511 AA; 55366 MW; 08F6F7672C948E2C CRC64;

Query Match 42.98; Score 6; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
|||||
Db 472 KHTGGG 477

RESULT 2

PHYA_SOLITU STANDARD; PRT: 1123 AA.

AC P30733;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phytochrome A.

DE PHYA.

GN Solanum tuberosum (Potato).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

ON NCBI_TaxID=4113;

XX [1]

RY SEQUENCE FROM N.A.

RC STRAIN=cv. Desiree;

RC MEDLINE=92163018; PubMed=1536928;

RX Hayer A., Gatz C.;

RA "Isolation and characterization of a cDNA-clone coding for potato

RT type A phytochrome.";

RL Plant Mol. Biol. 18:535-544(1992).

CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCOVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

CC -1- SUBUNIT: HOMODIMER.

CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.

CC -----

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CC -----

CC EMBL: S84872; AAB21533.2; -.

CC PIR: S20497; S20497.

CC InterPro: IPR003594; ATPbind_ATPase.

CC InterPro: IPR003018; GAF.

CC InterPro: IPR004359; HIS_KIN_sig.

CC InterPro: IPR003661; His_kinA.

CC InterPro: IPR001610; PAC.

CC InterPro: IPR000700; PAS-assoc_C.

CC InterPro: IPR000014; PAS_domain.

CC InterPro: IPR001294; phytochrome.

CC Pfam: PF00360; phytochrome; 1.

CC Pfam: PF00512; signal; 1.

CC Pfam: PF00989; PAS; 2.

CC Pfam: PF01590; GAF; 1.

CC Pfam: PF02518; HATPase_C; 1.

CC PRINTS: PR01033; PHYTOCHROME.

CC SMART: SM00065; GAF; 1.

CC SMART: SM00387; HATPase_C; 1.

CC SMART: SM00388; HisKA; 1.

CC SMART: SM00086; PAC; 1.

CC SMART: SM00091; PAS; 2.

CC TIGRfam: TIGR00229; sensory_box; 1.

CC PROSITE: PS50109; HIS_KIN; 1.

CC PROSITE: PS50113; PAC; 1.

CC PROSITE: PS50112; PAS; 2.

CC PROSITE: PS00245; PHYTOCHROME_1; 1.

DR PROSITE: PS50046; PHYTOCHROME_2; 1.

KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;

KW Repeat; Multigene family.

FT DOMAIN 617 687 PAS 1.

FT DOMAIN 690 746 PAC.

FT DOMAIN 747 821 PAS 2.

FT DOMAIN 901 1118 HISTIDINE KINASE.

FT BINDING 323 323 CHROMOPHORE.

SQ SEQUENCE 1123 AA; 124689 MW; 3A97062A5DFB29EA CRC64;

Query Match 42.9%; Score 6; DB 1; Length 1123;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8

Db 1058 HTGGGV 1063

IIIIII

RESULT 3

PHY1_TOBAC

ID PHY1_TOBAC STANDARD; PRT: 1124 AA.

AC P33530;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phytochrome A1.

DE PHYAL.

GN Nicotiana tabacum (Common tobacco).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

OC NCBI_TaxID=4097;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=94143494; PubMed=8310074;

RX Adam E., Deak M., Kay S., Chua N.H., Nagy F.;

RT "sequence of a tobacco (Nicotiana tabacum) gene coding for type A

RT phytochrome.";

RT Plant Physiol. 101:1407-1408(1993).

CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCOVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

CC -1- SUBUNIT: HOMODIMER.

CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.

CC -----

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CC -----

CC EMBL: X66784; CAA47284.1; -.

CC InterPro: IPR003594; ATPbind_ATPase.

CC InterPro: IPR003018; GAF.

CC InterPro: IPR004359; HIS_KIN_sig.

CC InterPro: IPR003661; His_kinA.

CC InterPro: IPR001610; PAC.

CC InterPro: IPR000700; PAS-assoc_C.

CC TIGRfam: TIGR00229; sensory_box; 1.

CC PROSITE: PS50109; HIS_KIN; 1.

CC PROSITE: PS50113; PAC; 1.

CC PROSITE: PS50112; PAS; 2.

CC PROSITE: PS00245; PHYTOCHROME_1; 1.

```
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HATPase_c; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRfams; TIGR00229; sensory_box; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50113; PAC; 1.
DR PROSITE; PS50112; PAS; 2.
DR PROSITE; PS50045; PHYTOCHROME_1; 1.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 617 687 PAS 1.
FT DOMAIN 690 746 PAC.
FT DOMAIN 747 821 PAS 2.
FT DOMAIN 901 1118 HISTIDINE KINASE.
FT BINDING 323 323 CHROMOPHORE (BY SIMILARITY).
SQ SEQUENCE 1124 AA; 124296 MW; 4C2938CFE9A5F130 CRC64;

Query Match 42.9%; Score 6; DB 1; Length 1124;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
Db 1058 HTGGGV 1063
|||||

RESULT 4
YYI4_HUMAN STANDARD; PRT; 68 AA.
ID YYI4_HUMAN
AC Q9UI56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Very very hypothetical protein from MEG3 locus (protein PRO0518).
GN MEG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Fetal liver;
RA Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
RA Liu M., He F.;
RT "Functional prediction of the coding sequences of 50 new genes deduced
RT by analysis of cDNA clones from human fetal liver."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
PROBABLE FUNCTION AS A RNA.
RP Miyoshi N., Wagatsuma H., Wakana S., Shirolishi T., Nomura M.,
RA Aisaka K., Kohda T., Surani M.A., Kaneko-Ishino T., Ishino F.;
RT "Identification of an imprinted gene, Meg3/Gtl2 and its human
RT homologue MEG3, first mapped on mouse distal chromosome 12 and human
RT chromosome 14q."
RL Genes Cells 5:211-220(2000).
CC -!- CAUTION: There is no evidence of expression of this protein. The
CC MEG3 (Maternally Expressed) gene probably encodes for a RNA.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M37996; AAA29829.1; -
DR HSSP; P28827; IIRPM.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR SMART; SM00012; PTPC_DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; PARTIAL.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 13566 MW; 1FBF565A3D1F8945 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTG 5
Db 106 AKHTG 110
|||||

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CC -----
EMBL; AF090934; AAF24048.1; -
DR DR MIM; 605636; -
DR Genew; HGNC:14575; MEG3.
DR Hypothetical protein.
SQ SEQUENCE 68 AA; 7791 MW; DDC6B78EC2981B99 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 68;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGG 6
Db 22 KHTGG 26
|||||

RESULT 5
PT11_STYPL STANDARD; PRT; 114 AA.
ID PT11_STYPL
AC P28203;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Protein-tyrosine phosphatase 11 (EC 3.1.3.48) (Fragment).
GN STY 11.
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91139172; PubMed=1704870;
RA Matthews R.J., Flores E., Thomas M.L.;
RT "Protein tyrosine phosphatase domains from the protochordate Styela
RT plicata."
RL Immunogenetics 33:33-41(1991).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -----
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CC -----
EMBL; M37996; AAA29829.1; -
DR HSSP; P28827; IIRPM.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR SMART; SM00012; PTPC_DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; PARTIAL.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 13566 MW; 1FBF565A3D1F8945 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTG 5
Db 106 AKHTG 110
|||||
```

```
RESULT 6
THH2_BRANA          STANDARD;          PRT;    119 AA.
AC Q39362;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioresoxin H-type 2 (TRX-H-2).
GN THL-2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Pistill;
RX MEDLINE=96434547; PubMed=8837514;
RA Bower M.S., Matias D.D., Fernandes-Carvalho E., Mazzurco M., Gu T.,
RA Rothstein S.J., Goring D.R.;
RT "Two members of the thioresoxin-h family interact with the kinase
RT domain of a Brassica S locus receptor kinase.";
RL Plant Cell 8:1641-1650(1996).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of the active center dithiol to a disulfide.
CC The H form is known to activate a number of cytosolic enzymes (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN FLORAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT H-TYPE.
-----
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-----
DR EMBL; U59380; BAB53695.1; -
DR HSP; P10599; IERV.
DR InterPro; IPR000063; Thiores.
DR Pfam; PF00085; thiores; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFS; TIGR01068; thioresoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Redox-active center; Electron transport; Multigene family.
KW DISULFID 40 43 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 119 AA; 12949 MW; 84A9985C618B1246 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AKHTG 5
Db 111 AKHTG 115
RESULT 7
RS1A_HUMAN          STANDARD;          PRT;    129 AA.
AC P39027; P39031; Q9BV24;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S15a.
GN RPS15A.
OS Homo sapiens (Human), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
-----
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-----
DR EMBL; X84407; CAA59127.1; -
DR EMBL; AB062400; BAB93487.1; -
DR EMBL; BC001697; AAH01697.1; -
DR EMBL; BC030569; AAH30569.1; -
DR EMBL; AB007154; BAA28592.1; -
DR EMBL; X77953; CAA54918.1; -
DR PIR; S22051; S22051.
DR PIR; JC2234; JC2234.
DR Genew; HGNC:10389; RPS15A.
DR MIM; 603674; -
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00410; Ribosomal_S8; 1.
DR Prodom; PD001098; Ribosomal_S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Ribosomal protein.
FT INIT_MET 0
FT CONFLICT 39 39 V -> L (IN REF. 2).
FT CONFLICT 78 78 F -> S (IN REF. 4; AAH01697).
SQ SEQUENCE 129 AA; 14708 MW; 4D95D7EE94E3A1E2 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 58;
```

```
OX NCBI_TaxID=9606, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RA Schwabe G.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Carcinoma;
RA Mays G., Burchert-Graeve M.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RA Shichiho S., Itoh K.;
RT "Identification of immuno-peptidmics that recognized by tumor-reactive
RT CTL generated from TIL of colon cancer patients.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Eye, and Skin;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE OF 43-53 FROM N.A.
RP SPECIES=Human;
RX MEDLINE=98248690; PubMed=9582194;
RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes.";
RL Genome Res. 8:503-523(1998).
[6]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-37.
RP SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94242014; PubMed=8185605;
RA Chan Y.-L., Olivera J., Paz V., Wool I.G.;
RT "The primary structure of rat ribosomal protein S15a.";
RL Biochem. Biophys. Res. Commun. 200:1498-1504(1994).
CC -1- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS
CC 23 TO 36 DUE TO PROBABLE FRAMESHIFT ERRORS.
-----
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-----
DR EMBL; X62691; CAA44568.1; ALT_FRAME.
DR EMBL; X84407; CAA59127.1; -
DR EMBL; AB062400; BAB93487.1; -
DR EMBL; BC001697; AAH01697.1; -
DR EMBL; BC030569; AAH30569.1; -
DR EMBL; AB007154; BAA28592.1; -
DR EMBL; X77953; CAA54918.1; -
DR PIR; S22051; S22051.
DR PIR; JC2234; JC2234.
DR Genew; HGNC:10389; RPS15A.
DR MIM; 603674; -
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00410; Ribosomal_S8; 1.
DR Prodom; PD001098; Ribosomal_S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Ribosomal protein.
FT INIT_MET 0
FT CONFLICT 39 39 V -> L (IN REF. 2).
FT CONFLICT 78 78 F -> S (IN REF. 4; AAH01697).
SQ SEQUENCE 129 AA; 14708 MW; 4D95D7EE94E3A1E2 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 58;
```



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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KHTGG 6
|||||
Db 118 KHTGG 122

RESULT 8
RS1A_ICTPU
ID RS1A_ICTPU STANDARD; PRT; 129 AA.
AC Q90YQ8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S15a.
GN RPS15A.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12095691;
RA Karsi A., Patterson A., Peng J., Liu Z.-J.;
RT "Translational machinery of channel catfish: I. A transcriptomic
RT approach to the analysis of 32 40S ribosomal protein genes and their
RT expression.";
RL Gene 291:177-186(2002).
CC -!- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF402824; AAK95198.1; ALT INIT.
DR InterPro: IPR000630; Ribosomal_S8.
DR Pfam: PF00410; Ribosomal_S8; 1.
DR PROSITE: PS00053; RIBOSOMAL_S8; 1.
KW Ribosomal protein.
FT INIT_MET 0
SQ SEQUENCE 129 AA; 14613 MW; 503D34786583D7A7 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KHTGG 6
|||||
Db 118 KHTGG 122

RESULT 9
RL15_HAEIN
ID RL15_HAEIN STANDARD; PRT; 144 AA.
AC P44353;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L15.
GN RPL5 OR RPL15 OR H10797.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;

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RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: U32762; AAC22455.1; -.
DR TIGR: H10797; -.
DR InterPro: IPR001196; Ribosomal_L15.
DR Pfam: PF00256; L15; 1.
DR TIGRFAMs: TIGR01071; rplO_bact; 1.
DR PROSITE: PS00475; RIBOSOMAL_L15; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 144 AA; 15072 MW; F0CFC80684DC64C5 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TGGGV 8
|||||
Db 42 TGGGV 46

RESULT 10
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,

```

CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC
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 CC
 CC EMBL; U22516; AAA91366.1; -
 CC PIR; A35932; A35932.
 CC HSSP; P03950; 1A4Y.
 CC MGD; MGI:88022; Ang.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis,
 CC Protein synthesis inhibitor; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 145 ANGIOGENIN.
 CC MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 CC SIMILARITY).
 CC ACT_SITE 37 37 BY SIMILARITY.
 CC ACT_SITE 64 64 BY SIMILARITY.
 CC ACT_SITE 137 137 BY SIMILARITY.
 CC DISULFID 50 104 BY SIMILARITY.
 CC DISULFID 63 115 BY SIMILARITY.
 CC DISULFID 81 130 BY SIMILARITY.
 CC SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
 CC
 CC Query Match 35.7%; Score 5; DB 1; Length 145;
 CC Best Local Similarity 100.0%; Pred. No. 64; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 KHTGG 6
 CC |
 CC |
 CC |
 CC |
 CC DB 105 KHTGG 109
 CC
 CC RESULT 11
 CC PLMN_RAT
 CC ID PLMN_RAT STANDARD; PRT; 169 AA.
 CC AC Q01177;
 CC DT 01-APR-1993 (Rel. 25, Created)
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Plasminogen (EC 3.4.21.7) (Fragment).
 CC GN PLG.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=91250378; PubMed=1645711;
 CC RA Kanakas J.J.; Makker S.P.;
 CC RT Identification of the rat Heymann nephritis autoantigen (GP330) as a
 CC receptor site for plasminogen.;
 CC RL J. Biol. Chem. 266:10825-10829(1991).
 CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC
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 CC
 CC EMBL; M62832; AAA41884.1; -
 CC PIR; A40522; A40522.
 CC HSSP; P00747; LPMK.
 CC MEROPS; S01.233; -
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Ser-protease_Try.
 CC Pfam; PF00051; Kringle; 2.
 CC ProDom; PD000395; Kringle; 2.
 CC SMART; SM00130; KR; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS50070; KRINGLE_2; 2.
 CC PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.
 CC PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 CC PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 CC Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 CC Tissue remodeling; Blood coagulation; Kringle; Repeat.
 CC NON_TER 1 1
 CC DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
 CC DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
 CC DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
 CC DISULFID 34 112 BY SIMILARITY.
 CC DISULFID 55 95 BY SIMILARITY.
 CC DISULFID 83 107 BY SIMILARITY.
 CC NON_TER 169 169
 CC SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;
 CC
 CC Query Match 35.7%; Score 5; DB 1; Length 169;
 CC Best Local Similarity 100.0%; Pred. No. 72; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 4 TGGGV 8
 CC |
 CC |
 CC |
 CC |
 CC DB 115 TGGGV 119
 CC
 CC RESULT 12
 CC FMKA_ECOLI
 CC ID FMKA_ECOLI STANDARD; PRT; 181 AA.
 CC AC P04738;
 CC DT 13-AUG-1987 (Rel. 05, Created)
 CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
 CC DE K88 fimbrial protein A precursor.
 CC GN FAEC.
 CC OS Escherichia coli.
 CC OG Plasmid pF205.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Escherichia.
 CC OX NCBI_TaxID=562;

```

[1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=84264326; PubMed=6086572;
RT "K88ab gene of Escherichia coli encodes a fimbria-like protein
distinct from the K88ab fimbrial adhesin.";
RL J. Bacteriol. 159:482-487(1984).
[2]
RP SEQUENCE OF 160-181 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86176742; PubMed=2870470;
RA Mooi F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;
RT "Regulation and structure of an Escherichia coli gene coding for an
outer membrane protein involved in export of K88ab fimbrial
subunits.";
RL Nucleic Acids Res. 14:2443-2457(1986).
-!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
-!- SUBUNIT: K88 FIMBRIA, 0.1-1 MICROMETER IN LENGTH AND 7 NANOMETERS
IN DIAMETER, IS COMPOSED OF ABOUT 100 IDENTICAL SUBUNITS.
-!- SUBCELLULAR LOCATION: PREDOMINANTLY LOCATED AT THE TIP OF THE
FIMBRIAE.
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-----
EMBL; X00940; CAA25454.1; -.
DR EMBL; X03675; CAA27312.1; -.
KW Fimbria; Signal; Plasmid.
FT SIGNAL 1 21
FT CHAIN 22 181 K88 FIMBRIAL PROTEIN A.
FT DISULFID 37 84 PROBABLE.
SQ SEQUENCE 181 AA; 13066 MW; 44EA049DA025D011 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
DB 14 TGGGV 18

RESULT 13
VP50_BPAPS
ID VP50_BPAPS STANDARD; PRT; 184 AA.
AC Q91P8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative protein P50.
GN 50
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC unclassified Podoviridae.
OX NCBI_TaxID=106199;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
RA van der Wilk F., Dullemans A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113(1999).
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-----
DR EMBL; AF157835; AAF03993.1; -.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 20416 MW; EB705FA272B6768F CRC64;

Query Match 35.7%; Score 5; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
DB 160 TGGGV 164

RESULT 14
AROK_SYNY3
ID AROK_SYNY3 STANDARD; PRT; 189 AA.
AC P72796;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN AROK OR SLL1669.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC -!- SIMILARITY: BELONGS TO THE SHIKIMATE KINASE FAMILY.
-----
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-----
EMBL; D90300; BAA16811.1; -.
DR HSP; P10880; ISHK.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT NP_BIND 19 26 ATP (POTENTIAL).
SQ SEQUENCE 189 AA; 20697 MW; 41727D4EC6E585D9 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Fri Mar 14 09:39:59 2003

QY 4 TGGGV 8
 |||||
 Db 88 TGGGV 92

RESULT 15
 VG23_BPMD2
 ID VG23_BPMD2 STANDARD; PRT; 197 AA.
 AC Q38362; O64217;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Major tail protein GP23 (Major coat protein).
 GN 23.
 OS Mycobacteriophage D29.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC unclassified Siphoviridae.
 OX NCBI_TaxID=28369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shramm Y., Wyse J., Mink S., Suissa M., Kuhn J.;
 RT "Cloning, sequence and expression of the gene coding for the major
 RL coat protein of Mycobacteriophage D29.";
 RN Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98300335; PubMed=9636706;
 RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
 RT "Genome structure of mycobacteriophage D29: implications for phage
 evolution.";
 RL J. Mol. Biol. 279:143-164(1998).
 CC -----
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 CC -----
 DR EMBL; X70353; CANA9811.1; -.
 KW Coats protein.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT CONFLICT 25 25 H -> P (IN REF. 1).
 FT CONFLICT 176 176 K -> E (IN REF. 1).
 SQ SEQUENCE 197 AA; 21183 MW; 548580298149564D CRC64;

Query Match 35.7%; Score 5; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. NO. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DPIDY 14
 |||||
 Db 86 DPIDY 90

Search completed: March 13, 2003, 15:32:06
 Job time : 9.53846 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:28:09 ; Search time 26.9231 Seconds
(without alignments)
107.144 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 14

Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rvirus:*
- 16: sp-bacteriap:*
- 17: sp-archeap:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	42.9	114	10 Q9SVK9	Q9svk9 arabidopsis
2	6	42.9	131	4 Q8WY0	Q8wy0 homo sapien
3	6	42.9	164	16 Q98HY2	Q98hy2 rhizobium l
4	6	42.9	181	13 Q91665	Q91665 xenopus lae
5	6	42.9	192	5 Q9N6S3	Q9n6s3 leishmania
6	6	42.9	193	16 Q9PDE3	Q9pde3 xylella fas
7	6	42.9	381	16 Q9DC19	Q9dc19 rhizobium l
8	6	42.9	436	16 Q9K6F3	Q9k6f3 bacillus ha
9	6	42.9	474	16 Q98MD0	Q98md0 rhizobium l
10	6	42.9	502	16 Q8Y012	Q8y012 ralstonia s
11	6	42.9	511	4 Q9BUL4	Q9bul4 homo sapien
12	6	42.9	511	11 Q9DBF1	Q9dbf1 mus musculu
13	6	42.9	614	16 Q98212	Q98212 rhizobium l
14	6	42.9	1068	10 Q9FF3	Q9fff3 arabidopsis
15	6	42.9	1123	10 Q41331	Q41331 lycopersico
16	5	35.7	46	15 Q80812	Q80812 human t-lym

17	5	35.7	52	12 Q98809	Q98809 yam mosaic
18	5	35.7	53	15 Q992L1	Q992l1 human t-cel
19	5	35.7	57	10 Q9SAT4	Q9sat4 nicotiana t
20	5	35.7	71	5 Q9NAJ8	Q9naj8 caenorhabdi
21	5	35.7	72	10 Q9IX10	Q9ix10 arabidopsis
22	5	35.7	75	17 Q26464	Q26464 methanobact
23	5	35.7	77	15 Q9198	Q9198 human t-lym
24	5	35.7	78	5 Q8WR25	Q8wr25 anopheles g
25	5	35.7	85	11 Q9JHY3	Q9jhy3 mus musculu
26	5	35.7	90	16 Q931P1	Q931p1 staphylococ
27	5	35.7	94	5 Q9VM00	Q9vm00 drosophila
28	5	35.7	101	8 Q08712	Q08712 nicotiana s
29	5	35.7	102	2 Q9LCA9	Q9lca9 rhodocycilus
30	5	35.7	103	16 Q9FJ66	Q9fj66 streptomyce
31	5	35.7	107	2 Q51490	Q51490 pseudomonas
32	5	35.7	109	10 Q9FJ20	Q9fj20 arabidopsis
33	5	35.7	110	11 Q9D905	Q9d9u5 mus musculu
34	5	35.7	111	5 Q8WPS3	Q8wps3 trypanosoma
35	5	35.7	117	2 Q9RH52	Q9rh52 streptomyce
36	5	35.7	117	11 Q9D466	Q9d466 mus musculu
37	5	35.7	118	6 Q95JT4	Q95jt4 macaca fasc
38	5	35.7	119	16 Q9RF97	Q9rf97 bacillus ha
39	5	35.7	122	10 Q9LW24	Q9lw24 arabidopsis
40	5	35.7	124	8 Q35862	Q35862 schistosoma
41	5	35.7	127	13 Q90YQ8	Q90yq8 ictalurus p
42	5	35.7	128	8 Q954T6	Q954t6 dugesia pol
43	5	35.7	130	4 Q9BV24	Q9bv24 homo sapien
44	5	35.7	130	5 Q77395	Q77395 plasmodium
45	5	35.7	130	13 Q91A74	Q91a74 paralichthy

ALIGNMENTS

RESULT 1

Q9SVK9 ID Q9SVK9 PRELIMINARY; PRT; 114 AA.
AC Q9SVK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical 12.9 kDa protein.
GN F18B3.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M., F.,
RA Meves H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
RA Salanoubat M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049862; CAB42919.1; -;
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12923 MW; F8156E1465887DBB CRC64;

Query Match 42.9%; Score 6; DB 10; Length 114;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGVWDP 11

|||||

Db 99 GGVWDP 104

RESULT 2

Q8WY0

ID	Q8WY0	PRELIMINARY;	PRT;	131 AA.
AC	Q8WY0;			
DT	01-MAR-2002 (TReMBLrel. 20, Created)			
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)			
DE	Hypothetical 13.9 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,			
RA	Wan D.F., Gu J.R.;			
RT	"Novel human cDNA clones with function of inhibiting cancer cell			
RT	growth."			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF289615; AAL5799.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 131 AA; 13879 MW; BID6A5917F3608ED CRC64;			
	Query Match	42.9%;	Score 6; DB 4; Length 131;	
	Best Local Similarity	100.0%;	Pred. No. 21;	
	Matches	6; Conservative	0; Mismatches	0; Indels
	Gaps	0;		
QY	4 TGGGVW 9			
Db	29 TGGGVW 34			
	RESULT 3			
Q98HY2	PRELIMINARY;	PRT;	164 AA.	
ID	Q98HY2			
AC	Q98HY2;			
DT	01-OCT-2001 (TReMBLrel. 18, Created)			
DT	01-OCT-2001 (TReMBLrel. 18, Last sequence update)			
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)			
DE	Hypothetical protein ms18626.			
GN	MS18626.			
OS	Rhizobium loti (Mesorhizobium loti).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Phyllobacteriaceae; Mesorhizobium.			
OX	NCBI_TaxID=381;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MAFF303099;			
RX	MEDLINE=21082930; PubMed=11214968;			
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,			
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,			
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,			
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,			
RA	Takeuchi C., Yamada M., Tabata S.;			
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium			
RT	Mesorhizobium loti."			
RL	DNA Res. 7:331-338(2000).			
DR	EMBL; AP003000; BAB49734.1; -			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 164 AA; 16680 MW; 8489A02A3C55D76D CRC64;			
	Query Match	42.9%;	Score 6; DB 16; Length 164;	
	Best Local Similarity	100.0%;	Pred. No. 26;	
	Matches	6; Conservative	0; Mismatches	0; Indels
	Gaps	0;		
QY	1 AKHTGG 6			
Db	90 AKHTGG 95			
	RESULT 4			
Q91665	PRELIMINARY;	PRT;	181 AA.	
ID	Q91665			
AC	Q91665;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			

DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)			
DE	CTX (Fragment).			
GN	Gl.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FF;			
RX	MEDLINE=96210130; PubMed=8625968;			
RA	Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M.,			
RA	Du Pasquier L.;			
RT	"CTX, a novel molecule specifically expressed on the surface of			
RT	cortical thymocytes in Xenopus."			
RL	Eur. J. Immunol. 26:780-791(1996).			
DR	EMBL; U43393; AAC59860.1; -			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003600; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00410; IG-like; 1.			
FT	NON_TER 1			
SQ	SEQUENCE 181 AA; 19380 MW; 6A558F6C824EDC16 CRC64;			
	Query Match	42.9%;	Score 6; DB 13; Length 181;	
	Best Local Similarity	100.0%;	Pred. No. 28;	
	Matches	6; Conservative	0; Mismatches	0; Indels
	Gaps	0;		
QY	3 HTGGGV 8			
Db	154 HTGGGV 159			
	RESULT 5			
Q9N6S3	PRELIMINARY;	PRT;	192 AA.	
ID	Q9N6S3			
AC	Q9N6S3;			
DT	01-OCT-2000 (TReMBLrel. 15, Created)			
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)			
DE	L7535.14.			
GN	L822.2 OR L7535.14.			
OS	Leishmania major.			
OC	Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.			
OX	NCBI_TaxID=5664;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRIEDLIN;			
RA	Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,			
RA	Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRIEDLIN;			
RA	Myler P.J.;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC005893; AAF31031.1; -			
DR	EMBL; AC005767; AAF27953.1; -			
DR	EMBL; AC005766; AAF28379.1; -			
SQ	SEQUENCE 192 AA; 19650 MW; 0CE9460B1FB5A9C4 CRC64;			
	Query Match	42.9%;	Score 6; DB 5; Length 192;	
	Best Local Similarity	100.0%;	Pred. No. 30;	
	Matches	6; Conservative	0; Mismatches	0; Indels
	Gaps	0;		
QY	3 HTGGGV 8			
Db	129 HTGGGV 134			

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RESULT 6
Q9PDE3 ID Q9PDE3 PRELIMINARY; PRT; 193 AA.
AC Q9PDE3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Disulfide oxidoreductase.
GN XF1436.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Froime M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Slyks M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003973; AAF84245.1; -.
DR InterPro; IPR001853; DSSA.
DR InterPro; IPR000063; Thiorid.
DR Pfam; PF01323; DSSA; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 193 AA; 21305 MW; 552DC6D86B4F555D CRC64;

Query Match 42.9%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDP 11
Db 68 GGWDP 73

RESULT 7
Q98C19 ID Q98C19 PRELIMINARY; PRT; 381 AA.
AC Q98C19;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical protein mlr5331.
GN MLR5331.
OS Rhizobium loti (Mesorhizobium loti).

Query Match 42.9%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDP 11
Db 68 GGWDP 73

RESULT 8
Q9K6F3 ID Q9K6F3 PRELIMINARY; PRT; 436 AA.
AC Q9K6F3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH oxidase (nox).
GN BH3776.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -/- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AF001519; BAB07495.1; -.
DR HSSP; P37062; INHP.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR001103; Pyridine_redox_2.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004099; Pyr_redox_dim.
DR Pfam; PF00070; pyr_redox; 1.

```

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Yamada S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AF003006; BAB51802.1; -.
 DR InterPro; IPR000160; GGDEF.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-associ_C.
 DR InterPro; IPR000014; PAS_domain.
 DR InterPro; IPR003975; Shal_channel.
 DR Pfam; PF00990; GGDEF; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01497; SHALCHANNEL.
 DR SMART; SM00267; DUF1; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 1.
 DR TIGRFAMs; TIGR00254; GGDEF; 1.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 381 AA; 41817 MW; 7CDACEER8F6E32B4 CRC64;

Query Match 42.9%; Score 6; DB 16; Length 381;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGWVD 10
 Db 138 GGWVD 143

RESULT 8
 Q9K6F3 ID Q9K6F3 PRELIMINARY; PRT; 436 AA.
 AC Q9K6F3;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE NADH oxidase (nox).
 GN BH3776.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -/- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL; AF001519; BAB07495.1; -.
 DR HSSP; P37062; INHP.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR000205; NAD_binding.
 DR InterPro; IPR001103; Pyridine_redox_2.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF00070; pyr_redox; 1.

DE DNA segment, Chr 18, Wayne state University 181, expressed (Unknown)

DE (Protein for MGC:18699).

GN D18WSu181E.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gyojbori T., Bono H., Kasakawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Salivary Gland;

RA Strausberg R.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

DR EMBL; AK004991; BAB23726.1; -.

DR EMBL; BC012407; AAH12407.1; -.

DR MGD; MGI:107847; D18WSu181E.

DR InterPro; IPR002086; Aldehyde_dehydr.

DR Pfam; PF00171; aldedh; 1

DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.

DR Oxidoreductase.

KW OXIDOREDUCTASE.

SQ SEQUENCE 511 AA; 53644 MW; 37952CEC7C5F3A85 CRC64;

Query Match 42.9%; Score 6; DB 11; Length 511;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7

DB 472 KHTGGG 477

RESULT 13

Q98212 PRELIMINARY; PRT; 614 AA.

AC Q98212;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE DNA methyltransferase.

GN ML19056.

OS Rhizobium loti (Mesorhizobium loti).

OG Plasmid pMla.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003015; BAB54474.1; -.

DR InterPro; IPR001091; CN4_MetTransf.

DR InterPro; IPR002295; D21N6_mtfase.

DR InterPro; IPR002941; N6/N4_Mtase.

DR InterPro; IPR002052; N6_Mtase.

DR Pfam; PF01553; N6/N4_Mcase; 1.

DR PRINTS; PR00506; D21N6MTFRASE.

DR PRINTS; PR00508; S21N4MTFRASE.

DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.

KW Transferase; Methyltransferase; Plasmid; Complete proteome.

SQ SEQUENCE 614 AA; 69230 MW; 14507EDDAE0FBCE CRC64;

Query Match 42.9%; Score 6; DB 16; Length 614;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8

DB 116 HTGGGV 121

RESULT 14

Q9FFF3 PRELIMINARY; PRT; 1068 AA.

AC Q9FFF3;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Low density lipoprotein B-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Magnoliophyta; Streptophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=97471969; PubMed=9330910;

RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,

RA Miyajima N., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned pl clones.";

RL DNA Res. 4:215-230(1997).

DR EMBL; AB005242; BAB09597.1; -.

KW Lipoprotein.

SQ SEQUENCE 1068 AA; 118802 MW; D696E592DD4B991C CRC64;

Query Match 42.9%; Score 6; DB 10; Length 1068;

Best Local Similarity 100.0%; Pred. No. 1.4e-02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGVW 9

DB 484 TGGGVW 489

RESULT 15

Q41331 PRELIMINARY; PRT; 1123 AA.

ID Q41331;

AC Q41331;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE PHYA protein (Phytochrome A).

GN GN

OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. UC82B;
RX MEDLINE=96346008; PubMed=9681030;
RA Lazarova G.I., Cordonnier-Pratt M.M., Kerckhoffs L.J.,
RA Brandstadter J., Matsui M., Pratt L.H., Kendrick R.E.;
RT "Molecular analysis of PHA in wild-type and phytochrome A-deficient
mutants of tomato."
RL Plant J. 14:653-662(1998).
RN [2]
RP SEQUENCE OF 165-277 FROM N.A.
RC STRAIN=UC-82B;
RX MEDLINE=96191281; PubMed=8616214;
RA Hauser B.A., Cordonnier-Pratt M.M., Daniel-Vedele F., Pratt L.H.;
RT "The phytochrome gene family in tomato includes a novel subfamily."
RL Plant Mol. Biol. 29:1143-1155(1995).
DR EMBL; AJ001916; CAA05089.1; -
DR EMBL; U32345; AAC49297.1; -
DR EMBL; AJ001915; CAA05088.1; -
DR EMBL; AJ001913; CAA05086.1; -
DR EMBL; AJ001914; CAA05087.1; -
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRfams; TIGR00229; sensory_box; 1.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Phytochrome.
SQ SEQUENCE 1123 AA; 124659 MW; 0432ADCCCFDF0FB1 CRC64;

Query Match 42.9%; Score 6; DB 10; Length 1123;
Best Local Similarity 100.0%; Pred. No. 1.5e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 HTGGGV 8
| | | | |
Db 1058 HTGGGV 1063

Search completed: March 13, 2003, 15:33:05
Job time : 29.9231 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 6.40769 Seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	85	100.0	121	22	AAE12706 Human PH1 Fab anti
2	85	100.0	381	22	AAE12707 Human b1vPH1-IL-2
3	85	100.0	451	22	AAE12715 Human recombinant
4	84	98.8	14	22	AAE12764 Human PH1 Fab anti
5	82	96.5	14	22	AAE12758 Human PH1 Fab anti
6	81	95.3	14	22	AAE12770 Human PH1 Fab anti
7	80	94.1	14	22	AAE12748 Human PH1 Fab anti
8	80	94.1	14	22	AAE12769 Human PH1 Fab anti
9	79	92.9	14	22	AAE12771 Human PH1 Fab anti
10	78	91.8	14	22	AAE12719 Human PH1 Fab anti

11	78	91.8	14	22	AAE12740 Human PH1 Fab anti
12	78	91.8	14	22	AAE12741 Human PH1 Fab anti
13	78	91.8	14	22	AAE12759 Human PH1 Fab anti
14	78	91.8	14	22	AAE12762 Human PH1 Fab anti
15	77	90.6	14	22	AAE12749 Human PH1 Fab anti
16	77	90.6	14	22	AAE12754 Human PH1 Fab anti
17	77	90.6	14	22	AAE12773 Human PH1 Fab anti
18	76	89.4	14	22	AAE12746 Human PH1 Fab anti
19	76	89.4	14	22	AAE12747 Human PH1 Fab anti
20	76	89.4	14	22	AAE12753 Human PH1 Fab anti
21	76	89.4	14	22	AAE12774 Human PH1 Fab anti
22	75	88.2	14	22	AAE12742 Human PH1 Fab anti
23	75	88.2	14	22	AAE12743 Human PH1 Fab anti
24	75	88.2	14	22	AAE12768 Human PH1 Fab anti
25	74	87.1	14	22	AAE12750 Human PH1 Fab anti
26	74	87.1	14	22	AAE12772 Human PH1 Fab anti
27	73	85.9	14	22	AAE12718 Human PH1 Fab anti
28	73	85.9	14	22	AAE12744 Human PH1 Fab anti
29	73	85.9	14	22	AAE12751 Human PH1 Fab anti
30	73	85.9	14	22	AAE12756 Human PH1 Fab anti
31	73	85.9	14	22	AAE12766 Human PH1 Fab anti
32	73	85.9	16	22	AAE12735 Human PH1 Fab anti
33	72	84.7	14	22	AAE12755 Human PH1 Fab anti
34	72	84.7	14	22	AAE12761 Human PH1 Fab anti
35	72	84.7	14	22	AAE12763 Human PH1 Fab anti
36	72	84.7	14	22	AAE12765 Human PH1 Fab anti
37	72	84.7	14	22	AAE12767 Human PH1 Fab anti
38	72	84.7	16	22	AAE12734 Human PH1 Fab anti
39	71	83.5	16	22	AAE12736 Human PH1 Fab anti
40	70	82.4	14	22	AAE12717 Human PH1 Fab anti
41	70	82.4	14	22	AAE12720 Human PH1 Fab anti
42	70	82.4	14	22	AAE12739 Human PH1 Fab anti
43	69	81.2	14	22	AAE12738 Human PH1 Fab anti
44	69	81.2	14	22	AAE12757 Human PH1 Fab anti
45	68	80.0	14	22	AAE12745 Human PH1 Fab anti

ALIGNMENTS

```

RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX
AC AAE12706;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody variable heavy chain region (VH).
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT Location/Qualifiers
FT 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
FT /note= "VH domain"
FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

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DR N-PSDB; AAD20745.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX
 PS Claim 12; Page 106-108; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (19) heavy chain region (variable VH and CH constant heavy chain).
 XX
 SQ Sequence 451 AA;

Query Match 100.0%; Score 85; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

|||||||

Db 97 AKHTGGGVWDPIDY 110

RESULT 4

AAE12764

ID AAE12764 standard; peptide; 14 AA.

XX AAE12764;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #31.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX /label= Framework_region_3

XX Region 3..14

XX /label= Complementarity_determining_region_3

XX WO200175110-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

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XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 123; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 98.8%; Score 84; DB 22; Length 14;

Best Local Similarity 92.9%; Pred. No. 5.8e-07;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

|||||||

Db 1 AKHTGGGVWDPIDY 14

RESULT 5

AAE12758

ID AAE12758 standard; peptide; 14 AA.

XX AAE12758;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #25.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX /label= Framework_region_3

XX Region 3..14

XX /label= Complementarity_determining_region_3

XX WO200175110-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX

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XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

XX Example 2; Page 122; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating MUC1-expressing

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX

XX Sequence 14 AA;

SQ

Query Match 96.5%; Score 82; DB 22; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.2e-06;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPIDY 14

DB 1 AKHTGGGVNDPIDY 14

|||||

RESULT 6

AAE12770

ID AAE12770 standard; peptide; 14 AA.

XX

AC AAE12770;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #37.

XX

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FH Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

XX 11-OCT-2001.

XX

XX 30-MAR-2001; 2001WO-US10589.

PF

XX 30-MAR-2000; 2000US-0538913.

PR

XX (DYAX-) DYAX CORP.

PA

XX Hoogenboom HRJM, Henderixx MPG;

PI

XX WPI; 2001-626437/72.

DR

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 125; 126pp; English.

XX

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX

XX Sequence 14 AA;

SQ

Query Match 95.3%; Score 81; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGGVNDPIDY 14

DB 2 KHTGGGVNDPIDY 14

|||||

RESULT 7

AAE12748

ID AAE12748 standard; peptide; 14 AA.

XX

AC AAE12748;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

XX

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FH Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

XX 11-OCT-2001.

XX

XX 30-MAR-2001; 2001WO-US10589.

PF

XX 30-MAR-2000; 2000US-0538913.

PR

XX (DYAX-) DYAX CORP.

PA

XX Hoogenboom HRJM, Henderixx MPG;

PI

XX WPI; 2001-626437/72.

DR

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

XX Example 2; Page 120; 126pp; English.

PS

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PHI Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;

Query Match 94.1%; Score 80; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.6e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
 |||||:|||||:|
 Db 1 AKHTGGGVWDPIN 14

RESULT 8
 AAEL2769
 ID AAEL2769 standard; peptide; 14 AA.
 AC AAEL2769;

DT 04-JAN-2002 (first entry)
 DE Human PHI Fab antibody VH region FR3-CDR3 variant #36.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PHI antibody; variant.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2 /label= Framework_region_3
 FT Region 3..14 /label= Complementarity_determining_region_3
 FT
 FT
 FT

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PS Example 2; Page 124; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PHI Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;

Query Match 94.1%; Score 80; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.6e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
 |||||:|||||:|
 Db 1 AKHTGGGVWNPIDY 14

RESULT 9
 AAEL2771
 ID AAEL2771 standard; peptide; 14 AA.
 AC AAEL2771;

DT 04-JAN-2002 (first entry)

XX Human PHI Fab antibody VH region FR3-CDR3 variant #38.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PHI antibody; variant.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2 /label= Framework_region_3
 FT Region 3..14 /label= Complementarity_determining_region_3
 FT
 FT
 FT

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PS Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 92.9%; Score 79; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 3.7e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AKHTGGVWDPIDY 14
 DB 1 AKHTGAGVWDPIDY 14
 RESULT 10
 AAE12719
 ID AAE12719 standard; peptide; 14 AA.
 AC AAE12719;
 XX
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #3.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 XX WO200175110-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 XX (DYAX-) DYAX CORP.
 XX
 XX Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 2; Page 75; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and x-ray film.

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AKHTGGVWDPIDY 14
 DB 1 AKHTGGVWDPIDY 14
 RESULT 11
 AAE12740
 ID AAE12740 standard; peptide; 14 AA.
 AC AAE12740;
 XX
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 XX WO200175110-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 XX (DYAX-) DYAX CORP.
 XX
 XX Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 119; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and x-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPID 13
 | | | | | | | | | | | | | | |
 Db 1 AKHTGGGVNDPID 13

RESULT 12
 AAEL12741
 ID AAEL12741 standard; peptide; 14 AA.
 XX
 AC AAEL12741;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #8.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PD 30-MAR-2001; 2001WO-US10589.
 XX
 PF 30-MAR-2000; 2000US-0538913.
 XX
 PR (DYAX-) DYAX CORP.
 XX
 PA Hoogenboom HRJM, Henderikx MPG;
 XX
 PI WPI; 2001-626437/72.
 XX
 DR Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 119; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and x-ray film.
 XX MUC1-specific binding member is useful for treating cancer, preferably
 XX adenocarcinoma, in an individual, where the cancer is present in tissue
 XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX binding member is useful for diagnosing and imaging MUC1-expressing

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPID 14
 | | | | | | | | | | | | | | |
 Db 1 AKHTGGGVNDPID 14

RESULT 13
 AAEL12759
 ID AAEL12759 standard; peptide; 14 AA.
 XX
 AC AAEL12759;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #26.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PD 30-MAR-2001; 2001WO-US10589.
 XX
 PF 30-MAR-2000; 2000US-0538913.
 XX
 PR (DYAX-) DYAX CORP.
 XX
 PA Hoogenboom HRJM, Henderikx MPG;
 XX
 PI WPI; 2001-626437/72.
 XX
 DR Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 122; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and x-ray film.
 XX MUC1-specific binding member is useful for treating cancer, preferably
 XX adenocarcinoma, in an individual, where the cancer is present in tissue
 XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 XX
 SQ Sequence 14 AA;

Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIY 14
 |||||
 Db 1 AKHTGGGVWDPIY 14

RESULT 14
 AAEL2762
 ID AAEL2762 standard; peptide; 14 AA.
 XX
 AC AAEL2762;
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #29.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 123; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 The binding of MUC1-specific binding member to MUC1 is detected by a
 detection method selected from enzyme-linked immunosorbent assay,
 magnetic resonance imaging, scintillation counting, and X-ray film.
 MUC1-specific binding member is useful for treating cancer, preferably
 adenocarcinoma, in an individual, where the cancer is present in tissue
 of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 binding member is useful for diagnosing and imaging MUC1-expressing
 cancer cells and tissues, for purifying or isolating non-glycosylated,
 underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 XX
 SQ Sequence 14 AA;

Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPID 13
 |||||
 Db 1 AKHTGGGVWDPID 13

RESULT 15
 AAEL2749
 ID AAEL2749 standard; peptide; 14 AA.
 XX
 AC AAEL2749;
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #16.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 120; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 The binding of MUC1-specific binding member to MUC1 is detected by a
 detection method selected from enzyme-linked immunosorbent assay,
 magnetic resonance imaging, scintillation counting, and X-ray film.
 MUC1-specific binding member is useful for treating cancer, preferably
 adenocarcinoma, in an individual, where the cancer is present in tissue
 of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 binding member is useful for diagnosing and imaging MUC1-expressing
 cancer cells and tissues, for purifying or isolating non-glycosylated,
 underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX
SQ

Sequence 14 AA;

Query Match 90.6%; Score 77; DB 22; Length 14;

Best Local Similarity 85.7%; Pred. No. 7.9e-06;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPIDY 14

I:|||||I:|

Db 1 ARHTGGGVNDPINY 14

Search completed: March 13, 2003, 15:14:41

Job time : 6.40769 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 2.15385 Seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 85
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCITUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	55.3	573	1	US-08-200-512-2
2	43.5	51.2	774	4	US-09-346-237-8
3	42	49.4	421	3	US-09-032-372-3
4	41	48.2	160	4	US-09-370-838-189
5	40	47.1	123	6	5171845-1
6	40	47.1	544	4	US-08-687-590-30
7	38	44.7	28	3	US-08-978-741-14
8	38	44.7	28	4	US-09-333-729A-14
9	38	44.7	109	4	US-09-134-001C-3523
10	38	44.7	328	4	US-09-300-672-2
11	38	44.7	397	3	US-08-978-741-6
12	38	44.7	397	4	US-09-333-729A-7
13	38	44.7	447	3	US-08-508-761B-6
14	38	44.7	738	1	US-07-985-458-3
15	38	44.7	941	4	US-09-074-658-75
16	38	44.7	944	2	US-08-867-941-23
17	38	44.7	944	4	US-08-867-941-24
18	38	44.7	944	4	US-09-074-658-23
19	38	44.7	944	4	US-09-074-658-24
20	37	43.5	409	3	US-09-075-215A-17
21	37	43.5	720	4	US-09-296-284-25
22	37	43.5	754	4	US-09-296-284-4
23	37	43.5	848	4	US-08-976-255-10
24	37	43.5	983	4	US-09-134-001C-3814
25	36	42.4	20	4	US-08-992-877-65
26	36	42.4	79	2	US-08-499-676A-13
27	36	42.4	152	3	US-08-916-043-2

28	36	42.4	152	6	5212286-6	Patent No. 5212286
29	36	42.4	300	4	US-09-134-001C-4385	Sequence 4385, Ap
30	36	42.4	384	3	US-09-071-434-3	Sequence 3, Appli
31	36	42.4	627	2	US-08-466-589-6	Sequence 6, Appli
32	36	42.4	627	2	US-08-700-636-6	Sequence 6, Appli
33	36	42.4	627	3	US-08-467-574-6	Sequence 6, Appli
34	36	42.4	627	4	US-09-217-345-6	Sequence 6, Appli
35	36	42.4	627	4	US-08-487-596-6	Sequence 6, Appli
36	36	42.4	881	4	US-09-413-814-44	Sequence 44, Appli
37	36	42.4	1090	4	US-09-346-237-5	Sequence 5, Appli
38	36	42.4	1096	4	US-09-346-237-6	Sequence 6, Appli
39	35.5	41.8	579	1	US-08-126-564A-31	Sequence 31, Appl
40	35.5	41.8	579	5	PCT-US94-09143-31	Sequence 31, Appl
41	35.5	41.8	659	1	US-08-240-049B-16	Sequence 16, Appl
42	35.5	41.8	659	1	US-08-259-148A-20	Sequence 20, Appl
43	35.5	41.8	659	1	US-08-484-054-20	Sequence 20, Appl
44	35.5	41.8	659	2	US-07-876-941A-20	Sequence 20, Appl
45	35.5	41.8	659	4	US-08-477-292-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-200-512-2
; Sequence 2, Application US/08200512
; Patent No. 5674718
; GENERAL INFORMATION:
; APPLICANT: BRIAND, MICHELLE
; APPLICANT: PLESIAT, PATRICK
; TITLE OF INVENTION: DNA SEGMENTS AND TRANS-
; TITLE OF INVENTION: FORMED MICROORGANISMS COMPRISING THE DELTA'-
; TITLE OF INVENTION: DEHYDROGENASE GENE, AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,512
; FILING DATE: 17-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,660
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00094
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A.
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1116-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: (212) 661-8002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PROTEIN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: PSEUDOMONAS TESTOSTERONI
FEATURE: (R, repeat if necessary)
NAME/KEY: PROTEIN
LOCATION: 1...573
OTHER INFORMATION: /note = Delta
OTHER INFORMATION: dehydrogenase protein of Pseudomonas
OTHER INFORMATION: testosterone
US-08-200-512-2

Query Match 55.3%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 7.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14
:|||:| | :|
Db 47 SGGGIWPLNY 57

RESULT 2

US-09-346-237-8
Sequence 8, Application US/09346237A

Patent No. 6265197
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629,200-US
CURRENT APPLICATION NUMBER: US/09/346,237A
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 60/094,353
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8

LENGTH: 774

TYPE: PRT

ORGANISM: Favobacterium odoratum

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(774)

OTHER INFORMATION: Isoamylase

US-09-346-237-8

Query Match 51.2%; Score 43.5; DB 4; Length 774;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTG-GGVWDPID 13
||| ||| | |
Db 329 HTGEGGAWSPD 340

RESULT 3

US-09-032-372-3
Sequence 3, Application US/09032372

Patent No. 6008337

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Yue, Henry

APPLICANT: Lal, Preeti

TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0478 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLANNOT23
CLONE: 1693222

US-09-032-372-3

Query Match 49.4%; Score 42; DB 3; Length 421;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDP 11
||| | | | | |
Db 274 AKHTGGGVWDP 284

RESULT 4

US-09-370-838-189
Sequence 189, Application US/09370838

Patent No. 6444425

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Roadoh

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

FILE REFERENCE: 210121.475C1

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: US 09/285,323

EARLIER FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 189

LENGTH: 160

TYPE: PRT

ORGANISM: Homo sapien

US-09-370-838-189

Query Match 48.2%; Score 41; DB 4; Length 160;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
||| | | | | |
Db 149 AKHTGGGVW 157

RESULT 5
5171845-1
; Patent No. 5171845
; APPLICANT: SPIK, GENEVIEVE; TARTAR, ANDRE; MONTREUIL, JEAN
; TITLE OF INVENTION: PROTEIN HOMOLOGUE OF HUMAN ANGIOGENIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392.977
; FILING DATE: 18-NOV-1988
; SEQ ID NO: 1:
; LENGTH: 123
5171845-1

Query Match 47.1%; Score 40; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
|| ||| |
DB 85 GGGVWDPIDY 94

RESULT 6
US-08-687-590-30
; Sequence 30, Application US/08687590
; Patent No. 6255070
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith Robert
; APPLICANT: Kubota, Hiroshi
; APPLICANT: Ashworth, Alan
; TITLE OF INVENTION: Folding Proteins
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,590
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00192
; FILING DATE: 31-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401791.0
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9418234.2
; FILING DATE: 09-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 084619-00000005
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-687-590-30

Query Match 47.1%; Score 40; DB 4; Length 544;
Best Local Similarity 46.2%; Pred. No. 95;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 AKHTGGGVWDPID 13
|:| |:| |:
DB 466 ARHAQGGMWYGV 478

RESULT 7
US-08-978-741-14
; Sequence 14, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
; APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Fucosyltransferase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,741
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792498
; FILING DATE: 31
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1041P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-978-741-14

Query Match 44.7%; Score 38; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVWDPIDY 14
| | | | |
DB 8 HMPAGSWDPAGY 19

RESULT 8
US-09-333-729A-14
; Sequence 14, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041P1-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 14
; LENGTH: 28

;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid insert encoded protein.
; NAME/KEY: unsure
; LOCATION: 23, 25
; OTHER INFORMATION: unknown amino acid
US-09-333-729A-14

Query Match 44.7%; Score 38; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVWDPIDY 14
| | | | |
DB 8 HMPAGSWDPAGY 19

RESULT 9
US-09-134-001C-3523
; Sequence 3523, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3523
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3523

Query Match 44.7%; Score 38; DB 4; Length 109;
Best Local Similarity 45.5%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPID 13
| | | | |
DB 27 HTLEGIWHPVE 37

RESULT 10
US-09-300-672-2
; Sequence 2, Application US/09300672
; Patent No. 6248937
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-Li
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
; FILE REFERENCE: 480.89(HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Arabidopsis
US-09-300-672-2

Query Match 44.7%; Score 38; DB 4; Length 328;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 HTGGGVWDPID 13
| | | | |
DB 311 HNWGSIWDFID 321

RESULT 11
US-08-978-741-6
; Sequence 6, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
; APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Fucosyltransferase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,741
; FILING DATE: 26-No. 6100076-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792498
; FILING DATE: 31
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1041P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-978-741-6

Query Match 44.7%; Score 38; DB 3; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVWDPIDY 14
| | | | |
DB 32 HMPAGSWDPAGY 43

RESULT 12
US-09-333-729A-7
; Sequence 7, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041P1-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 7
; LENGTH: 397

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid insert encoded protein.
US-09-333-729A-7

Query Match 44.7%; Score 38; DB 4; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVDPIDY 14
| | | | |
Db 32 HMPAGSWDPAGY 43

RESULT 13
US-08-508-761B-6
; Sequence 6, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Arnel
; APPLICANT: Purification, Relano
; APPLICANT: Duchiron, Francis
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; TITLE OF INVENTION: Secretion Especially in Corynebacteria
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-761B-6

Query Match 44.7%; Score 38; DB 3; Length 447;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HTGGGVWD 10
| | | | |
Db 304 HTDGS1WD 311

RESULT 14

US-07-985-458-3
; Sequence 3, Application US/07985458
; Patent No. 5344777
; GENERAL INFORMATION:
; APPLICANT: Tamaki, Toshiaki;
; APPLICANT: Takamura, Hiroshi;
; APPLICANT: Tayama, Kenji;
; APPLICANT: Fukaya, Masahiro;
; APPLICANT: Okumura, Hajime and
; APPLICANT: Kawamura, Yoshiya
; TITLE OF INVENTION: Structural Gene of Membrane-Bound
; TITLE OF INVENTION: Alcohol Dehydrogenase Complex, Plasmid
; TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
; TITLE OF INVENTION: Bacteria
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frischauf, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72 mb
; COMPUTER: IBM PC compatible (NEC PC-9801 ES)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/985,458
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,221
; FILING DATE: 20-FEB-1991
; APPLICATION NUMBER: 73440/1990
; FILING DATE: 26-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910134/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MATURE PEPTIDE
; LOCATION: 36 to 738
; IDENTIFICATION METHOD: N-terminal sequences of the
; IDENTIFICATION METHOD: purified protein having a molecular weight of about
; IDENTIFICATION METHOD: 72,000
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter altoacetigenes
; STRAIN: MH-24
; PUBLICATION INFORMATION:
; AUTHORS: Tamaki, Toshiaki;
; AUTHORS: Fukaya, Masahiro;
; AUTHORS: Takamura, Hiroshi;
; AUTHORS: Tayama, Kenji;
; AUTHORS: Okumura, Hajime;
; AUTHORS: Kawamura, Yoshiya;
; AUTHORS: Nishiyama, Makoto;
; AUTHORS: Horinouchi, Sueharu and
; AUTHORS: Beppu, Teruhiko
; TITLE: Cloning and Sequencing of the Gene Cluster
; TITLE: Encoding Two Subunits of Membrane-Bound
; TITLE: Alcohol Dehydrogenase from Acetobacter
; TITLE: polyoxogenes

JOURNAL: Biochimica et Biophysica Acta.
VOLUME: 1088
PAGES: 292-300
DATE: 1991
US-07-985-458-3

Query Match 44.7%; Score 38; DB 1; Length 738;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGVWDPIDY 14
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Db 276 GGTWDSIVY 285

RESULT 15
US-09-074-658-75
; Sequence 75, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-75

Query Match 44.7%; Score 38; DB 4; Length 941;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 3 HTGGG-VWDPIDY 14
: |||| : ||: ||
Db 326 YTGGRILPDPMDY 339

Search completed: March 13, 2003, 15:18:41
Job time : 3.15385 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 1.99231 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGVNDPIDY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	85	100.0	121	10	US-09-822-698A-3
2	85	100.0	381	10	US-09-822-698A-5
3	85	100.0	451	10	US-09-822-698A-26
4	84	98.8	14	10	US-09-822-698A-99
5	82	96.5	14	10	US-09-822-698A-93
6	81	95.3	14	10	US-09-822-698A-105
7	80	94.1	14	10	US-09-822-698A-83
8	80	94.1	14	10	US-09-822-698A-104
9	79	92.9	14	10	US-09-822-698A-106
10	78	91.8	14	10	US-09-822-698A-31
11	78	91.8	14	10	US-09-822-698A-75
12	78	91.8	14	10	US-09-822-698A-76
13	78	91.8	14	10	US-09-822-698A-94
14	78	91.8	14	10	US-09-822-698A-97
15	77	90.6	14	10	US-09-822-698A-84
16	77	90.6	14	10	US-09-822-698A-89
17	77	90.6	14	10	US-09-822-698A-108
18	76	89.4	14	10	US-09-822-698A-81
19	76	89.4	14	10	US-09-822-698A-82

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20 76 89.4 14 10 US-09-822-698A-88 Sequence 88, Appl
21 76 89.4 14 10 US-09-822-698A-109 Sequence 109, Appl
22 75 88.2 14 10 US-09-822-698A-77 Sequence 77, Appl
23 75 88.2 14 10 US-09-822-698A-78 Sequence 78, Appl
24 75 88.2 14 10 US-09-822-698A-103 Sequence 103, Appl
25 74 87.1 14 10 US-09-822-698A-85 Sequence 85, Appl
26 74 87.1 14 10 US-09-822-698A-107 Sequence 107, Appl
27 73 85.9 14 10 US-09-822-698A-30 Sequence 30, Appl
28 73 85.9 14 10 US-09-822-698A-79 Sequence 79, Appl
29 73 85.9 14 10 US-09-822-698A-86 Sequence 86, Appl
30 73 85.9 14 10 US-09-822-698A-91 Sequence 91, Appl
31 73 85.9 14 10 US-09-822-698A-101 Sequence 101, Appl
32 73 85.9 16 10 US-09-822-698A-67 Sequence 67, Appl
33 72 84.7 14 10 US-09-822-698A-90 Sequence 90, Appl
34 72 84.7 14 10 US-09-822-698A-96 Sequence 96, Appl
35 72 84.7 14 10 US-09-822-698A-98 Sequence 98, Appl
36 72 84.7 14 10 US-09-822-698A-100 Sequence 100, Appl
37 72 84.7 14 10 US-09-822-698A-102 Sequence 102, Appl
38 72 84.7 16 10 US-09-822-698A-65 Sequence 65, Appl
39 71 83.5 16 10 US-09-822-698A-69 Sequence 69, Appl
40 70 82.4 14 10 US-09-822-698A-29 Sequence 29, Appl
41 70 82.4 14 10 US-09-822-698A-32 Sequence 32, Appl
42 70 82.4 14 10 US-09-822-698A-74 Sequence 74, Appl
43 69 81.2 14 10 US-09-822-698A-73 Sequence 73, Appl
44 69 81.2 14 10 US-09-822-698A-92 Sequence 92, Appl
45 68 80.0 14 10 US-09-822-698A-80 Sequence 80, Appl

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ALIGNMENTS

```

RESULT 1
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

```

```

Query Match 100.0%; Score 85; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AKHTGGVNDPIDY 14
      |||||
DB 97 AKHTGGVNDPIDY 110

```

```

RESULT 2
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US

```

```
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine biVPH1-IL-2
US-09-822-698A-5
```

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Query Match 100.0%; Score 85; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AKHTGGGVWDPIDY 14
|||||
Db 97 AKHTGGGVWDPIDY 110
|||||
```

```
RESULT 3
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26
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Query Match 100.0%; Score 85; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AKHTGGGVWDPIDY 14
|||||
Db 97 AKHTGGGVWDPIDY 110
|||||
```

```
RESULT 4
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99
```

```
Query Match 98.8%; Score 84; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.9e-07;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AKHTGGGVWDPIDY 14
|||||
Db 1 AKHTGGGVWDPIDY 14
|||||
```

```
RESULT 5
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93
```

```
Query Match 96.5%; Score 82; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AKHTGGGVWDPIDY 14
|||||
Db 1 AKHTGGGVWDPIDY 14
|||||
```

```
RESULT 6
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105
```

```
Query Match 95.3%; Score 81; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 KHTGGGVWDPIDY 14
|||||

Db 2 KHTGGGVWDPIDY 14
|||||

RESULT 7

US-09-822-698A-83

; Sequence 83, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 83

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-83

Query Match 94.1%; Score 80; DB 10; Length 14;

Best Local Similarity 92.9%; Pred. No. 3.2e-06;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
|||||

Db 1 AKHTGGGVWDPIDY 14
|||||

RESULT 8

US-09-822-698A-104

; Sequence 104, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 104

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-104

Query Match 94.1%; Score 80; DB 10; Length 14;

Best Local Similarity 92.9%; Pred. No. 3.2e-06;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
|||||

Db 1 AKHTGGGVWDPIDY 14
|||||

RESULT 9

US-09-822-698A-106

; Sequence 106, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 106

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-106

Query Match 92.9%; Score 79; DB 10; Length 14;

Best Local Similarity 92.9%; Pred. No. 4.5e-06;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
|||||

Db 1 AKHTGGGVWDPIDY 14
|||||

RESULT 10

US-09-822-698A-31

; Sequence 31, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 31

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: region of a MUC1-specific binding member

US-09-822-698A-31

Query Match 91.8%; Score 78; DB 10; Length 14;

Best Local Similarity 92.9%; Pred. No. 6.4e-06;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
|||||

Db 1 AKHTGGGVWDPIDY 14
|||||

RESULT 11

US-09-822-698A-75

; Sequence 75, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPID 13
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPID 13

RESULT 12

US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1

GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 76

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-76

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPIGY 14

RESULT 13

US-09-822-698A-94
; Sequence 94, Application US/09822698A
; Patent No. US20020146750A1

GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 94

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-94

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPIHY 14

RESULT 14

US-09-822-698A-97

; Sequence 97, Application US/09822698A

; Patent No. US20020146750A1

GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 97

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-97

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPID 13
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPID 13

RESULT 15

US-09-822-698A-84

; Sequence 84, Application US/09822698A

; Patent No. US20020146750A1

GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 84

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-84

Query Match 90.6%; Score 77; DB 10; Length 14;
Best Local Similarity 85.7%; Pred. No. 9.1e-06;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPINY 14

Search completed: March 13, 2003, 15:30:31
Job time : 1.99231 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model
Run on: March 13, 2003, 15:14:49 ; Search time 29,8308 seconds
(without alignments)
302.582 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 85
Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Pending_Patents_AA_Main:*
- 1: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/paa/US10_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/paa/US11_COMB.pep.*
 - 7: /cgn2_6/ptodata/2/paa/US12_COMB.pep.*
 - 8: /cgn2_6/ptodata/2/paa/US13_COMB.pep.*
 - 9: /cgn2_6/ptodata/2/paa/US14_COMB.pep.*
 - 10: /cgn2_6/ptodata/2/paa/US15_COMB.pep.*
 - 11: /cgn2_6/ptodata/2/paa/US16_COMB.pep.*
 - 12: /cgn2_6/ptodata/2/paa/US17_COMB.pep.*
 - 13: /cgn2_6/ptodata/2/paa/US18_COMB.pep.*
 - 14: /cgn2_6/ptodata/2/paa/US19_COMB.pep.*
 - 15: /cgn2_6/ptodata/2/paa/US20_COMB.pep.*
 - 16: /cgn2_6/ptodata/2/paa/US21_COMB.pep.*
 - 17: /cgn2_6/ptodata/2/paa/US22_COMB.pep.*
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 - 20: /cgn2_6/ptodata/2/paa/US25_COMB.pep.*
 - 21: /cgn2_6/ptodata/2/paa/US26_COMB.pep.*
 - 22: /cgn2_6/ptodata/2/paa/US27_COMB.pep.*
 - 23: /cgn2_6/ptodata/2/paa/US28_COMB.pep.*
 - 24: /cgn2_6/ptodata/2/paa/US29_COMB.pep.*
 - 25: /cgn2_6/ptodata/2/paa/US30_COMB.pep.*
 - 26: /cgn2_6/ptodata/2/paa/US31_COMB.pep.*
 - 27: /cgn2_6/ptodata/2/paa/US32_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	121	19	US-09-538-913-3
2	85	100.0	121	22	US-09-822-698A-3
3	85	100.0	381	19	US-09-538-913-5
4	85	100.0	381	22	US-09-822-698A-5
5	85	100.0	451	22	US-09-822-698A-26
6	84	98.8	14	22	US-09-822-698A-99

7	82	96.5	14	22	US-09-822-698A-93	Sequence 93, Appl
8	81	95.3	14	22	US-09-822-698A-105	Sequence 105, Appl
9	80	94.1	14	22	US-09-822-698A-83	Sequence 83, Appl
10	80	94.1	14	22	US-09-822-698A-104	Sequence 104, Appl
11	79	92.9	14	22	US-09-822-698A-106	Sequence 106, Appl
12	78	91.8	14	22	US-09-822-698A-31	Sequence 31, Appl
13	78	91.8	14	22	US-09-822-698A-75	Sequence 75, Appl
14	78	91.8	14	22	US-09-822-698A-94	Sequence 94, Appl
15	78	91.8	14	22	US-09-822-698A-97	Sequence 97, Appl
16	77	90.6	14	22	US-09-822-698A-84	Sequence 84, Appl
17	77	90.6	14	22	US-09-822-698A-89	Sequence 89, Appl
18	77	90.6	14	22	US-09-822-698A-108	Sequence 108, Appl
19	77	90.6	14	22	US-09-822-698A-81	Sequence 81, Appl
20	76	89.4	14	22	US-09-822-698A-82	Sequence 82, Appl
21	76	89.4	14	22	US-09-822-698A-88	Sequence 88, Appl
22	76	89.4	14	22	US-09-822-698A-109	Sequence 109, Appl
23	76	89.4	14	22	US-09-822-698A-77	Sequence 77, Appl
24	75	88.2	14	22	US-09-822-698A-78	Sequence 78, Appl
25	75	88.2	14	22	US-09-822-698A-103	Sequence 103, Appl
26	75	88.2	14	22	US-09-822-698A-85	Sequence 85, Appl
27	74	87.1	14	22	US-09-822-698A-107	Sequence 107, Appl
28	74	87.1	14	22	US-09-822-698A-30	Sequence 30, Appl
29	73	85.9	14	22	US-09-822-698A-79	Sequence 79, Appl
30	73	85.9	14	22	US-09-822-698A-86	Sequence 86, Appl
31	73	85.9	14	22	US-09-822-698A-91	Sequence 91, Appl
32	73	85.9	14	22	US-09-822-698A-101	Sequence 101, Appl
33	73	85.9	14	22	US-09-822-698A-90	Sequence 90, Appl
34	73	85.9	14	22	US-09-822-698A-96	Sequence 96, Appl
35	72	84.7	14	22	US-09-822-698A-98	Sequence 98, Appl
36	72	84.7	14	22	US-09-822-698A-100	Sequence 100, Appl
37	72	84.7	14	22	US-09-822-698A-65	Sequence 65, Appl
38	72	84.7	14	22	US-09-822-698A-69	Sequence 69, Appl
39	72	84.7	14	22	US-09-822-698A-32	Sequence 32, Appl
40	71	83.5	16	22	US-09-822-698A-74	Sequence 74, Appl
41	71	83.5	16	22	US-09-822-698A-73	Sequence 73, Appl
42	70	82.4	14	22		
43	70	82.4	14	22		
44	70	82.4	14	22		
45	69	81.2	14	22		

ALIGNMENTS

RESULT 1
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match 100.0%; Score 85; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKHTGGGVWDPIDY 14
Db 97 AKHTGGGVWDPIDY 110

RESULT 2

```
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 85; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
Db 97 AKHTGGGVWDPIDY 110
|||||

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for bivPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match 100.0%; Score 85; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
Db 97 AKHTGGGVWDPIDY 110
|||||

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
US-09-822-698A-5

Query Match 100.0%; Score 85; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
Db 97 AKHTGGGVWDPIDY 110
|||||

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match 100.0%; Score 85; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
Db 97 AKHTGGGVWDPIDY 110
|||||

RESULT 6
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99
```

```
Query Match          98.8%; Score 84; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 7e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||
Db 1 AKHTGGVWDPIDY 14
   |||||

RESULT 7
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match          96.5%; Score 82; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.4e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||
Db 1 AKHTGGVWDPIDY 14
   |||||

RESULT 8
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match          95.3%; Score 81; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGVWDPIDY 14
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Db 2 KHTGGVWDPIDY 14
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RESULT 9
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US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match          94.1%; Score 80; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||
Db 1 AKHTGGVWDPIDY 14
   |||||

RESULT 10
US-09-822-698A-104
; Sequence 104, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 104
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-104

Query Match          94.1%; Score 80; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||
Db 1 AKHTGGVWDPIDY 14
   |||||

RESULT 11
US-09-822-698A-106
; Sequence 106, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
```

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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106

Query Match          92.9%; Score 79; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   ||||| |||||
Db 1 AKHTGAGVWDPIDY 14

RESULT 12
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   ||||| |||||
Db 1 AKHTGGVWDPIGY 14

RESULT 13
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match          91.8%; Score 78; DB 22; Length 14;
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Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPID 13
   ||||| |||||
Db 1 AKHTGGVWDPID 13

RESULT 14
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   ||||| |||||
Db 1 AKHTGGVWDPIGY 14

RESULT 15
US-09-822-698A-94
; Sequence 94, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 94
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-94

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   ||||| |||||
Db 1 AKHTGGVWDPIHY 14

Search completed: March 13, 2003, 15:28:04
Job time : 31.0808 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 5.11538 Seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US05_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	45	52.9	218	6	US-10-282-122A-50009
2	44	51.8	330	6	US-10-366-683-23794
3	43	50.6	57	1	PCT-US02-32727-17567
4	43	50.6	57	5	US-09-978-825-17567
5	43	50.6	57	6	US-10-057-498-17567
6	43	50.6	799	6	US-10-282-122A-49879
7	42	49.4	152	6	US-10-156-761-10926
8	41	48.2	222	5	US-09-724-676-80033
9	41	48.2	222	5	US-09-724-676A-80033
10	41	48.2	251	6	US-10-282-122A-46525
11	41	48.2	264	1	PCT-US02-40225-3079
12	41	48.2	264	6	US-10-320-797-3079
13	41	48.2	275	5	US-09-724-676-80034
14	41	48.2	275	5	US-09-724-676A-80034
15	41	48.2	295	5	US-09-724-676-80022
16	41	48.2	295	5	US-09-724-676-80028
17	41	48.2	295	5	US-09-724-676-80037
18	41	48.2	295	5	US-09-724-676A-80022
19	41	48.2	295	5	US-09-724-676A-80028
20	41	48.2	295	5	US-09-724-676A-80037
21	41	48.2	300	6	US-10-282-122A-46309
22	41	48.2	348	5	US-09-724-676-80023
23	41	48.2	348	5	US-09-724-676-80029
24	41	48.2	348	5	US-09-724-676-80038
25	41	48.2	348	5	US-09-724-676A-80023
26	41	48.2	348	5	US-09-724-676A-80029

27	41	48.2	348	5	US-09-724-676A-80038
28	41	48.2	385	5	US-09-724-676-80041
29	41	48.2	385	5	US-09-724-676A-80041
30	41	48.2	420	5	US-09-724-676-80025
31	41	48.2	420	5	US-09-724-676A-80025
32	41	48.2	438	5	US-09-724-676-80020
33	41	48.2	438	5	US-09-724-676A-80020
34	41	48.2	473	5	US-09-724-676-80026
35	41	48.2	473	5	US-09-724-676-80035
36	41	48.2	473	5	US-09-724-676A-80026
37	41	48.2	473	5	US-09-724-676A-80035
38	41	48.2	687	6	US-10-369-493-7152
39	41	48.2	692	6	US-10-369-493-4397
40	41	48.2	710	6	US-10-156-761-14284
41	41	48.2	795	6	US-10-282-122A-47364
42	40.5	47.6	672	6	US-10-156-761-8104
43	40	47.1	34	6	US-10-203-138A-13646
44	40	47.1	93	1	PCT-US02-32727-9150
45	40	47.1	93	5	US-09-978-825-9150

ALIGNMENTS

RESULT 1

US-10-282-122A-50009
Sequence 50009, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELTRA 034A
CURRENT APPLICATION NUMBER: US/10282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50009
LENGTH: 218
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50009

Query Match 52.9%; Score 45; DB 6; Length 218;
Best Local Similarity 58.3%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDPID 13
Db 79 EHGGLYQPID 90

RESULT 2
US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rudenfield, Marc J.
; APPLICANT: Nollong, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 51.8%; Score 44; DB 6; Length 330;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGVWDPID 13
Db 101 GSVWDPID 108

RESULT 3
PCT-US02-32727-17567
; Sequence 17567, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-17567

Query Match 50.6%; Score 43; DB 1; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
Db 17 RHSGGGRWPP 26

RESULT 4
US-09-978-825-17567
; Sequence 17567, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-17567

Query Match 50.6%; Score 43; DB 5; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
Db 17 RHSGGGRWPP 26

RESULT 5
US-10-057-498-17567
; Sequence 17567, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-17567

Query Match 50.6%; Score 43; DB 6; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
Db 17 RHSGGGRWPP 26

RESULT 6
US-10-282-122A-49879
; Sequence 49879, Application US/10282122A

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49879
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49879

Query Match 50.6%; Score 43; DB 6; Length 799;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPTDY 14
| | | | | | | | | | | | | | | |
Db 511 AAETGGQWEPKRY 524

RESULT 7
US-10-156-761-10926
; Sequence 10926, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

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; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10926
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10926

Query Match 49.4%; Score 42; DB 6; Length 152;
Best Local Similarity 32.1%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 16; Gaps 1;

QY 2 KHTG-----GGVWDPID 13
| | | | | | | | | | | | | | | |
Db 104 RHTGGEWTTGDDHWRTDGLRLWDPID 131

RESULT 8
US-09-724-676-80033
; Sequence 80033, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80033
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80033

Query Match 48.2%; Score 41; DB 5; Length 222;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
| | | | | | | | | |
Db 76 AKHTPGGPW 84

RESULT 9
US-09-724-676A-80033
; Sequence 80033, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80033
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-80033

Query Match 48.2%; Score 41; DB 5; Length 222;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
| | | | | | | | | |
Db 76 AKHTPGGPW 84

RESULT 10
US-10-282-122A-46525
; Sequence 46525, Application US/10282122A
; GENERAL INFORMATION:

```

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46525
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46525

Query Match      48.2%; Score 41; DB 6; Length 251;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TGGGVWDPI 12
      |||||
Db     152 TGGGGWGPI 160

RESULT 11
PCT-US02-40225-3079
; Sequence 3079, Application PC/TUS0240225
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-228
; CURRENT APPLICATION NUMBER: PCT/US02/40225
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT

US-09-822-698a-3_copy_97_110_1.rapn

; ORGANISM: Cryptococcus neoformans
PCT-US02-40225-3079

Query Match      48.2%; Score 41; DB 1; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      3 HTGGGVWDPI 13
      :| ||| |
Db     233 YKGTGVWTPVD 243

RESULT 12
US-10-320-797-3079
; Sequence 3079, Application US/10320797
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS A
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3079

Query Match      48.2%; Score 41; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      3 HTGGGVWDPI 13
      :| ||| |
Db     233 YKGTGVWTPVD 243

RESULT 13
US-09-724-676-80034
; Sequence 80034, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 80034
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (97)-(98)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (107)..(107)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676-80034

Query Match      48.2%; Score 41; DB 5; Length 275;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AKHTGGGVW 9
      |||||
```


Db 76 AKHTPGGPW 84

RESULT 14

US-09-724-676A-80034
 ; Sequence 80034, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 80034
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (97)..(98)
 ; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (107)..(107)
 ; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-09-724-676A-80034

Query Match 48.2%; Score 41; DB 5; Length 275;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9

||||||

Db 76 AKHTPGGPW 84

RESULT 15

US-09-724-676-80022
 ; Sequence 80022, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 80022
 ; LENGTH: 295
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-724-676-80022

Query Match 48.2%; Score 41; DB 5; Length 295;
 Best Local Similarity 77.8%; Pred. No. 2.8e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9

||||||

Db 149 AKHTPGGPW 157

Search completed: March 13, 2003, 15:29:46
 Job time : 6.11538 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: March 13, 2003, 15:12:09 ; Search time 2.42308 seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110

Perfect score: 85
Sequence: 1 AKHTGGGVDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	55.3	573	2 A41319	3-oxosteroid 1-dehydrogenase
2	45	52.9	381	2 B97182	acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum
3	44	51.8	125	1 B43825	angiotensin - rabbit
4	43	50.6	71	2 A34768	ORF1 protein - Orf
5	43	50.6	304	2 H82984	hypothetical prote
6	43	50.6	435	2 H87412	conserved hypothet
7	43	50.6	536	2 T08241	gas-vesicle operon
8	43	50.6	536	2 S15183	gas-vesicle operon
9	42.5	50.0	597	2 G75070	hypothetical prote
10	42.5	50.0	598	2 B71095	hypothetical prote
11	42	49.4	255	2 S26020	cytochrome-c oxida
12	41	48.2	42	2 E95061	peptide pheromone
13	41	48.2	182	2 S77005	Anrl protein - yea
14	41	48.2	300	2 F69997	hypothetical prote
15	40	47.1	114	2 T08411	hypothetical prote
16	40	47.1	158	2 E86498	pts IIA protein [i
17	40	47.1	158	2 E72124	pts IIA protein -
18	40	47.1	193	2 C82683	disulfide oxidore
19	40	47.1	241	2 AC0596	histidine utilizat
20	40	47.1	291	2 E71491	probable geranyl t
21	40	47.1	338	2 H84173	acetoin utilizatio
22	40	47.1	345	2 E80817	hypothetical prote
23	40	47.1	345	2 C90974	hypothetical prote
24	40	47.1	345	2 A85677	unknown protein en
25	40	47.1	345	2 E85821	unknown protein en
26	40	47.1	347	2 F90904	hypothetical prote
27	40	47.1	347	2 G85712	unknown protein en
28	40	47.1	473	2 JC1184	hypothetical 50.8K
29	40	47.1	478	1 I47154	transcription fact

30	40	47.1	544	2 S43058	ccrta protein eta
31	40	47.1	600	2 D84588	hypothetical prote
32	40	47.1	738	2 C97420	probable 3-hydroxy
33	40	47.1	738	2 AD2638	enoyl-CoA hydratase
34	40	47.1	784	2 T45697	hypothetical prote
35	39.5	46.5	285	2 B86687	conserved hypothet
36	39	45.9	163	2 T34604	hypothetical prote
37	39	45.9	237	2 A82607	hypothetical prote
38	39	45.9	260	2 C75454	hypothetical prote
39	39	45.9	312	2 T36986	probable ribosylgl
40	39	45.9	370	2 F86338	protein F2D10.2 [i
41	39	45.9	386	2 S74778	hypothetical prote
42	39	45.9	418	2 S42031	LDJ2 protein - lee
43	39	45.9	434	1 S49457	pyrimidine-nucleos
44	39	45.9	518	2 S42387	MPP protein homol
45	39	45.9	524	2 S30575	glycoprotein precu

ALIGNMENTS

RESULT 1

A41319

3-oxosteroid 1-dehydrogenase (EC 1.3.99.4) - Comamonas testosteroni

C:Species: Comamonas testosteroni

C>Date: 05-Jun-1992 #sequence_revision 28-Apr-1993 #text_change 29-Sep-1999

C:Accession: A41319

R:Plesiat, P.; Grandguillot, M.; Harayama, S.; Vragar, S.; Michel-Briand, Y.

J. Bacteriol. 173, 7219-7227, 1991

A>Title: Cloning, sequencing, and expression of the Pseudomonas testosteroni gene enc

A:Reference number: A41319; MUID:92041619; PMID:1657885

A:Accession: A41319

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-573 <PLE>

A:Cross-references: GB:M68488; NID:g485378; PIDN:AAA25679.1; PID:g485379

A>Note: the authors translated the codon ACC for residue 497 as Tyr

C:Superfamily: 3-oxosteroid 1-dehydrogenase; 3-oxosteroid 1-dehydrogenase homology

C:Keywords: oxidoreductase

F:450-548/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match

Best Local Similarity 55.3%; Score 47; DB 2; Length 573;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVDPIDY 14

DB 47 SGGGIWIPLY 57

||||:|:|

RESULT 2

B97182

acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: B97182

R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97182

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 <KUR>

A:Cross-references: GB:AF001437; PIDN:AAK80245.1; PID:gl5025293; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2288

Query Match

Best Local Similarity 52.9%; Score 45; DB 2; Length 381;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 HTGGGVWD 10
|||||
Db 223 HTGGGGWD 230

RESULT 3
B43825
angiotensin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernme
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29833
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Note: submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 51.8%; Score 44; DB 1; Length 125;
Best Local Similarity 53.8%; Pred. No. 8.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 2 KHTGGGVWDPIDY 14
|||||
Db 82 KHVGGSPWPCRY 94

RESULT 4
A34768
ORF1 protein - Orf virus (strain NZ2)
C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C:Accession: A34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the para
A:Reference number: A34768; MUID:90266454; PMID:2129563
A:Accession: A34768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <FRA>
A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46787.1; PID:g332563

Query Match 50.6%; Score 43; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 7.1; Mismatches 4; Indels 1; Gaps 0;
Matches 5; Conservative 4;

QY 4 TGGGVWDPID 13
|||||
Db 32 SGGGIWGPLE 41

RESULT 5
H82984
hypothetical protein PA5284 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H82984
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: H82950; MUID:20437337; PMID:10984043
A:Accession: H82984
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004941; GB:AE00491; NID:g9951596; PIDN:AAG08669.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5284

Query Match 50.6%; Score 43; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 6 GGVWDPID 13
|||||
Db 75 GSVWDPDV 82

RESULT 6
B87412
conserved hypothetical protein CC1313 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87412
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: B87249; MUID:21173698; PMID:11259647
A:Accession: B87412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <STO>
A:Cross-references: GB:AE005673; NID:g13422654; PIDN:AAK23294.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1313

Query Match 50.6%; Score 43; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 44; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 3 HTGGGVWDPI 12
|||||
Db 372 HNPGGFWDPL 381

RESULT 7
T08241
gas-vesicle operon protein gvpD - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N:Alternate names: hypothetical protein H0263
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C:Accession: T08241
R:Ng, W.V.; Gufvo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid o
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08241
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-536 <NGW>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822302; HALOSP:H0263
A:Experimental source: strain NRC-1
C:Genetics:
A:Gene: gvpD; HALOSP:H0263
A:Genome: plasmid pNRC100

Query Match 50.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. No. 54; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 4 TGGGVWDPI 12
|||||
```

Db 247 TGNGTWDPL 255

RESULT 8

S15183
gas-vesicle operon protein gvpD - Halobacterium salinarum plasmids pHH1 and pNRC100
C:Species: Halobacterium salinarum
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C:Accession: S15183; S06185
R:Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A:Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in
A:Reference number: S15183; MUID:92065812; PMID:1956294
A:Accession: S15183
A:Molecule type: DNA
A:Residues: 1-536 <HOR>
A:CROSS-references: EMBL:X55648; NID:g43516; PID:g43517
A:Experimental source: plasmid pHH1
A:Genetics: PHH
A:Note: the authors translated the codon ACG for residue 531 as Ile
R:Jones, J.G.; Hackett, N.R.; Halladay, J.T.; Scothorn, D.J.; Yang, C.F.; Ng, W.L.; Dass
Nucleic Acids Res. 17, 7785-7793, 1989
A:Title: Analysis of insertion mutants reveals two new genes in the pNRC100 gas vesicle
A:Reference number: S06184; MUID:90016863; PMID:2552415
A:Accession: S06185
A:Molecule type: DNA
A:Residues: 1-536 <JON>
A:CROSS-references: EMBL:X15374; NID:g43502; PID:g43504
A:Experimental source: plasmid pNRC100
A:Genetics: NRC
A:Note: the source is designated as Halobacterium halobium
C:Genetics: <NRC>
A:Gene: gvpD
A:Genome: plasmid pNRC100
C:Genetics: <PHH>
A:Gene: gvpD
A:Genome: plasmid pHH1

Query Match 50.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGGGVWDPI 12
| | | | |

Db 247 TGNGTWDPL 255

RESULT 9
G75070
hypochemical protein PAR0644 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75070
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: G75070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-597 <KAW>
A:CROSS-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49868.1; PID:g545836
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAR0644

Query Match 50.0%; Score 42.5; DB 2; Length 597;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTGGGVWDPI 14
| | | | |

Db 21 HDGSG-WDPIKY 31

RESULT 10

B71095
hypochemical protein PH1023 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: B71095
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: B71095
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-598 <KAW>
A:CROSS-references: GB:AP000004; NID:g3236131; PIDN:BAA30120.1; PID:g3257437
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH1023

Query Match 50.0%; Score 42.5; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTGGGVWDPI 14
| | | | |

Db 21 HDGSG-WDPIKY 31

RESULT 11
S26020
cytochrome-c oxidase (EC 1.9.3.1) chain III - pig roundworm mitochondrion
C:Species: mitochondrion Ascaris suum (pig roundworm)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 07-Dec-1999
C:Accession: S26020; S25793
R:Okimoto, R.; Macfarlane, J.L.; Clary, D.O.; Wolstenholme, D.R.
Genetics 130, 471-498, 1992
A:Title: The mitochondrial genomes of two nematodes, Caenorhabditis elegans and Ascar
A:Reference number: S26014; MUID:92201635; PMID:1551572
A:Accession: S26020
A:Molecule type: DNA
A:Residues: 1-255 <OKI>
A:CROSS-references: EMBL:X54253; NID:g13971; PIDN:CAA38169.1; PID:g575347
A:Note: the authors translated the initiation codon GTG for residue 1 as Val
R:Okimoto, R.; Macfarlane, J.L.; Wolstenholme, D.R.
Nucleic Acids Res. 18, 6113-6118, 1990
A:Title: Evidence for the frequent use of TTG as the translation initiation codon of
A:Reference number: S13139; MUID:91045077; PMID:2235493
A:Accession: S25793
A:Molecule type: DNA
A:Residues: 1-25 <OK2>
A:CROSS-references: EMBL:X54253
A:Note: the authors translated the initiation codon GTG for residue 1 as Val
C:Genetics:
A:Gene: COIII
A:Genome: mitochondrion
A:Genetic code: SGC4
A:Start codon: GTG
A:Superfamily: cytochrome-c oxidase chain III
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr

Query Match 49.4%; Score 42; DB 2; Length 255;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPI 12
| | | | |

Db 106 HDVGGVWSPI 115

RESULT 12

E95061
peptide pheromone B1pC [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95061
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-42 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74686.1; PID:g14972003; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0528

Query Match 48.2%; Score 41; DB 2; Length 42;
Best Local Similarity 54.5%; Pred. No. 8.6;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGGGVWDPIDY 14
|||||:|:|
Db 22 TGGGLWEDLLY 32

RESULT 13

S17005
AHT1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: activator of hexose transport; protein H9332.3; protein YHR093w
C:Species: Saccharomyces cerevisiae
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 29-Oct-1999
C:Accession: S17005; S46717
R:Oezcan, S.; Ciriacy, M.
submitted to the EMBL Data Library, May 1991
A:Reference number: S17005
A:Accession: S17005
A:Molecule type: DNA
A:Residues: 1-182 <QEZ>
A:Cross-references: EMBL:X59464; NID:g3354; PIDN:CAA42071.1; PID:g663230
A:Experimental source: strain MC 971 B
R:Vaudin, M.
submitted to The EMBL Data Library, May 1994
A:Description: The sequence of S. cerevisiae cosmid 9332.
A:Reference number: S46715
A:Accession: S46717
A:Molecule type: DNA
A:Residues: 1-182 <VAU>
A:Cross-references: EMBL:U00060; NID:g487928; PIDN:AA68925.1; PID:g487931; MIPS:YHR093w
C:Genetics:
A:Gene: SGD:AHT1
A:Cross-references: SGD:S0001135; MIPS:YHR093w
A:Map position: 8R
C:Superfamily: Saccharomyces AHT1 protein

Query Match 48.2%; Score 41; DB 2; Length 182;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGVWDPID 13
|||||:|:|
Db 44 GGGIWPME 52

RESULT 14

F69997
hypothetical protein ytnm - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: F69997
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95061
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-42 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74686.1; PID:g14972003; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0528

Query Match 48.2%; Score 41; DB 2; Length 300;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPI 12
|||||:|:|
Db 148 ADATGGGGWGPV 159

RESULT 15

T08411
hypothetical protein F18B3.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Oct-1999
C:Accession: T08411
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16409
A:Accession: T08411
A:Molecule type: DNA
A:Residues: 1-114 <QUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.180
A:Map position: 3
C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 47.1%; Score 40; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGVWDPI 11
|||||
Db 99 GGVWDPI 104

Search completed: March 13, 2003, 15:17:52
Job time : 4.42308 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 1.4 seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	%	Score	Length	ID	Description
1	47	55.3	573	1	30ID_COMTE	O06401 comamonas t
2	44	51.8	125	1	ANGI_RABIT	P31347 oryctolagus
3	43	50.6	536	1	GVDL_HALNI	P13043 halobacteri
4	43	50.6	1371	1	PUR2_CHITE	O26255 c trifuncti
5	42	49.4	255	1	COX3_ASCSU	P24879 ascaris suu
6	41	48.2	182	1	AHT1_YEAST	P29589 saccharomyc
7	40	47.1	478	1	OCT2_PIG	O29013 sus scrofa
8	40	47.1	544	1	TCPH_MOUSE	P80313 mus musculu
9	39	45.9	418	1	DNJ2_ALLPO	P42824 allium porr
10	39	45.9	434	1	PDP_BACSU	P39142 bacillus su
11	39	45.9	518	1	YNV6_CAEEL	P34569 caenorhabdi
12	39	45.9	543	1	TCPH_HUMAN	O99832 homo sapien
13	39	45.9	579	1	YR47_CAEEL	O09563 caenorhabdi
14	39	45.9	807	1	YAK1_YEAST	P14680 saccharomyc
15	39	45.9	868	1	PRTT_PORGI	P43158 porphyromon
16	39	45.9	983	1	4ET_MOUSE	O9est3 mus musculu
17	39	45.9	985	1	4ET_HUMAN	Q9nra8 homo sapien
18	38	44.7	185	1	EFP_DEIRA	P99y32 deinococcus
19	38	44.7	256	1	YM56_YEAST	O03691 saccharomyc
20	38	44.7	272	1	COX3_PYLII	O37600 pylaella l
21	38	44.7	387	1	YB96_YEAST	P38332 saccharomyc
22	38	44.7	420	1	TABA_PSESZ	P31851 pseudomonas
23	38	44.7	447	1	DHEA_CORGL	P31026 corynebacte
24	38	44.7	521	1	GLGA_METJA	O59001 methanococc
25	38	44.7	534	1	AWT1_CAEEL	P54145 caenorhabdi
26	38	44.7	628	1	BGAL_LACAC	O07684 lactobacill
27	38	44.7	637	1	TRGS_ECOLI	O00184 escherichia
28	38	44.7	643	1	YK09_CAEEL	P34304 caenorhabdi
29	38	44.7	738	1	DHET_ACEPO	P28036 acetobacter
30	38	44.7	739	1	DHET_ACEEU	O44002 acetobacter
31	38	44.7	943	1	LBPA_NEIMB	O06379 neisseria m
32	38	44.7	944	1	LBPA_NEIMA	Q9JCK4 neisseria m
33	38	44.7	1276	1	PMP6_CHLPN	O9z899 chlamydia p

34 37 43.5 32 1 GHR4_RAT
35 37 43.5 145 1 ANGI_MOUSE
36 37 43.5 204 1 ADEN_ADEP3
37 37 43.5 238 1 PRRC_RAT
38 37 43.5 242 1 Y252_MYCGE
39 37 43.5 319 1 TAL_RALSO
40 37 43.5 344 1 PUR5_ECOLI
41 37 43.5 344 1 PUR5_HAEIN
42 37 43.5 357 1 YFOB_SCHPO
43 37 43.5 382 1 SUC1_ARCFU
44 37 43.5 408 1 HUT1_RALSO
45 37 43.5 497 1 ACCD_CUSRE

p33581 rattus norv
p21570 mus musculu
Q84177 porcine ade
P33579 rattus norv
P47494 mycoplasma
Q8Y014 raistonia s
P08178 escherichia
P43848 haemophilus
Q10170 schizosacch
O28732 archaeglob
Q8wx31 raistonia s
P31562 cuscita ref

ALIGNMENTS

RESULT 1
30ID_COMTE
ID 30ID_COMTE STANDARD; PRT; 573 AA.
AC Q06401;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxosteroid 1-dehydrogenase (EC 1.3.99.4)
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 17410;
RX MEDLINE=92041619; PubMed=1657885;
RA Plesiat P., Grandguillot M., Hatayama S., Vragar S., Michel-Briand Y.;
RT "Cloning, sequencing, and expression of the Pseudomonas testosteroni
gene encoding 3-oxosteroid delta 1-dehydrogenase."
RL J. Bacteriol. 173:7219-7227(1991).
CC -!- FUNCTION: DEHYDROGENATES STEROIDS BY INTRODUCING A DOUBLE
BOND IN STEROID RING A.
CC -!- CATALYTIC ACTIVITY: A 3-oxosteroid + acceptor = a 3-oxo-delta(1)-
steroid + reduced acceptor.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: FIRST STEP IN STEROID CATABOLISM.
CC -!- SUBCELLULAR LOCATION: Inner membrane.
CC -----
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CC -----
CC EMBL; M68488; AAA25679.1; -.
CC EMBL; A22347; CAA01596.1; -.
CC PIR; A41319; A41319.
KW Oxidoreductase; Flavoprotein; Inner membrane; Steroid metabolism;
KW FAD.
FT NP_BIND 7 36 FAD (BY SIMILARITY).
SQ SEQUENCE 573 AA; 62672 MW; 8E941AF569897734 CRC64;
Query Match 55.3%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 5.5;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 4 TGGGVWDPIDY 14
:|||||:
Db 47 SGGGIWIPLYN 57
RESULT 2
ANGI_RABIT
ID ANGI_RABIT STANDARD; PRT; 125 AA.
AC P31347;

DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin (EC 3.1.27.-)
GN ANG.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR; B43825; B43825.
DR PIR; S29833; S29833.
DR HSP; P03950; 1A4Y.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SMW0092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 13 13 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 114 114 BY SIMILARITY.
FT DISULFID 26 81 BY SIMILARITY.
FT DISULFID 39 92 BY SIMILARITY.
FT DISULFID 57 107 BY SIMILARITY.
SQ SEQUENCE 125 AA; 14361 MW; 3A737E595D767B04 CRC64;
Query Match 51.88; Score 44; DB 1; Length 125;
Best Local Similarity 53.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 2 KHTGGVWVDIPY 14
Db 82 KHVGSPPWPCRY 94
RESULT 3
GVDL HALN1 STANDARD; PRT; 536 AA.
ID P13043; Q9H119;
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN GvpD protein 1.
DE (GVPD11 OR GVPD OR VNG5029C) AND (GVPD12 OR VNG6028G).
OS Halobacterium sp. (strain NRC-1), and
OS Halobacterium sp. (strain NRC-817).
OC Plasmid pNRC100, Plasmid pNRC200, and plasmid pHHL.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091, 148370;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=pNRC100;
RX Jones J.G., Hackett N.R., Halladay J.T., Scothorn D.J.,
RA Yang C.-F., Ng W.-L., Dassarma S.;
RT "Analysis of insertion mutants reveals two new genes in the pNRC100
RT gas vesicle gene cluster of Halobacterium halobium.";
RL Nucleic Acids Res. 17:7785-7794(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=pNRC100;
RX MEDLINE=91323716; PubMed=1864501;
RA Jones J.G., Young D.C., Dassarma S.;
RT "Structure and organization of the gas vesicle gene cluster on the
RT Halobacterium halobium plasmid pNRC100.";
RL Gene 102:117-122(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=pNRC100;
RX MEDLINE=99063795; PubMed=9847077;
RA Ng W.V., Clufo S.A., Smith T.M., Bungarner R.E., Baskin D., Faust J.,
RA Hall B., Loretz C., Seto J., Slagel J., Hood L., Dassarma S.;
RT "Snapshot of a large dynamic replicon in a halophilic archaeon:
RT megaplasmid or minichromosome?";
RL Genome Res. 8:1131-1141(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=pNRC200;
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebbard H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-817; PLASMID=pHHL;
RX MEDLINE=92065812; PubMed=1956294;
RA Horne M., Englert C., Wimmer C., Pfeifer F.;
RT "A DNA region of 9 kbp contains all genes necessary for gas vesicle
RT synthesis in halophilic archaeobacteria.";
RL Mol. Microbiol. 5:1159-1174(1991).
CC -1- FUNCTION: MAY PLAY A ROLE IN AN ENERGY REQUIRING PROCESS SUCH AS
CC ASSEMBLY OF GAS VESICLES IN ADDITION TO A POSSIBLE STRUCTURAL OR
CC REGULATORY FUNCTION.
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CC EMBL; X15374; CAA33435.1; -
DR EMBL; M58557; AAA98195.1; -
DR EMBL; AF016485; AAC82808.1; -
DR EMBL; AE005141; AAG20725.1; -
DR EMBL; X55648; CAA39171.1; -
DR PIR; S06185; S06185.
DR PIR; S15183; S15183.
KW Gas vesicle; Plasmid; ATP-binding; Complete proteome.
FT NP_BIND 39 46 ATP (POTENTIAL).
SQ SEQUENCE 536 AA; 59342 MW; 3FC4E4F8F129F9CD CRC64;
Query Match 50.6%; Score 43; DB 1; Length 536;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;


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QY 4 TGGGWDPI 12
Db 247 TGGTWDPI 255

RESULT 4
PUR2_CHITE STANDARD; PRT; 1371 AA.
AC Q26255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trifunctional purine biosynthetic protein adenosine-3 [Includes:
DE Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide
DE ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase);
DE Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (AIRS)
DE (Phosphoribosyl-aminimidazole synthetase) (AIR synthetase);
DE Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR
DE transformylase) (5'-phosphoribosylglycinamide transformylase)].
GN GART.
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92389366; PubMed=1518084;
RA Clark D.V., Henikoff S.;
RT "Unusual organizational features of the Drosophila Gart locus are not
RT conserved within Diptera.";
RL J. Mol. Evol. 35:51-59(1992).
CC -|- CATALYTIC ACTIVITY: ATP + 5-phospho-D-riboseylamine + glycine = ADP
CC + phosphate + N(1)-(5-phospho-D-riboseyl)glycinamide.
CC -|- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-
CC ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-
CC phospho-D-riboseyl)glycinamide.
CC -|- CATALYTIC ACTIVITY: ATP + 2-(formamido)-N(1)-(5-phospho-D-
CC ribosyl)acetamide = ADP + phosphate + 5-amino-1-(5-phospho-D-
CC ribosyl)imidazole.
CC -|- PATHWAY: SECOND, THIRD AND FIFTH STEPS IN DE NOVO PURINE
CC BIOSYNTHESIS.
CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GARS FAMILY.
CC -|- SIMILARITY: TO OTHER AIRS AND GART FROM BACTERIA AND EUKARYOTES.
CC -----
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CC -----
DR EMBL; S43653; AAB23115.1; -.
DR HSSP; P08178; 1CLI.
DR InterPro: IPR000728; AIRS_related.
DR InterPro: IPR001555; GART.
DR InterPro: IPR001115; Gars.
DR InterPro: IPR004733; PurM_cligase.
DR InterPro: IPR004607; PurM.
DR InterPro: IPR002376; formyl_transf.
DR Pfam; PF00551; formyl_transf; 1.
DR Pfam; PF00586; AIRS; 2.
DR Pfam; PF01071; GARS; 1.
DR Pfam; PF02769; AIRS_C; 2.
DR Pfam; PF02842; GARS_B; 1.
DR Pfam; PF02843; GARS_C; 1.
DR Pfam; PF02844; GARS_N; 1.
DR TIGRFAMS; TIGR00639; PurM; 1.
DR TIGRFAMS; TIGR00877; purD; 1.
DR TIGRFAMS; TIGR00878; purM; 2.
DR PROSITE; PS00184; GARS; 1.
DR PROSITE; PS00373; GART; 1.

KW Multifunctional enzyme; Purine biosynthesis; Ligase; Transferase.
FT DOMAIN 1 433 GARS.
FT DOMAIN 434 1171 AIRS.
FT DOMAIN 1172 1371 GART.
FT ACT_SITE 1315 BY SIMILARITY.
SQ SEQUENCE 1371 AA; 149103 MW; 7BF4664DB1538946 CRC64;

Query Match 50.6%; Score 43; DB 1; Length 1371;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGWDPI 12
Db 1057 TGGGLWDNI 1065

RESULT 5
COX3_ASCSU STANDARD; PRT; 255 AA.
ID COX3_ASCSU
AC F24879;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COIII.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OG Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body wall muscle, and Egg;
RX MEDLINE=92201635; PubMed=1551572;
RA Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial genomes of two nematodes, Caenorhabditis elegans
RT and Ascaris suum.";
RL Genetics 130:471-498(1992).
CC -|- FUNCTION: Subunits I, II and III form the functional core of
CC the enzyme complex.
CC -|- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54253; CAA38169.1; -.
DR PIR; S26020; S26020.
DR InterPro: IPR000298; Cytc_oxdse_III.
DR Pfam; PF00510; COX3; 1.
DR ProDom; PD000382; Cytc_oxdse_III; 1.
DR PROSITE; PS00253; COX3; 1.
DR OXidoreductase; Mitochondrion; Transmembrane.
SQ SEQUENCE 255 AA; 29094 MW; 05A992684AC92755 CRC64;

Query Match 49.4%; Score 42; DB 1; Length 255;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGWDPI 12
Db 106 HDVGGVMSPI 115

RESULT 6
AHT1_YEAST STANDARD; PRT; 182 AA.
ID AHT1_YEAST

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AC P29589: P38807:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hexose transport activator protein.
GN AHT1 OR YHR093W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MC 971 B.
RC Oezcan S., Cirilacy M.;
RA Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RC MEDLINE=94378003; PubMed=8091229;
RX Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favella A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -----
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CC -----
DR EMBL; X59464; CAA42071.1; -
DR EMBL; U00060; AAB68925.1; -
DR PIR; S17005; S17005.
DR PIR; S46717; S46717.
DR SGD; S0001135; AHT1.
SQ SEQUENCE 182 AA; 19776 MW; 7B0723BAA1066713 CRC64;

Query Match 48.28; Score 41; DB 1; Length 182;
Best Local Similarity 55.68; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPID 13
DB 44 GGGINGPME 52
|||||
STANDARD; PRT; 478 AA.

RESULT 7
OCT2_PIG
ID OCT2_PIG STANDARD; PRT; 478 AA.
AC Q29013; Q29089;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Octamer-binding transcription factor 2 (OTF-2) (Lymphoid-restricted
DE immunoglobulin octamer binding protein NF-A2) (OCT-2 factor).
GN POU2F2 OR OTF2 OR OCT2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95030552; PubMed=7943947;
RA Tuggie C.K., Helm J., Rothschild M.F.;

RT "Cloning, sequencing and restriction fragment length polymorphism
RT analysis of a porcine cDNA for OCT2.";
RL Anim. Genet. 25:141-145(1994).
RN [2]
RN SEQUENCE OF 210-350 FROM N.A.
RC STRAIN=Duroc;
RX MEDLINE=94095558; PubMed=8270542;
RA Tuggie C.K.;
RT "Cloning and sequence analysis of the swine Oct-2 POU-domain genomic
RT region.";
RL J. Anim. Sci. 71:3172-3172(1993).
CC -!- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR THAT SPECIFICALLY
CC BINDS TO THE OCTAMER MOTIF ('ATTGTCAT') AND PLAYS AN IMPORTANT
CC ROLE IN REGULATING TRANSCRIPTION IN A NUMBER OF TISSUES IN
CC ADDITION TO ACTIVATING IMMUNOGLOBULIN GENE EXPRESSION (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN B-CELLS (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC -!- CLASS-2 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -----
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CC -----
DR EMBL; U00794; AAA80148.1; -
DR EMBL; L03842; AAA74657.1; -
DR HSSP; P09086; LHDP.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000972; Octamer-bind_TF.
DR InterPro; IPR000327; POU_domain.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00157; pou; 1.
DR PRINTS; PR00029; OCTAMER.
DR PRINTS; PR00028; POUDOMAIN.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000583; POU_domain; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
KW Homeobox; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein.
FT DOMAIN 199 269 POU.
FT DNA_BIND 297 356 HOMEBOX.
FT DOMAIN 389 410 LEUCINE-ZIPPER.
FT DOMAIN 77 80 POLY-PRO.
FT DOMAIN 417 424 GLY-RICH.
FT DOMAIN 437 440 POLY-PRO.
FT CONFLICT 212 212 Q -> V (IN REF. 2).
FT CONFLICT 215 215 I -> M (IN REF. 2).
FT CONFLICT 222 222 G -> V (IN REF. 2).
FT CONFLICT 233 233 G -> A (IN REF. 2).
FT CONFLICT 238 238 Q -> K (IN REF. 2).
FT CONFLICT 285 285 R -> S (IN REF. 2).
SQ SEQUENCE 478 AA; 51098 MW; FD196758B603B718 CRC64;

Query Match 47.18; Score 40; DB 1; Length 478;
Best Local Similarity 54.58; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14
DB 466 TGGGLWNPAPY 476
|||||
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RESULT 8
TCPL_MOUSE
ID TCPL_MOUSE STANDARD; PRT; 544 AA.
AC P80313;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta).
GN CCT7 OR COT7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Testis;
RX MEDLINE=95041331; PubMed=7953530;
RA Kubota H., Hynes G., Carne A., Ashworth A., Willison K.R.;
RT "Identification of six Tcp-1-related genes encoding divergent
subunits of the TCP-1-containing chaperonin.";
RL Curr. Biol. 4:89-99(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99269022; PubMed=10336634;
RA Kubota H., Yokota S., Yanagi H., Yura T.;
RT "Structures and coregulated expression of the genes encoding mouse
cytosolic chaperonin CCT subunits.";
RL Eur. J. Biochem. 262:492-500(1999).
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
ACTIN AND TUBULIN.
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
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-----
EMBL: Z31399; CAA83274.1; -.
DR EMBL; AB022160; BA81878.1; -.
DR PIR; S43058; S43058.
DR HSP; P48424; IAE6.
DR MGD; MGI:107184; Cct7.
DR InterPro; IPR002194; Chaperonin_TCP-1.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; Cpn60_TCP1.1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00750; TCP1_1; 1.
DR PROSITE; PS00751; TCP1_2; 1.
DR PROSITE; PS00995; TCP1_3; 1.
KW Chaperone; ATP-binding; Multigene family.
SQ SEQUENCE 544 AA; 59652 MW; 0BD7AD35456EE677 CRC64;

Query Match 47.1%; Score 40; DB 1; Length 544;
Best Local Similarity 46.2%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKHTGGVNDPID 13
DB 466 ARHAQGMWYVD 478

RESULT 9
DNJ2_ALLPO
ID DNJ2_ALLPO STANDARD; PRT; 418 AA.
AC P42824;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ protein homolog 2.
GN LDJ2.
OS Allium porrum (Leek).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4681;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessoule J.J., Testet E., Cassagne C.;
RT "Cloning of a new isoform of a DnaJ protein from Allium porrum
epidermal cells.";
RL Plant Physiol. Biochem. 32:723-727(1994).
CC -!- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 CR DOMAIN.
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EMBL: X77632; CAA54720.1; -.
DR HSP; P25685; LDJ1.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF00684; DnaJ_CXXCXG; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXG; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
KW Chaperone; Repeat; Prenylation; Lipoprotein; Multigene family.
FT DOMAIN 11 76 J-DOMAIN.
FT DOMAIN 83 88 POLY-GLY.
FT REPEAT 148 155 GLY-RICH.
FT REPEAT 164 171 CXXCXGXG MOTIF.
FT REPEAT 191 198 CXXCXGXG MOTIF.
FT REPEAT 207 214 CXXCXGXG MOTIF.
FT LIPID 415 415 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 418 AA; 46584 MW; DCE2A4DF192329E6 CRC64;

Query Match 45.9%; Score 39; DB 1; Length 418;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGVGWDPID 13
DB 85 GGVGWDPID 93

RESULT 10
PDP_BACSU
ID PDP_BACSU STANDARD; PRT; 434 AA.
AC P39142;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) (PNP).
GN *Bacillus subtilis*.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RX SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96134975; PubMed=8550462;
RA Saxild H.H., Andersen L.N., Hammer K.;
RT induction by deoxyribonucleosides, and transcriptional regulation by
RT the deOR-encoded DeOR repressor protein.";
RL J. Bacteriol. 178:424-434(1996).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=168 / HGSC1A1;
RX MEDLINE=97021444; PubMed=8867804;
RA Yoshida K.-I., Fujimura M., Yanai N., Fujita Y.;
RT "Cloning and sequencing of a 23-kb region of the *Bacillus subtilis*
RT genome between the *tol* and *hut* operons.";
RL DNA Res. 2:295-301(1995).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Berruyer M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Connerston I.F., Cummings N.J., Daniel R.A.,
RA Denton K.B., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klearr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krohn S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Potwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Sordo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*.";
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: Pyrimidine nucleoside + phosphate = pyrimidine
CC + alpha-D-ribose 1-phosphate.
CC -!- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
CC PHOSPHORYLASES FAMILY.
CC -----
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CC -----
CC EMBL; X82174; CAA57664.1; -.
CC EMBL; D45912; BAA08339.1; -.
CC EMBL; 299124; CAB15976.1; -.
DR

HSSP; P77836; 1BRW.
DR Subtilist; BG10985; pdp.
DR InterPro; IPR000312; Glycos_transf_3.
DR InterPro; IPR000053; Thymid_phosphils.
DR Pfam; PF00591; Glycos_transf_3; 1.
DR Pfam; PF02885; Glycos_trans_3N; 1.
DR ProDom; PD005916; Thymid_phosphils; 1.
DR PROSITE; PS00647; Thymid_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase; Complete proteome.
SQ SEQUENCE 434 AA; 46532 MW; E451CF497ECF5B30 CRC64;
Query Match 45.9%; Score 39; DB 1; Length 434;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 KHTGGGVW 9
Db 81 KHTGGGVW 88
||: ||||
RESULT 11
YINV6_CAEEL
ID YINV6_CAEEL STANDARD; PRT; 518 AA.
AC P34569; P34570;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 59.0 kDa protein T16H12.6 in chromosome III.
GN T16H12.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC -----
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CC -----
CC EMBL; Z30662; CAA83141.1; -.
CC PIR; S42387; S42387.
DR WormPep; T16H12.6; CE00627.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR PROSITE; PS00097; BTB; FALSE_NEG.
KW Hypothetical protein; Repeat.
FT DOMAIN 1 98 BTB.
FT REPEAT 205 255 KELCH 1.
FT REPEAT 256 302 KELCH 2.
FT REPEAT 308 354 KELCH 3.
FT REPEAT 356 402 KELCH 4.
FT REPEAT 404 450 KELCH 5.
FT REPEAT 452 498 KELCH 6.
SQ SEQUENCE 518 AA; 59036 MW; 117A355F4EAD6A9F CRC64;
Query Match 45.9%; Score 39; DB 1; Length 518;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 HTGGGVWDPI 12

```
Db 368 HOGGEVYDPV 377
Query Match 45.9%; Score 39; DB 1; Length 543;
Best Local Similarity 46.2%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 12
TCFH_HUMAN
ID TCPTH_HUMAN STANDARD; PRT; 543 AA.
AC Q99832; O14871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-complex protein 1, eta subunit (TCP-1-eta) (HIV-1 Nef
DE interacting protein).
DE CC17 OR CCH1 OR NIP1-1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9503262; PubMed=9819444;
RT "Maturation of human cyclin E requires the function of eukaryotic
RT chaperonin CCT.";
RL Mol. Cell. Biol. 18:7584-7589(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 13-424 FROM N.A.
RA Fukushi M., Kimura T., Yamamoto N.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC ACTIN AND TUBULIN (BY SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
CC
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CC
CC -----
CC EMBL; AF026292; AAC96011.1; -.
CC EMBL; BC019296; AAH19296.1; -.
CC EMBL; U83843; AAB41437.1; -.
CC HSSP; P48424; 1A6D.
CC GenSeq; HGNC:1622; CCT7.
CC MIM; 605140; -.
CC InterPro; IPR002194; Chaperonin_TCP-1.
CC InterPro; IPR002423; Cpn60/TCP-1.
CC Pfam; PF00118; cpn60_TCP1.1.
CC PRINTS; PR00304; TCOMPLEXTCP1.
CC PROSITE; PS00750; TCP1_1; 1.
CC PROSITE; PS00751; TCP1_2; 1.
CC PROSITE; PS00995; TCP1_3; 1.
CC Chaperone; ATP-binding; Multigene family.
FT CONFLICT 282 283 HH -> RQ (IN REF. 3).
FT CONFLICT 293 293 L -> P (IN REF. 3).
FT CONFLICT 336 336 A -> P (IN REF. 3).
FT CONFLICT 364 364 C -> L (IN REF. 3).
FT CONFLICT 374 376 LRG -> SPC (IN REF. 3).
FT CONFLICT 407 407 A -> P (IN REF. 3).
FT CONFLICT 411 411 A -> P (IN REF. 3).
SQ SEQUENCE 543 AA; 59366 MW; 9F1E33FA80E6238E CRC64;

Query Match 45.9%; Score 39; DB 1; Length 579;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 HTGGGVNDPI 12
Db 429 HOGGEVYDPV 438
Query Match 45.9%; Score 39; DB 1; Length 579;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
YAKL_YEAST
ID YAKL_YEAST STANDARD; PRT; 807 AA.
AC P14680;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Query Match 45.9%; Score 39; DB 1; Length 543;
Best Local Similarity 46.2%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AKHTGGVNDPID 13
Db 466 ARHAQGGTWYGDV 478
Query Match 45.9%; Score 39; DB 1; Length 543;
Best Local Similarity 46.2%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 13
YR47_CAEEL
ID YR47_CAEEL STANDARD; PRT; 579 AA.
AC Q09563;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 66.0 kDa protein F47D12.7 in chromosome III.
GN F47D12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Taich A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U22831; AAK20068.1; -.
CC WormPep; F47D12.7; CE01951.
CC InterPro; IPR000210; BTB_POZ.
CC InterPro; IPR001798; Kelch.
CC Pfam; PF00651; BTB; 1.
CC Pfam; PF01344; Kelch; 6.
CC PRINTS; PR00501; KELCHREPEAT.
CC SMART; SM00225; BTB; 1.
CC PROSITE; PS50097; BTB; 1.
CC Hypothetical protein; Repeat.
FT DOMAIN 51 119 BTB.
FT REPEAT 266 316 KELCH 1.
FT REPEAT 317 363 KELCH 2.
FT REPEAT 369 415 KELCH 3.
FT REPEAT 417 463 KELCH 4.
FT REPEAT 465 511 KELCH 5.
FT REPEAT 513 559 KELCH 6.
SQ SEQUENCE 579 AA; 66042 MW; 3FE770B5E4C2D32F CRC64;
```

DE Protein kinase YAK1 (EC 2.7.1.1.-).
GN YAK1 OR YJL141C OR J0652.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90108683; PubMed=2558053;
RA Garrett S., Broach J.;
RT "Loss of Ras activity in Saccharomyces cerevisiae is suppressed by
RT disruptions of a new kinase gene, YAK1, whose product may act
RT downstream of the cAMP-dependent protein kinase.";
RL Genes Dev. 3:1336-1348(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / FY1679;
RA MEDLINE=96406771; PubMed=8813765;
RA Katsoulou C., Ternita M., Tavernarakis N., Alexandraki D.;
RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT chromosome X reveals 14 known genes and 13 new open reading frames
RT including homologues of genes clustered on the right arm of
RT chromosome XI.";
RL Yeast 12:787-797(1996).
CC -!- FUNCTION: THIS PROTEIN OCCURS IN REVERTANT RAS/CAMP MUTANTS
CC YEAST AND MAY BE INVOLVED IN CELL-CYCLE REGULATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB/DRK SUBFAMILY.
CC
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CC
CC EMBL; X16056; CA34192.1; -;
DR EMBL; X87371; CA60814.1; -;
DR EMBL; 249417; CA89437.1; -;
DR PIR; A32582; A32582.
DR HSP; P24941; IAO1.
DR SGD; S0003677; YAK1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 56 85 GLN-RICH.
FT DOMAIN 369 704 PROTEIN KINASE.
FT NP_BIND 375 383 ATP (BY SIMILARITY).
FT BINDING 398 398 ATP (BY SIMILARITY).
FT ACT_SITE 496 496 BY SIMILARITY.
FT MOD_RES 127 127 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 206 206 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 240 240 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 295 295 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 807 AA; 91245 MW; E0B7C56FAA35E056 CRC64;

Query Match 45.9%; Score 39; DB 1; Length 807;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 HTGGGVDP 11
| | | | |
DB 43 HMGRIWNP 51

RESULT 15
PRTT_PORGI
ID PRTT_PORGI STANDARD; PRT; 868 AA.
AC P43158;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Thiol protease/hemagglutinin prtr precursor (EC 3.4.22.-).
GN PRTT.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 53977;
RA MEDLINE=93114862; PubMed=8093357;
RA Oototo J.-I., Kuramitsu H.K.;
RT "Isolation and characterization of the Porphyromonas gingivalis prtr
RT gene, coding for protease activity.";
RL Infect. Immun. 61:1117-123(1993).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RX STRAIN=ATCC 53977;
RX MEDLINE=95105001; PubMed=7806362;
RA Madden T.E., Clark V.L., Kuramitsu H.K.;
RT "Revised sequence of the Porphyromonas gingivalis prtr cysteine
RT protease/hemagglutinin gene: homology with streptococcal pyrogenic
RT exotoxin B/streptococcal proteinase.";
RL Infect. Immun. 63:238-247(1995).
CC -!- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGININE-CONTAINING PEPTIDE
CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
CC
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CC
CC EMBL; M83096; -; NOT_ANNOTATED_CDS.
DR MEROPS; C10.002; -;
DR InterPro; IPR000200; Peptidase_C10.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01640; Peptidase_C10; 1.
DR PRINTS; PR00757; STREPTOPAIN.
KW Hydrolase; Thiol protease; Signal; Hemagglutinin.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 ? POTENTIAL.
FT CHAIN ? 868 THIOL PROTEASE/HEMAGGLUTININ PRTT.
FT ACT_SITE 184 184 BY SIMILARITY.
FT ACT_SITE 327 327 BY SIMILARITY.
SQ SEQUENCE 868 AA; 96444 MW; 45436EFE32779323 CRC64;
Query Match 45.9%; Score 39; DB 1; Length 868;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GVWDPTD 13
| | | | |
DB 736 GFWDPTD 742

Search completed: March 13, 2003, 15:15:15
Job time : 3.4 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:11:14 ; Search time 5.06154 seconds
(without alignments)
569.918 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 85
Sequence: 1 AKHTGGGWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	54.1	171	13 Q98U44	Q98U44 mantidactyl
2	46	54.1	177	13 Q98U43	Q98U43 aglyptodact
3	46	54.1	177	13 Q98U41	Q98U41 boophis tep
4	46	54.1	177	13 Q98U33	Q98U33 nyctibatr
5	46	54.1	177	13 Q98U32	Q98U32 nyctibatr
6	46	54.1	177	13 Q98U26	Q98U26 micrixalus
7	46	54.1	177	13 Q98U25	Q98U25 micrixalus
8	46	54.1	177	13 Q98U24	Q98U24 indirana sp
9	46	54.1	177	13 Q98U20	Q98U20 phyllautus m
10	46	54.1	177	13 Q98U19	Q98U19 phyllautus m
11	45	52.9	131	4 Q8WYX0	Q8WYX0 homo sapien
12	45	52.9	177	13 Q98U42	Q98U42 boophis xer
13	45	52.9	177	13 Q98U21	Q98U21 rhacophorus
14	45	52.9	381	16 Q97G57	Q97G57 clostridium
15	44	51.8	489	2 P72455	P72455 streptomyces
16	43.5	51.2	762	2 Q9RM63	Q9RM63 myroides od

17	43	50.6	51	2	Q9F2F8	Q9F2F8 streptococ
18	43	50.6	71	12	Q85298	Q85298 orf virus.
19	43	50.6	102	2	Q9LCA9	Q9LCA9 rhodocyclu
20	43	50.6	304	16	Q9HTS0	Q9HTS0 pseudomonas
21	43	50.6	435	16	Q9A8P0	Q9A8P0 caulobacter
22	43	50.6	762	2	Q9RQ15	Q9RQ15 neisseria d
23	42.5	50.0	597	17	Q9V038	Q9V038 pyrococcus
24	42.5	50.0	597	17	Q8U2G5	Q8U2G5 pyrococcus
25	42.5	50.0	598	17	O58774	O58774 pyrococcus
26	42	49.4	174	13	Q8U4U5	Q8U4U5 mantella ma
27	42	49.4	174	13	Q8RU64	Q8RU64 oryza sativ
28	42	49.4	458	10	Q8RU64	Q8RU64 oryza sativ
29	41	48.2	502	16	O8Y012	O8Y012 raietonia s
30	41	48.2	42	16	O8Y012	O8Y012 streptococ
31	41	48.2	300	16	O34430	O34430 bacillus su
32	41	48.2	324	10	Q9LVM5	Q9LVM5 arabidopsis
33	41	48.2	399	4	Q9Y5P5	Q9Y5P5 homo sapien
34	41	48.2	420	4	O9NWC3	O9NWC3 homo sapien
35	41	48.2	420	4	O961J6	O961J6 homo sapien
36	41	48.2	695	2	O934G0	O934G0 pseudomonas
37	41	48.2	792	4	O9H0D2	O9H0D2 homo sapien
38	41	48.2	801	16	O8XV55	O8XV55 raietonia s
39	41	48.2	1022	2	O93G16	O93G16 bifidobacte
40	41	48.2	1023	2	O9X6Y5	O9X6Y5 bifidobacte
41	41	48.2	1044	2	O9F4D6	O9F4D6 bifidobacte
42	40.5	47.6	1456	2	O9F636	O9F636 stigmatella
43	40.5	47.6	181	10	O9C5D5	O9C5D5 arabidopsis
44	40.5	47.6	388	10	O9M8R4	O9M8R4 arabidopsis
45	40	47.1	56	2	O9RMH8	O9RMH8 lactobacilli
	40	47.1	114	10	Q9SVK9	Q9SVK9 arabidopsis

ALIGNMENTS

RESULT 1

Q98U44 ID Q98U44 PRELIMINARY; PRT; 171 AA.
AC Q98U44;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Mantidactylus cf. ulcersus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Mantidactylus.
OX NCBI_TaxID=129014;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249165; AAG49808.1; .
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; Tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 19816 MW; 50CEFFA8130D2A7B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 171;

Best Local Similarity 70.0%; Pred. No. 11;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGWDPIDY 14

|||||:|||

Db 133 GGGWENIDY 142

RESULT 2

Q98043 ID Q98U43 PRELIMINARY; PRT; 177 AA.
 AC Q98U43;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Aglyptodactylus madagascariensis (Madagascar jumping frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;
 OC Aglyptodactylus.
 OX NCBI_TaxID=68424;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249166; AAG49809.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20410 MW; A4E5A34F90563FF1 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
 |||||: ||:

DB 133 GGGVWENIDF 142

RESULT 3

Q98041 ID Q98U41 PRELIMINARY; PRT; 177 AA.
 AC Q98U41;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Boophis tephraeomystax.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;
 OC Boophis.
 OX NCBI_TaxID=68440;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249168; AAG49811.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20542 MW; 22C28DBB1217467B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;

Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
 |||||: ||:

DB 133 GGGVWENIDF 142

RESULT 4

Q98U33 ID Q98U33 PRELIMINARY; PRT; 177 AA.
 AC Q98U33;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Nyctibatrachus major.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Nyctibatrachus.
 OX NCBI_TaxID=129023;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249176; AAG49819.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20589 MW; 1B647613316D7C42 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
 |||||: ||:

DB 133 GGGVWENIDF 142

RESULT 5

Q98U32 ID Q98U32 PRELIMINARY; PRT; 177 AA.
 AC Q98U32;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Nyctibatrachus aliciae.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Nyctibatrachus.
 OX NCBI_TaxID=129021;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249177; AAG49820.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20556 MW; 2C67161CD96FB382 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 6
 ID Q98U26 PRELIMINARY; PRT; 177 AA.
 AC Q98U26;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus fuscus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OX NCBI_TaxID=129016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249183; AAG49826.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20560 MW; A76738DA4102C9CE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 7
 ID Q98U25 PRELIMINARY; PRT; 177 AA.
 AC Q98U25;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus kottigeharensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OX NCBI_TaxID=130786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs

RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249184; AAG49827.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20574 MW; 05A658678D3BF9D4 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 8
 ID Q98U24 PRELIMINARY; PRT; 177 AA.
 AC Q98U24;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Indirana sp. 1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Indirana.
 OX NCBI_TaxID=147865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249185; AAG49828.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20434 MW; 29EB35222BA6D60B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 9
 ID Q98U20 PRELIMINARY; PRT; 177 AA.
 AC Q98U20;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Philautus microlymanus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=129024;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249189; AAG49832.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20464 MW; 4E2C1654EA212ADE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142

RESULT 10
Q98019 PRELIMINARY; PRT; 177 AA.
AC Q98019;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Philautus wynaedensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=130794;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249190; AAG49833.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20516 MW; 51214062A98389DE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142
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```
ID Q8WY0 PRELIMINARY; PRT; 131 AA.
AC Q8WY0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 52.9%; Score 45; DB 4; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVWDP 11
DB 40 TGGGVWQP 47

RESULT 12
Q98042 PRELIMINARY; PRT; 177 AA.
AC Q98042;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=128996;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249167; AAG49810.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20587 MW; DB6493AF16D0F020 CRC64;

Query Match 52.9%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142

RESULT 13
Q98021 PRELIMINARY; PRT; 177 AA.
ID Q98021
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AC Q98U21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Rhacophorus malabaricus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Rhacophorus.
OX NCBI_TaxID=129031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RL Reveal Co-variation between Larval and Adult Traits.";
DR EMBL: AF249188; AAG49831.1; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR Pfam: PF00264; tyrosinase; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE: PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT 177
FT 177
SQ SEQUENCE 177 AA; 20426 MW; 16A9E9F4F1BE2035 CRC64;

Query Match 52.9%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWFIDY 14
Db 133 GGGVWENVDF 142
|||||:|:|

RESULT 14
Q97GS7
ID Q97GS7 PRELIMINARY; PRT; 381 AA.
AC Q97GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Acyl-protein synthetase, luxE.
GN CAC2288.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007729; AAK80245.1; -.
KW Complete proteome.
SQ SEQUENCE 381 AA; 43104 MW; 68D07900AC06AA70 CRC64;

Query Match 52.9%; Score 45; DB 16; Length 381;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HTGGGVWD 10
Db 223 HTGGGGWD 230
|||||

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RESULT 15
P72455
ID P72455 PRELIMINARY; PRT; 489 AA.
AC P72455;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH:N-amidino-scylo-L-inosamine oxidoreductase.
GN STSB.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=97385085; PubMed=9238101;
RA Ahlert J., Distler J., Mansouri K., Piepersberg W.;
RT "Identification of stsc, the gene encoding the L-glutamine:scyllo-
RL inosose aminotransferase from streptomycin-producing Streptomyces.";
DR Arch. Microbiol. 168:102-113(1997).
DR EMBL: Y08763; CAA70011.1; -.
DR InterPro: IPR000205; NAD_binding.
SQ SEQUENCE 489 AA; 51576 MW; 73B6863C3FAA3C93 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 489;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGVWDP 11
Db 166 SGGGLWDP 173
|||||

Search completed: March 13, 2003, 15:17:00
Job time : 7.06154 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:59 ; Search time 29.0769 Seconds
(without alignments)
54.992 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying Chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	14	AAE12770	Human PH1 Fab anti
2	12	100.0	121	AAE12706	Human PH1 Fab anti
3	12	100.0	381	AAE12707	Human blvPH1-IL-2
4	12	100.0	451	AAE12715	Human recombinant
5	11	91.7	14	AAE12740	Human PH1 Fab anti
6	11	91.7	14	AAE12762	Human PH1 Fab anti
7	11	91.7	16	AAE12734	Human PH1 Fab anti
8	10	83.3	14	AAE12718	Human PH1 Fab anti
9	10	83.3	14	AAE12719	Human PH1 Fab anti
10	10	83.3	14	AAE12720	Human PH1 Fab anti

11	10	83.3	14	22	AAE12741	Human PH1 Fab anti
12	10	83.3	14	22	AAE12742	Human PH1 Fab anti
13	10	83.3	14	22	AAE12743	Human PH1 Fab anti
14	10	83.3	14	22	AAE12744	Human PH1 Fab anti
15	10	83.3	14	22	AAE12748	Human PH1 Fab anti
16	10	83.3	14	22	AAE12749	Human PH1 Fab anti
17	10	83.3	14	22	AAE12751	Human PH1 Fab anti
18	10	83.3	14	22	AAE12753	Human PH1 Fab anti
19	10	83.3	14	22	AAE12754	Human PH1 Fab anti
20	10	83.3	14	22	AAE12755	Human PH1 Fab anti
21	10	83.3	14	22	AAE12759	Human PH1 Fab anti
22	10	83.3	14	22	AAE12761	Human PH1 Fab anti
23	10	83.3	14	22	AAE12763	Human PH1 Fab anti
24	10	83.3	14	22	AAE12765	Human PH1 Fab anti
25	10	83.3	14	22	AAE12766	Human PH1 Fab anti
26	10	83.3	14	22	AAE12767	Human PH1 Fab anti
27	10	83.3	14	22	AAE12772	Human PH1 Fab anti
28	10	83.3	14	22	AAE12774	Human PH1 Fab anti
29	10	83.3	16	22	AAE12735	Human PH1 Fab anti
30	9	75.0	14	22	AAE12746	Human PH1 Fab anti
31	9	75.0	14	22	AAE12747	Human PH1 Fab anti
32	9	75.0	14	22	AAE12756	Human PH1 Fab anti
33	9	75.0	14	22	AAE12757	Human PH1 Fab anti
34	9	75.0	14	22	AAE12758	Human PH1 Fab anti
35	9	75.0	14	22	AAE12764	Human PH1 Fab anti
36	9	75.0	14	22	AAE12768	Human PH1 Fab anti
37	8	66.7	14	22	AAE12771	Human PH1 Fab anti
38	8	66.7	14	22	AAE12773	Human PH1 Fab anti
39	7	58.3	14	22	AAE12745	Human PH1 Fab anti
40	7	58.3	14	22	AAE12769	Human PH1 Fab anti
41	7	58.3	16	22	AAE12722	Human PH1 Fab anti
42	7	58.3	16	22	AAE12723	Human PH1 Fab anti
43	7	58.3	16	22	AAE12724	Human PH1 Fab anti
44	7	58.3	16	22	AAE12725	Human PH1 Fab anti
45	7	58.3	16	22	AAE12726	Human PH1 Fab anti

ALIGNMENTS

RESULT 1
AAE12770
ID AAE12770 standard; peptide; 14 AA.
XX
AC AAE12770;
XX
XX 04-JAN-2002 (first entry)
DT Human PH1 Fab antibody VH region FR3-CDR3 variant #37.
DE Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody; variant.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..2
FT /label= Framework_region_3
FT Region 3..14
FT /label= Complementarity_determining_region_3
XX
XX WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
PI

XX WPI; 2001-626437/72.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 125; 126pp; English.
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 Query Match 100.0%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWDPIDY 14

RESULT 2
 AAE12706
 ID AAE12706 standard; Protein; 121 AA.
 XX AAE12706;
 AC AAE12706;
 DT 04-JAN-2002 (first entry)
 XX Human PH1 Fab antibody variable heavy chain region (VH).
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody.
 XX Homo sapiens.

XX Key Location/Qualifiers
 XX Region 31..35
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT Region 50..66
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT Region 97..99
 FT /label= FR3
 FT /note= "Framework region 3"
 FT Region 97..112
 FT /note= "VH domain"
 FT Region 99..110
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 FT Region 111..112
 FT /label= FR4
 FT /note= "Framework region 4"

PN WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 PI WPI; 2001-626437/72.
 DR N-PSDB; AAD20731.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 2; Page 94-95; 126pp; English.
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
 CC antibody VH region.

XX Sequence 121 AA;
 Query Match 100.0%; Score 12; DB 22; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 Db 99 HTGGGVWDPIDY 110

RESULT 3
 AAE12707
 ID AAE12707 standard; Protein; 381 AA.
 XX AAE12707;
 AC AAE12707;
 DT 04-JAN-2002 (first entry)
 XX Human bivPH1-1L-2 immunocytokine protein.
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
 KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
 XX Homo sapiens.

XX OS
 XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.

PA (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI: 2001-626437/72.
 DR N-PSDB; AAD20732.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 9; Page 95-97; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human bivPH1-1L-2
 CC immunocytokine protein. bivPH1 is mucin specific binding portion.
 XX
 XX Sequence 381 AA;
 SQ
 Query Match 100.0%; Score 12; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DB 99 HTGGGVWDPIDY 110
 |||||
 RESULT 4
 AAE12715
 ID AAE12715 standard; Protein; 451 AA.
 XX
 AC AAE12715;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human recombinant immunoglobulin (Ig) heavy chain region.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
 KW heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; immunoglobulin; Ig.
 XX
 OS Homo sapiens.
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI: 2001-626437/72.
 DR N-PSDB; AAD20745.
 XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 12; Page 106-108; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
 XX
 XX Sequence 451 AA;
 SQ
 Query Match 100.0%; Score 12; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 5.7e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DB 99 HTGGGVWDPIDY 110
 |||||
 RESULT 5
 AAE12740
 ID AAE12740 standard; peptide; 14 AA.
 XX
 AC AAE12740;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT Region /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI: 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PT its portion for binding to an epitope of the protein core of mucin-1
 XX
 PS Example 2; Page 119; 126pp; English.
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 SQ
 Query Match 91.7%; Score 11; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVNDPID 11
 DB 3 HTGGGVNDPID 13
 |||||

RESULT 6
 AAE12762
 ID AAE12762 standard; peptide; 14 AA.

XX AAE12762;
 XX
 XX 04-JAN-2002 (first entry)

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #29.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1

Example 2; Page 123; 126pp; English.

PS The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 91.7%; Score 11; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVNDPID 11
 DB 3 HTGGGVNDPID 13
 |||||

RESULT 7
 AAE12734
 ID AAE12734 standard; peptide; 16 AA.

XX AAE12734;

XX 04-JAN-2002 (first entry)

DE Human PH1 Fab antibody variable heavy chain domain (VH) #13.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= FR3
 FT /note= "Framework region 3"
 FT Region 3..14
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 FT Region 15..16
 FT /label= FR4
 FT /note= "Framework region 4"

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20765.

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
PS Example 2; Page 52; 126pp; English.
XX
CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC domain.
XX
SQ Sequence 16 AA;

Query Match 91.7%; Score 11; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDPIDY 12
| | | | | | | | | |
Db 4 TGGGVWDPIDY 14

RESULT 8
AAE12718
ID AAE12718 standard; peptide; 14 AA.
XX
AC AAE12718;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody VH region FR3-CDR3 variant #2.
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..2
FT /label= Framework_region_3
FT Region 3..14
FT /label= Complementarity_determining_region_3
XX
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MPG;
XX
DR WPI; 2001-626437/72.
XX
PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -

PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
PS Claim 2; Page 75; 126pp; English.
XX
CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC region FR (framework region)3-CDR3 variant.
XX
SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
| | | | | | | | | |
Db 3 HTGGGVWDPI 12

RESULT 9
AAE12719
ID AAE12719 standard; peptide; 14 AA.
XX
AC AAE12719;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody VH region FR3-CDR3 variant #3.
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..2
FT /label= Framework_region_3
FT Region 3..14
FT /label= Complementarity_determining_region_3
XX
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MPG;
XX
DR WPI; 2001-626437/72.
XX
PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -

PS Claim 2; Page 75; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 10
 AAEL12720
 ID AAEL12720 standard; peptide; 14 AA.
 AC AAEL12720;
 XX
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #4.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 XX WO200175110-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 PF 30-MAR-2000; 2000US-0538913.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 XX Hoogenboom HRJM, Henderikx MPG;
 PI
 XX WPI; 2001-626437/72.
 DR
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 2; Page 75; 126pp; English.

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 11
 AAEL12741
 ID AAEL12741 standard; peptide; 14 AA.
 AC AAEL12741;
 XX
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #8.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 XX WO200175110-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 PF 30-MAR-2000; 2000US-0538913.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 XX Hoogenboom HRJM, Henderikx MPG;
 PI
 XX WPI; 2001-626437/72.
 DR
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 119; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;
 Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPI 10
 Db 3 HTGGGVWDPI 12
 |||||
 RESULT 12
 AAEL2742
 ID AAEL2742 standard; peptide; 14 AA.
 AC AAEL2742;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #9.
 XX
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 FT
 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 XX (DYAX-) DYAX CORP.
 XX
 XX Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 119; 126pp; English.
 PS
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;
 Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPI 10
 Db 3 HTGGGVWDPI 12
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 RESULT 13
 AAEL2743
 ID AAEL2743 standard; peptide; 14 AA.
 AC AAEL2743;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #10.
 XX
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
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 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 XX (DYAX-) DYAX CORP.
 XX
 XX Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 119; 126pp; English.
 PS
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
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Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 14
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 ID AAEL2744 standard; peptide; 14 AA.
 XX
 AC AAEL2744;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #11.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 119; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 15
 AAEL2748
 ID AAEL2748 standard; peptide; 14 AA.
 XX
 AC AAEL2748;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 XX WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 120; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

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 Job time : 29.0769 secs

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OM protein - protein search, using sw model

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(without alignments)
33.261 Million cell updates/sec

Title: US-09-822-698a-3_COPY_99_110

Sequence: 12
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Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents.AA.*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	50.0	95	4	US-08-928-383B-18
2	5	41.7	8	4	US-08-637-732A-34
3	5	41.7	8	4	US-08-637-732A-36
4	5	41.7	14	4	US-08-973-131-75
5	5	41.7	20	1	US-08-103-742-12
6	5	41.7	20	1	US-08-139-508-5
7	5	41.7	22	1	US-07-791-930C-9
8	5	41.7	22	1	US-08-173-515B-12
9	5	41.7	22	3	US-08-329-799-40
10	5	41.7	33	2	US-08-415-788-28
11	5	41.7	34	2	US-08-415-788-11
12	5	41.7	34	2	US-08-415-788-14
13	5	41.7	34	2	US-08-415-788-18
14	5	41.7	34	2	US-08-415-788-24
15	5	41.7	41	2	US-08-415-788-5
16	5	41.7	41	2	US-08-415-788-41
17	5	41.7	56	4	US-07-741-453A-47
18	5	41.7	58	4	US-09-605-785-553
19	5	41.7	116	2	US-08-428-197-10
20	5	41.7	116	5	PCT-US93-10555-10
21	5	41.7	187	4	US-09-117-257-23
22	5	41.7	187	4	US-08-945-476-23
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25	5	41.7	188	4	US-09-489-352-44
26	5	41.7	264	4	US-08-856-841-14
27	5	41.7	325	1	US-08-118-270-30

28	5	41.7	325	5	PCT-US93-08528-30	Sequence 30, Appl
29	5	41.7	329	1	US-08-348-792-12	Sequence 12, Appl
30	5	41.7	329	2	US-08-462-738-12	Sequence 12, Appl
31	5	41.7	329	4	US-09-199-955-12	Sequence 12, Appl
32	5	41.7	329	4	US-08-880-875-12	Sequence 12, Appl
33	5	41.7	343	1	US-08-348-792-10	Sequence 10, Appl
34	5	41.7	343	2	US-08-462-738-10	Sequence 10, Appl
35	5	41.7	343	4	US-09-199-955-10	Sequence 10, Appl
36	5	41.7	343	4	US-08-880-875-10	Sequence 10, Appl
37	5	41.7	356	4	US-08-259-451-17	Sequence 17, Appl
38	5	41.7	359	1	US-08-181-271A-98	Sequence 98, Appl
39	5	41.7	359	1	US-08-449-315-98	Sequence 98, Appl
40	5	41.7	359	1	US-08-444-803-98	Sequence 98, Appl
41	5	41.7	359	1	US-08-047-413-15	Sequence 15, Appl
42	5	41.7	359	1	US-08-449-043-98	Sequence 98, Appl
43	5	41.7	359	1	US-08-456-265A-98	Sequence 98, Appl
44	5	41.7	359	1	US-08-455-416-98	Sequence 98, Appl
45	5	41.7	359	1	US-08-455-244-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-08-928-383B-18
; Sequence 18, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cossackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-928-383B-18

Query Match 50.0%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGV 6

Db 88 HTGGG 93
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RESULT 2

US-08-637-732A-34
; Sequence 34, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,732A

; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-34

Query Match 41.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
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Db 1 HTGGG 5

RESULT 3

US-08-637-732A-36
; Sequence 36, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia

; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,732A
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-36

Query Match 41.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
|||||

Db 1 HTGGG 5

RESULT 4

US-08-973-131-75
; Sequence 75, Application US/08973131
; Patent No. 6326166
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Joel L.
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Chimeric DNA-binding proteins
; FILE REFERENCE: APV-022.02
; CURRENT APPLICATION NUMBER: US/08/973,131
; CURRENT FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: PCT/US95/16982
; EARLIER FILING DATE: 1995-12-29
; EARLIER APPLICATION NUMBER: 08/366,083
; EARLIER FILING DATE: 1994-12-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric motif
US-08-973-131-75

Query Match 41.7%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 HTGGG 7

RESULT 5

US-08-103-742-12
; Sequence 12, Application 08/103742


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; Patent No. 5420244
; GENERAL INFORMATION:
; APPLICANT: RUDOLPH, DONNA L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUKA
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/103,742
; FILING DATE: 06 AUG 1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRATT, GWENDOLYN D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-103-742-12

Query Match 41.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 11 WDPID 15

RESULT 6
US-08-199-508-5
; Sequence 5, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sonatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,508
; FILING DATE: February 18, 1994
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,536
; FILING DATE: February 23, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5717058ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 121 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
US-08-199-508-5

Query Match 41.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 8 WDPID 12

RESULT 7
US-07-791-930C-9
; Sequence 9, Application US/07791930C
; Patent No. 5360726
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: Polypeptides Enabling Sorting
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,930C
; FILING DATE: 1991 No. 5360726ember 12
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/612,200
; FILING DATE: No. 5360726ember 13, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
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;;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-07-791-930C-9

Query Match 41.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGWVD 8
| | | | |
Db 3 GGWVD 7

RESULT 8
US-08-173-515B-12
; Sequence 12, Application US/08173515B
; Patent No. 5525713
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: DNA Encoding Polypeptides
; TITLE OF INVENTION: Enabling Sorting of proteins to
; TITLE OF INVENTION: vacuoles of plants.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,515B
; FILING DATE: 1993 December 23
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,930
; FILING DATE: 1991 NO. 5525713ember 12
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5525713e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22

;;
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-08-173-515B-12

Query Match 41.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGWVD 8
| | | | |
Db 3 GGWVD 7

RESULT 9
US-08-329-799-40
; Sequence 40, Application US/08329799
; Patent No. 6054637
; GENERAL INFORMATION:
; APPLICANT: Boller, Thomas
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Ryals, John
; TITLE OF INVENTION: No. 6054637el Signal Sequences
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,799
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,521
; FILING DATE: 13-JUN-1991
; APPLICATION NUMBER: CH 2007/90-9
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: GA/5-18123/A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-329-799-40

Query Match 41.7%; Score 5; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGWD 8
Db 3 GGWD 7

RESULT 10

US-08-415-788-28
Sequence 28, Application US/08415788
Patent No. 5834591

GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,788
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,465
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SCHWENNING, LYNN E.
REGISTRATION NUMBER: 37,233
REFERENCE/DOCKET NUMBER: 29500-20046.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-788-28

Query Match 41.7%; Score 5; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
Db 13 HTGGG 17

RESULT 11

US-08-415-788-11
Sequence 11, Application US/08415788
Patent No. 5834591
GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,788
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,465
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SCHWENNING, LYNN E.
REGISTRATION NUMBER: 37,233
REFERENCE/DOCKET NUMBER: 29500-20046.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-788-11

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
Db 13 HTGGG 17

RESULT 12

US-08-415-788-14
Sequence 14, Application US/08415788
Patent No. 5834591

GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-14

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Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 HTGGG 5
    |||||
Db 13 HTGGG 17

```

```

RESULT 13
US-08-415-788-18
; Sequence 18, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-18

```

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Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 HTGGG 5
    |||||
Db 13 HTGGG 17

```

```

RESULT 14
US-08-415-788-24
; Sequence 24, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-24

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```

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 HTGGG 5
    |||||
Db 13 HTGGG 17

```

```

RESULT 15
US-08-415-788-5
; Sequence 5, Application US/08415788

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; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-5

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Query Match 41.7%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGG 5
Db 24 HTGGG 28

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Search completed: March 13, 2003, 15:34:10
Job time : 10.6154 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:33:09 ; Search time 9.69231 Seconds
(without alignments)
57.066 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	12	100.0	121	10	US-09-822-698A-3
3	12	100.0	381	10	US-09-822-698A-5
4	12	100.0	451	10	US-09-822-698A-26
5	11	91.7	14	10	US-09-822-698A-75
6	11	91.7	14	10	US-09-822-698A-97
7	11	91.7	16	10	US-09-822-698A-65
8	10	83.3	14	10	US-09-822-698A-30
9	10	83.3	14	10	US-09-822-698A-31
10	10	83.3	14	10	US-09-822-698A-32
11	10	83.3	14	10	US-09-822-698A-76
12	10	83.3	14	10	US-09-822-698A-77
13	10	83.3	14	10	US-09-822-698A-78
14	10	83.3	14	10	US-09-822-698A-79
15	10	83.3	14	10	US-09-822-698A-83
16	10	83.3	14	10	US-09-822-698A-84
17	10	83.3	14	10	US-09-822-698A-85
18	10	83.3	14	10	US-09-822-698A-88
19	10	83.3	14	10	US-09-822-698A-89

20 10 83.3 14 10 US-09-822-698A-90 Sequence 90, Appl
21 10 83.3 14 10 US-09-822-698A-94 Sequence 94, Appl
22 10 83.3 14 10 US-09-822-698A-96 Sequence 96, Appl
23 10 83.3 14 10 US-09-822-698A-98 Sequence 98, Appl
24 10 83.3 14 10 US-09-822-698A-100 Sequence 100, Appl
25 10 83.3 14 10 US-09-822-698A-101 Sequence 101, Appl
26 10 83.3 14 10 US-09-822-698A-102 Sequence 102, Appl
27 10 83.3 14 10 US-09-822-698A-107 Sequence 107, Appl
28 10 83.3 14 10 US-09-822-698A-109 Sequence 109, Appl
29 10 83.3 16 10 US-09-822-698A-67 Sequence 67, Appl
30 9 75.0 14 10 US-09-822-698A-81 Sequence 81, Appl
31 9 75.0 14 10 US-09-822-698A-82 Sequence 82, Appl
32 9 75.0 14 10 US-09-822-698A-91 Sequence 91, Appl
33 9 75.0 14 10 US-09-822-698A-92 Sequence 92, Appl
34 9 75.0 14 10 US-09-822-698A-93 Sequence 93, Appl
35 9 75.0 14 10 US-09-822-698A-99 Sequence 99, Appl
36 9 75.0 14 10 US-09-822-698A-103 Sequence 103, Appl
37 8 66.7 14 10 US-09-822-698A-106 Sequence 106, Appl
38 8 66.7 14 10 US-09-822-698A-108 Sequence 108, Appl
39 7 58.3 14 10 US-09-822-698A-80 Sequence 80, Appl
40 7 58.3 14 10 US-09-822-698A-104 Sequence 104, Appl
41 7 58.3 16 10 US-09-822-698A-41 Sequence 41, Appl
42 7 58.3 16 10 US-09-822-698A-43 Sequence 43, Appl
43 7 58.3 16 10 US-09-822-698A-45 Sequence 45, Appl
44 7 58.3 16 10 US-09-822-698A-47 Sequence 47, Appl
45 7 58.3 16 10 US-09-822-698A-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-09-822-698A-105

; Sequence 105, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 105

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-105

Query Match 100.0%; Score 12; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.2e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

Db 3 HTGGGVWDPIDY 14

RESULT 2

US-09-822-698A-3

; Sequence 3, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A


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QY 1 HTGGGVWDPI 11
Db 3 HTGGGVWDPI 13

RESULT 7
US-09-822-698A-65
; Sequence 65, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 65
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-65

Query Match 91.7%; Score 11; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 12
Db 4 TGGGVWDPI 14

RESULT 8
US-09-822-698A-30
; Sequence 30, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match 83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 9
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match 83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 11
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

Query Match 83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 12
US-09-822-698A-32
; Sequence 32, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

Query Match 83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12
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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
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Db 3 HTGGGVWDPI 12

```

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RESULT 12
US-09-822-698A-77
; Sequence 77, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 77
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-77

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

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RESULT 13
US-09-822-698A-78
; Sequence 78, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 78
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-78

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
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Db 3 HTGGGVWDPI 12

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RESULT 14
US-09-822-698A-79
; Sequence 79, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
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Db 3 HTGGGVWDPI 12

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RESULT 15
US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

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Search completed: March 13, 2003, 15:40:23
Job time : 9.69231 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:31:49 ; Search time 130.154 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110

Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
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- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	12	100.0	14	22	US-09-822-698A-105	Sequence 105, App
2	12	100.0	121	19	US-09-538-913-3	Sequence 3, Appli
3	12	100.0	121	22	US-09-822-698A-3	Sequence 3, Appli
4	12	100.0	381	19	US-09-538-913-5	Sequence 5, Appli
5	12	100.0	381	22	US-09-822-698A-5	Sequence 5, Appli
6	12	100.0	451	22	US-09-822-698A-26	Sequence 26, Appli

7	11	91.7	14	22	US-09-822-698A-75	Sequence 75, Appl
8	11	91.7	14	22	US-09-822-698A-97	Sequence 97, Appl
9	11	91.7	16	22	US-09-822-698A-65	Sequence 65, Appl
10	10	83.3	14	22	US-09-822-698A-30	Sequence 30, Appl
11	10	83.3	14	22	US-09-822-698A-31	Sequence 31, Appl
12	10	83.3	14	22	US-09-822-698A-32	Sequence 32, Appl
13	10	83.3	14	22	US-09-822-698A-76	Sequence 76, Appl
14	10	83.3	14	22	US-09-822-698A-77	Sequence 77, Appl
15	10	83.3	14	22	US-09-822-698A-78	Sequence 78, Appl
16	10	83.3	14	22	US-09-822-698A-79	Sequence 79, Appl
17	10	83.3	14	22	US-09-822-698A-83	Sequence 83, Appl
18	10	83.3	14	22	US-09-822-698A-84	Sequence 84, Appl
19	10	83.3	14	22	US-09-822-698A-86	Sequence 86, Appl
20	10	83.3	14	22	US-09-822-698A-88	Sequence 88, Appl
21	10	83.3	14	22	US-09-822-698A-89	Sequence 89, Appl
22	10	83.3	14	22	US-09-822-698A-90	Sequence 90, Appl
23	10	83.3	14	22	US-09-822-698A-94	Sequence 94, Appl
24	10	83.3	14	22	US-09-822-698A-96	Sequence 96, Appl
25	10	83.3	14	22	US-09-822-698A-98	Sequence 98, Appl
26	10	83.3	14	22	US-09-822-698A-100	Sequence 100, App
27	10	83.3	14	22	US-09-822-698A-101	Sequence 101, App
28	10	83.3	14	22	US-09-822-698A-102	Sequence 102, App
29	10	83.3	14	22	US-09-822-698A-107	Sequence 107, App
30	10	83.3	14	22	US-09-822-698A-109	Sequence 109, App
31	10	83.3	16	22	US-09-822-698A-67	Sequence 67, Appl
32	9	75.0	14	22	US-09-822-698A-81	Sequence 81, Appl
33	9	75.0	14	22	US-09-822-698A-82	Sequence 82, Appl
34	9	75.0	14	22	US-09-822-698A-91	Sequence 91, Appl
35	9	75.0	14	22	US-09-822-698A-92	Sequence 92, Appl
36	9	75.0	14	22	US-09-822-698A-93	Sequence 93, Appl
37	9	75.0	14	22	US-09-822-698A-99	Sequence 99, Appl
38	9	75.0	14	22	US-09-822-698A-103	Sequence 103, App
39	8	66.7	14	22	US-09-822-698A-106	Sequence 106, App
40	8	66.7	14	22	US-09-822-698A-108	Sequence 108, App
41	7	58.3	14	22	US-09-822-698A-80	Sequence 80, Appl
42	7	58.3	14	22	US-09-822-698A-104	Sequence 104, App
43	7	58.3	16	22	US-09-822-698A-41	Sequence 41, Appl
44	7	58.3	16	22	US-09-822-698A-43	Sequence 43, Appl
45	7	58.3	16	22	US-09-822-698A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoechst, Hendrix R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DXX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match	100.0%	Score 12;	DB 22;	Length 14;
Best Local Similarity	100.0%	Pred. No. 2.9e-05;		
Matches	12;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	HTGGGVWDPIDY 12		
Db	3	HTGGGVWDPIDY 14		

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RESULT 2
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match      100.0%; Score 12; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
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Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 12; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for biVPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 12; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine biVPHI-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 12; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
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Db 99 HTGGGVWDPIDY 110

RESULT 6
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26
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Query Match      100.0%; Score 12; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 12
   |||||
Db 99 HTGGGVWDPI 110

RESULT 7
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 8
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 9
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 9
```

```
US-09-822-698A-65
; Sequence 65, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 65
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-65

Query Match      91.7%; Score 11; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 12
   |||||
Db 4 TGGGVWDPI 14

RESULT 10
US-09-822-698A-30
; Sequence 30, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

RESULT 11
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
```

```
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 12
US-09-822-698A-32
; Sequence 32, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 13
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 14
US-09-822-698A-77
; Sequence 77, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 77
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-77

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 15
US-09-822-698A-78
; Sequence 78, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 78
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-78

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

Search completed: March 13, 2003, 15:39:00
Job time : 130.154 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:32:14 ; Search time 20.7692 Seconds
(without alignments)
75.113 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 596842 seqs, 130003698 residues

Word size : 0

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US16_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	50.0	55	1 PCT-US02-32727-11588	Sequence 11588, A
2	6	50.0	55	5 US-09-978-825-11588	Sequence 11588, A
3	6	50.0	55	6 US-10-057-498-11588	Sequence 11588, A
4	6	50.0	93	1 PCT-US02-32727-9150	Sequence 9150, Ap
5	6	50.0	93	5 US-09-978-825-9150	Sequence 9150, Ap
6	6	50.0	93	6 US-10-057-498-9150	Sequence 9150, Ap
7	6	50.0	330	6 US-10-366-683-23794	Sequence 23794, A
8	6	50.0	701	6 US-10-282-122A-62129	Sequence 62129, A
9	6	50.0	1583	1 PCT-US02-32727-15149	Sequence 15149, A
10	6	50.0	1583	5 US-09-978-825-15149	Sequence 15149, A
11	6	50.0	1583	6 US-10-057-498-15149	Sequence 15149, A
12	5	41.7	38	6 US-10-156-761-15030	Sequence 15030, A
13	5	41.7	51	5 US-09-724-676-87689	Sequence 87689, A
14	5	41.7	51	5 US-09-724-676A-87689	Sequence 87689, A
15	5	41.7	56	1 PCT-US02-32727-26391	Sequence 26391, A
16	5	41.7	56	5 US-09-978-825-26391	Sequence 26391, A
17	5	41.7	56	6 US-10-057-498-26391	Sequence 26391, A
18	5	41.7	58	5 US-09-593-793A-553	Sequence 553, App
19	5	41.7	58	6 US-10-294-025-553	Sequence 553, App
20	5	41.7	66	1 PCT-US02-32727-28218	Sequence 28218, A
21	5	41.7	66	5 US-09-978-825-28218	Sequence 28218, A
22	5	41.7	66	6 US-10-057-498-28218	Sequence 28218, A
23	5	41.7	67	1 PCT-US02-32727-9117	Sequence 9117, Ap
24	5	41.7	67	5 US-09-978-825-9117	Sequence 9117, Ap
25	5	41.7	67	6 US-10-057-498-9117	Sequence 9117, Ap
26	5	41.7	68	1 PCT-US02-32727-28689	Sequence 28689, A

27	5	41.7	68	5	US-09-978-825-28689	Sequence 28689, A
28	5	41.7	68	6	US-10-057-498-28689	Sequence 28689, A
29	5	41.7	77	5	US-09-724-676-87695	Sequence 87695, A
30	5	41.7	77	5	US-09-724-676A-87695	Sequence 87695, A
31	5	41.7	78	1	PCT-US02-32727-21401	Sequence 21401, A
32	5	41.7	78	5	US-09-978-825-21401	Sequence 21401, A
33	5	41.7	78	6	US-10-057-498-21401	Sequence 21401, A
34	5	41.7	84	5	US-09-724-676-87694	Sequence 87694, A
35	5	41.7	84	5	US-09-724-676A-87694	Sequence 87694, A
36	5	41.7	93	1	PCT-US02-32727-16769	Sequence 16769, A
37	5	41.7	93	5	US-09-978-825-16769	Sequence 16769, A
38	5	41.7	93	6	US-10-057-498-16769	Sequence 16769, A
39	5	41.7	94	6	US-10-363-929-159	Sequence 159, App
40	5	41.7	97	1	PCT-US02-32727-9048	Sequence 9048, Ap
41	5	41.7	97	5	US-09-978-825-9048	Sequence 9048, Ap
42	5	41.7	97	6	US-10-057-498-9048	Sequence 9048, Ap
43	5	41.7	102	1	PCT-US02-32727-25439	Sequence 25439, A
44	5	41.7	102	5	US-09-978-825-25439	Sequence 25439, A
45	5	41.7	102	6	US-10-057-498-25439	Sequence 25439, A

ALIGNMENTS

RESULT 1
PCT-US02-32727-11588
; Sequence 11588, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siquing
; APPLICANT: Jen, Shyan
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darlick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-11588

Query Match 50.0%; Score 6; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 2
US-09-978-825-11588
; Sequence 11588, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siquing

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; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-11588

Query Match          50.0%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 3
US-10-057-498-11588
; Sequence 11588, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-11588

Query Match          50.0%; Score 6; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 4
PCT-US02-32727-9150
; Sequence 9150, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

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; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-9150

Query Match          50.0%; Score 6; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 10 GGGVWD 15

RESULT 5
US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-9150

Query Match          50.0%; Score 6; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 10 GGGVWD 15

RESULT 6
US-10-057-498-9150
; Sequence 9150, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes

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US-10-057-498-9150

Query Match 50.0%; Score 6; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
| | | | |
DB 10 GGGVWD 15

RESULT 7

US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 50.0%; Score 6; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VWDPID 11
| | | | |
DB 103 VWDPID 108

RESULT 8

US-10-282-122A-62129
; Sequence 62129, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62129
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62129

Query Match 50.0%; Score 6; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
| | | | |
DB 75 HTGGGV 80

RESULT 9

PCT-US02-32727-15149
; Sequence 15149, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 15149
; LENGTH: 1583
; TYPE: PRT
; ORGANISM: Propionibacterium
PCT-US02-32727-15149

Query Match 50.0%; Score 6; DB 1; Length 1583;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
| | | | |
DB 1039 GGGVWD 1044

RESULT 10

US-09-978-825-15149
; Sequence 15149, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay

```

; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 15149
; LENGTH: 1583
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-15149

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```

Query Match          50.0%; Score 6; DB 5; Length 1583;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 GGGVWD 8
Db 1039 GGGVWD 1044

```

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RESULT 11
US-10-057-498-15149
; Sequence 15149, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 15149
; LENGTH: 1583
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-15149

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```

Query Match          50.0%; Score 6; DB 6; Length 1583;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 GGGVWD 8
Db 1039 GGGVWD 1044

```

```

RESULT 12
US-10-156-761-15030
; Sequence 15030, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089

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; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 15030
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-15030

```

```

Query Match          41.7%; Score 5; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGG 5
Db 14 HTGGG 18

```

```

RESULT 13
US-09-724-676-87689
; Sequence 87689, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87689
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-87689

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```

Query Match          41.7%; Score 5; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 TGGGV 6
Db 47 TGGGV 51

```

```

RESULT 14
US-09-724-676A-87689
; Sequence 87689, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87689
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-87689

```

```

Query Match          41.7%; Score 5; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 TGGGV 6
Db 47 TGGGV 51

```

```

RESULT 15
PCT-US02-32727-26391

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; Sequence 26391, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 26391
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-26391

Query Match          41.7%; Score 5; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGG 5
   |||||
Db 25 HTGGG 29

Search completed: March 13, 2003, 15:39:55
Job time : 21.7692 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model
Run on: March 13, 2003, 15:29:54 ; Search time 12,4615 Seconds
(without alignments)
92.574 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	50.0	114	2 T08411	hypothetical prote
2	6	50.0	193	2 C82683	disulfide oxidore
3	6	50.0	436	2 H84121	NADH oxidase (nox)
4	6	50.0	1123	2 S20497	phytochrome A - po
5	5	41.7	10	2 H60787	sperm-activating p
6	5	41.7	10	2 D60788	sperm-activating p
7	5	41.7	10	2 B60787	sperm-activating p
8	5	41.7	10	2 A60788	sperm-activating p
9	5	41.7	10	2 C60589	sperm-activating p
10	5	41.7	10	2 D60588	sperm-activating p
11	5	41.7	71	2 T26663	hypothetical prote
12	5	41.7	72	2 T48971	hypothetical prote
13	5	41.7	75	2 A69147	hypothetical prote
14	5	41.7	101	2 S22454	ribosomal protein
15	5	41.7	107	2 S58218	hypothetical prote
16	5	41.7	113	2 S25575	Ig heavy chain V r
17	5	41.7	119	2 D83723	hypothetical prote
18	5	41.7	119	2 T48745	hypothetical prote
19	5	41.7	120	2 C53482	transcription regu
20	5	41.7	133	2 C97301	uncharacterized co
21	5	41.7	144	2 F64094	ribosomal protein
22	5	41.7	145	2 D70938	hypothetical prote
23	5	41.7	150	2 A83482	exsF protein [limpo
24	5	41.7	155	2 C86206	hypothetical prote
25	5	41.7	158	2 C95159	shikimate kinase [
26	5	41.7	158	2 G98025	shikimate kinase (
27	5	41.7	160	2 G69376	conserved hypothet
28	5	41.7	163	2 A70847	hypothetical prote
29	5	41.7	168	2 D82310	CinA-related prote

30	5	41.7	169	2 A40522	plasmin (EC 3.4.21
31	5	41.7	175	2 A71680	cytochrome C (cycM
32	5	41.7	175	2 A97742	cytochrome c limpo
33	5	41.7	181	1 I41314	K88 fimbrial prote
34	5	41.7	185	2 F95008	acetyltransferase,
35	5	41.7	188	2 B95365	probable oxidoredu
36	5	41.7	189	1 S74659	shikimate kinase (
37	5	41.7	189	2 D69128	conserved hypothet
38	5	41.7	189	2 A87254	hypothetical prote
39	5	41.7	194	2 JC4589	immunoreactive pro
40	5	41.7	197	2 S25106	capsid protein - b
41	5	41.7	198	2 S30968	major tail protein
42	5	41.7	198	2 E72802	major tail subunit
43	5	41.7	198	2 S31937	coat protein - Myc
44	5	41.7	203	2 F70601	probable rimJ prot
45	5	41.7	205	2 C90140	conserved hypothet

ALIGNMENTS

RESULT 1

T08411
hypothetical protein F18B3.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08411
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16409
A:Accession: T08411
A:Molecule type: DNA
A:Residues: 1-114 <QUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.180
A:Map position: 3
C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 50.0%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	GGVWDP	9
Db	99	GGVWDP	104

RESULT 2

C82683
disulfide oxidoreductase XF1436 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82683
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <SUM>
A:Cross-references: GB:AE003973; GB:AE003849; NID:g9106438; PIDN:AAF84245.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorrry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XFL436

Query Match 50.0%; Score 6; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDP 9
 Db 68 GGVWDP 73

RESULT 3

H84121
 NADH oxidase (nox) BH3776 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H84121
 R:Takami, H.; Nakasono, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: H84121
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-436 <STO>
 A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA07495.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3776
 C:Superfamily: NADH peroxidase; dihydrolipoamide dehydrogenase homology

Query Match 50.0%; Score 6; DB 2; Length 436;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GVVWDP 10
 Db 424 GVVWDP 429

RESULT 4

S20497
 phytochrome A - potato
 C:Species: Solanum tuberosum (potato)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 30-Apr-1999
 C:Accession: S20497
 R:Heyer, A.; Gatz, C.
 Plant Mol. Biol. 18, 535-544, 1992
 A:Title: Isolation and characterization of a cDNA-clone coding for potato type A phytoch
 A:Reference number: S20497; MUID:92163018; PMID:1536928
 A:Accession: S20497
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1123 <HEY>
 C:Genetics:
 A:Gene: phyA
 C:Superfamily: phytochrome; phytochrome homology
 C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
 F:67-582/Domain: phytochrome homology <PHT>
 F:323/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 50.0%; Score 6; DB 2; Length 1123;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
 Db 1058 HTGGGV 1063

RESULT 5

H60787
 sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
 C:Species: Anthocidaris crassispina
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C:Accession: H60787
 R:Suzuki, N.; Kajilura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent
 A:Reference number: A60787; MUID:88242184; PMID:3378407
 A:Accession: H60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
 Db 5 TGGGV 9

RESULT 6

D60788
 sperm-activating peptide (Thr-5 speract) - sea urchin (Pseudocentrotus depressus)
 C:Species: Pseudocentrotus depressus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
 C:Accession: D60788
 R:Suzuki, N.; Kajilura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen
 A:Reference number: A60787; MUID:88242184; PMID:3378407
 A:Accession: D60788
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
 Db 5 TGGGV 9

RESULT 7

B60787
 sperm-activating peptide (Thr-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
 C:Species: Hemicentrotus pulcherrimus
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C:Accession: B60787
 R:Suzuki, N.; Kajilura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen
 A:Reference number: A60787; MUID:88242184; PMID:3378407
 A:Accession: B60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

D60588
sperm-activating peptide (Thr-5 SAP-I) - sea urchin (*Strongylocentrotus nudus*)
N; Alternate names: speract homolog
C; Species: *Strongylocentrotus nudus*
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
R; Accession: D60588
R; Yoshino, K.I.; Kajilura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, S.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A; Title: A halogenated amino acid-containing sperm activating peptide and its related peptides from the sea urchin, *Strongylocentrotus nudus*, and heterocentrotus mammillatus.

hypothetical protein MTH364 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69147
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
k1, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69147
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-75 <MTH>
A:Cross-references: GB:AE000822; GB:AE000666; NID:g2621420; PIDN:AAB84870.1; PID:g262142
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH364
A:Start codon: TTG

Query Match 41.7%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
|||||
Db 23 TGGGV 27

RESULT 14

S22454
ribosomal protein L2 REP - wood tobacco mitochondrion (fragment)
C:Species: mitochondrion Nicotiana sylvestris (wood tobacco)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 21-Jul-2000
C:Accession: S22454
R:Vitart, V.; de Paape, R.; Mathieu, C.; Chetrit, P.; Vedel, F.
Mol. Gen. Genet. 233, 193-200, 1992
A:Title: Amplification of substoichiometric recombinant mitochondrial DNA sequences in a
A:Reference number: S22454; MUID:92293115; PMID:1376403
A:Accession: S22454
A:Molecule type: DNA
A:Residues: 1-101 <VIT>
A:Cross-references: EMBL:X66519; NID:g396185; PIDN:CAA47138.1; PID:g396186
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: Escherichia coli ribosomal protein L2
C:Keywords: mitochondrion

Query Match 41.7%; Score 5; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
|||||
Db 73 TGGGV 77

RESULT 15

S58218
hypothetical protein 3 - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C:Accession: S58218
R:Lim, A.; de Vos, D.; Brauns, M.; Gaballa, A.; Hamers, R.; Cornelis, P.
submitted to the EMBL Data Library, August 1995
A:Description: Molecular cloning, nucleotide sequence, and characterization of OprL, a m
A:Reference number: S58216
A:Accession: S58218
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <LIM>
A:Cross-references: EMBL:Z50191; NID:g2251191; PIDN:CAA90572.1; PID:g929777

Query Match 41.7%; Score 5; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
|||||
Db 52 TGGGV 56

Search completed: March 13, 2003, 15:33:40
Job time : 12.4615 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:18:49 ; Search time 6.46154 Seconds
(without alignments)
77.027 Million cell updates/sec

Title: us-09-822-698a-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Description
1	6	50.0	1123	PHYA_SOLTU P30733 solanum tub
2	6	50.0	1124	PHY1_TOBAC P33530 nicotiana t
3	5	41.7	144	RL15_HAEIN P44353 haemophilus
4	5	41.7	169	PLMN_RAT Q01177 rattus norv
5	5	41.7	181	FMKA_ECOLI Q04738 escherichia
6	5	41.7	184	VP50_BPAPS Q9t1p8 bacterioph
7	5	41.7	189	AROK_SYNY3 P72196 synecocyst
8	5	41.7	197	VG23_BPMD2 Q38362 mycobacteri
9	5	41.7	197	VG23_BPMD5 Q05229 mycobacteri
10	5	41.7	223	RL4_MYCBO Q06045 mycobacteri
11	5	41.7	223	RL4_MYCTU P95050 mycobacteri
12	5	41.7	229	H1S4_PYRAE Q82y14 pyrobaculum
13	5	41.7	238	MOTB_TREPA Q07887 treponema p
14	5	41.7	241	PYRF_THETH P96076 thermus the
15	5	41.7	245	PFLA_HAEIN P43751 haemophilus
16	5	41.7	245	T2M4_METJA Q38723 methanococc
17	5	41.7	262	RS2_THEME Q9wzml thermotoga
18	5	41.7	265	H1S4_XYLEFA Q9pbc9 xylella fas
19	5	41.7	270	L181_CHLEU Q03965 chlamydomon
20	5	41.7	270	URED_SYNY3 P73047 synecocyst
21	5	41.7	285	NADC_MYCTU Q06594 mycobacteri
22	5	41.7	296	SAPR_STRPU P11761 strongyloc
23	5	41.7	297	E2Y3_CHLRE Q08356 chlamydomon
24	5	41.7	303	L722_SYNY3 P72667 synecocyst
25	5	41.7	304	LST_HAEIN Q48211 haemophilus
26	5	41.7	319	AES_ECOLI P23872 escherichia
27	5	41.7	325	YC83_MYCTU Q10611 mycobacteri
28	5	41.7	337	TAT_HTLV2 P03410 human t-cel
29	5	41.7	343	SLAM_MOUSE Q9qum4 mus musculu
30	5	41.7	344	JUNB_MOUSE P09450 mus musculu
31	5	41.7	344	JUNB_RAT P24898 rattus norv
32	5	41.7	349	MRAY_CHLPN Q92706 chlamydia p
33	5	41.7	350	REDD_STRCO P16922 streptomyce

34	5	41.7	358	1	TAT_HTLIA	P03409 human t-cel
35	5	41.7	358	1	TAT_HTLIC	P14079 human t-cel
36	5	41.7	370	1	EL3E_TOBAC	P23546 nicotiana t
37	5	41.7	370	1	EL3F_TOBAC	P27666 nicotiana t
38	5	41.7	371	1	EL3B_TOBAC	P15797 nicotiana t
39	5	41.7	374	1	ADH1_ALLMI	P80222 alligator m
40	5	41.7	387	1	YB96_YEAST	P38332 saccharomyc
41	5	41.7	406	1	METK_AERPE	Q9ybk2 aeropyrum p
42	5	41.7	417	1	ARCA_PSEAE	P13981 pseudomonas
43	5	41.7	420	1	ARCA_PSEPU	P41142 pseudomonas
44	5	41.7	421	1	SHIA_MOUSE	Q64264 mus musculu
45	5	41.7	422	1	SHIA_HUMAN	P08908 homo sapien

ALIGNMENTS

RESULT 1
PHYA_SOLTU STANDARD; PRT; 1123 AA.
ID PHYA_SOLTU
AC P30733;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome A.
GN PHYA.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree;
RX MEDLINE=92163018; PubMed=1536928;
RA Heyer A., Gatz C.;
RT "Isolation and characterization of a cDNA-clone coding for potato
RT type A phytochrome.";
RL Plant Mol. Biol. 18:535-544(1992).
CC -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -!- SUBUNIT: HOMODIMER.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC -----
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CC -----
CC EMBL; S84872; AAB21533.2; -.
CC PIR; S20497; S20497.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR004359; HIS_KIN_sig.
CC InterPro; IPR003661; His_kinA.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000700; PAS-assoc_C.

```

DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001294; Phytochrome.
DR Pfam: PF00360; phytochrome; 1.
DR Pfam: PF00512; signal; 1.
DR Pfam: PF00989; PAS; 2.
DR Pfam: PF01590; GAF; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR PRINTS: PR01033; PHYTOCHROME.
DR SMART: SM00065; GAF; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00086; PAS; 1.
DR SMART: SM00091; PAS; 2.
DR TIGRFAMS: TIGR00229; sensory_box; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50113; PAC; 1.
DR PROSITE: PS02112; PAS; 2.
DR PROSITE: PS00245; PHYTOCHROME_1; 1.
DR PROSITE: PS50046; PHYTOCHROME_2; 1.
DR Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 617 687 PAS 1.
FT DOMAIN 690 746 PAC.
FT DOMAIN 747 821 PAS 2.
FT DOMAIN 901 1118 HISTIDINE KINASE.
FT BINDING 323 323 CHROMOPHORE.
SQ SEQUENCE 1123 AA; 124689 MW; 3A97062A5DFB29EA CRC64;

Query Match 50.0%; Score 6; DB 1; Length 1123;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGV 6
Db 1058 HTGGGV 1063

RESULT 2
PHY1_TOBAC
ID PHY1_TOBAC STANDARD; PRT; 1124 AA.
AC P33530;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome A1.
GN PHYA1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94143494; PubMed=8310074;
RA Adam E., Deak M., Kay S., Chua N.H., Nagy F.;
RT "Sequence of a tobacco (Nicotiana tabacum) gene coding for type A
  phytochrome.";
RL Plant Physiol. 101:1407-1408(1993).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RUBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC PHOTOCYCLOPHYLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -1- SUBUNIT: HOMODIMER.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

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CC CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL: X66784; CAA47284.1; -.
CC DR InterPro: IPR003594; ATPbind_ATPase.
CC DR InterPro: IPR003018; GAF.
CC DR InterPro: IPR004359; HIS_KIN_sig.
CC DR InterPro: IPR003661; HIS_KIN_A.
CC DR InterPro: IPR001610; PAC.
CC DR InterPro: IPR000700; PAS-assoc_C.
CC DR InterPro: IPR000014; PAS_domain.
CC DR InterPro: IPR001294; Phytochrome.
CC DR Pfam: PF00360; phytochrome; 1.
CC DR Pfam: PF00512; signal; 1.
CC DR Pfam: PF00989; PAS; 2.
CC DR Pfam: PF01590; GAF; 1.
CC DR Pfam: PF02518; HATPase_c; 1.
CC DR PRINTS: PR01033; PHYTOCHROME.
CC DR SMART: SM00065; GAF; 1.
CC DR SMART: SM00387; HATPase_c; 1.
CC DR SMART: SM00388; HSKA; 1.
CC DR SMART: SM00086; PAC; 1.
CC DR SMART: SM00091; PAS; 2.
CC DR TIGRFAMS: TIGR00229; sensory_box; 1.
CC DR PROSITE: PS50109; HIS_KIN; 1.
CC DR PROSITE: PS50113; PAC; 1.
CC DR PROSITE: PS02112; PAS; 2.
CC DR PROSITE: PS00245; PHYTOCHROME_1; 1.
CC DR PROSITE: PS50046; PHYTOCHROME_2; 1.
CC KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
CC KW Repeat; Multigene family.
FT DOMAIN 617 687 PAS 1.
FT DOMAIN 690 746 PAC.
FT DOMAIN 747 821 PAS 2.
FT DOMAIN 901 1118 HISTIDINE KINASE.
FT BINDING 323 323 CHROMOPHORE (BY SIMILARITY).
SQ SEQUENCE 1124 AA; 124296 MW; 4C2938CFE9A5F130 CRC64;

Query Match 50.0%; Score 6; DB 1; Length 1124;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGV 6
Db 1058 HTGGGV 1063

RESULT 3
RL15_HAEIN
ID RL15_HAEIN STANDARD; PRT; 144 AA.
AC P44353;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L15.
GN RPL0 OR RPL15 OR H10797.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA

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RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32762; AAC22455.1; -.
DR TIGR; HI0797; -.
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR Pfam; PF01305; Ribosomal_L15; 1.
DR TIGRFAMs; TIGR01071; rplO_bact; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
DR Ribosomal protein; rRNA-binding; Complete proteome.
KW RIBOSOMAL L15; 15072 MW; FOCPC80684DC64C5 CRC64;
SQ
SEQUENCE 144 AA: 15072 MW; FOCPC80684DC64C5 CRC64;
-----
Query Match 41.7%; Score 5; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGGGV 6
Db 42 TGGGV 46
|||||
-----
RESULT 4
PLMN_RAT PLMN_RAT STANDARD; PRT; 169 AA.
AC Q01177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen."
RL J. Biol. Chem. 266:10825-10829(1991).
CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble

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CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
CC -----
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CC -----
DR EMBL; M62832; AAA41884.1; -.
DR PIR; A40522; A40522.
DR HSP; P00747; 1PMK.
DR MEROPS; S01.233; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 2.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
DR Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Repeat.
FT NON_TER 1
FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
FT DISULFID 34 112 BY SIMILARITY.
FT DISULFID 55 95 BY SIMILARITY.
FT DISULFID 83 107 BY SIMILARITY.
FT NON_TER 169
SQ SEQUENCE 169 AA: 18401 MW; 77A54214C49D010C CRC64;
-----
Query Match 41.7%; Score 5; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGGGV 6
Db 115 TGGGV 119
|||||
-----
RESULT 5
EMKA_ECOLI EMKA_ECOLI STANDARD; PRT; 181 AA.
AC P04738;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE K88 fimbrial protein A precursor.
GN FAPC.
OS Escherichia coli.
OG Plasmid pRW205.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=84264326; PubMed=6086572;
RA Mool F.R., van Buuren M., Koopman G., Roosendaal B., de Graaf F.K.;
RT "K88ab gene of Escherichia coli encodes a fimbria-like protein
RT distinct from the K88ab fimbrial adhesin."

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RL J. Bacteriol. 159:482-487(1984).
RN [2]
RP SEQUENCE OF 160-181 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86176742; PubMed=2870470;
RA Mooi F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;
RT "Regulation and structure of an Escherichia coli gene coding for an
RT outer membrane protein involved in export of K88ab fimbrial
RT subunits.";
RL Nucleic Acids Res. 14:2443-2457(1986).
CC -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL. ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -!- SUBUNIT: K88 FIMBRIA, 0.1-1 MICROMETER IN LENGTH AND 7 NANOMETERS
CC IN DIAMETER, IS COMPOSED OF ABOUT 100 IDENTICAL SUBUNITS.
CC -!- SUBCELLULAR LOCATION: PREDOMINANTLY LOCATED AT THE TIP OF THE
CC FIMBRIAE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00940; CAA25454.1; -.
CC EMBL; X03675; CAA27312.1; -.
CC FIMBRIA; Signal; Plasmid.
CC SGNAL 21
CC CHAIN 22 181 K88 FIMBRIAL PROTEIN A.
CC DISULFID 37 84 PROBABLE.
CC SEQUENCE 181 AA; 19066 MW; 44EA049DA025D011 CRC64;
CC -----
Query Match 41.7%; Score 5; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
DB 14 TGGGV 18

RESULT 6
VP50_BPAPS STANDARD; PRT; 184 AA.
AC Q9T1P8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE putative protein P50.
GN 50.
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC unclassified Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
RA van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RT the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113(1999).
CC -----
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CC -----
DR EMBL; AF157835; AAF03993.1; -.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 20416 MW; EB705FA272B6768F CRC64;

Query Match 41.7%; Score 5; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
DB 160 TGGGV 164

RESULT 7
AROK_SYNY3 STANDARD; PRT; 189 AA.
AC P72796;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN AROK OR SLL1669.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpou S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate -> ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE SHIKIMATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL; D90900; BAA16811.1; -.
DR HSSP; P10880; 1SHK.
DR InterPro; IPR000623; Shik_Kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT NP_BIND 19 26 ATP (POTENTIAL).
SQ SEQUENCE 189 AA; 20697 MW; 41727D4EC6E585D9 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
DB 88 TGGGV 92

RESULT 8
VG23_BPMD2
```


DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L4.
 GN RPLD OR RV0702 OR MT0729 OR MTCY210.21.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeter K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S
 CC rRNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; Z84395; CAB06465.1; -;
 DR EMBL; AE006966; AAK4960.1; -;
 DR TIGR; MT0729; -;
 DR TubercuList; RV0702; -;
 DR InterPro; IPR002136; Ribosomal_L4/L1E.
 DR Pfam; PF00573; Ribosomal_L4; 1.
 KW Ribosomal protein; rRNA-binding; Complete proteome.
 SQ SEQUENCE 223 AA; 23743 MW; E9AF8F30E35A66AB CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 223;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 TGGGV 6
 Db 91 TGGGV 95
 |||||

 RESULT 12
 HIS4_PYRAE
 ID HIS4_PYRAE STANDARD; PRT; 229 AA.
 AC Q8ZY14;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)
 DE

DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
 DE isomerase).
 GN HIS4 OR PAE0991.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 CC -!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
 CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
 CC [(5-phospho-1-deoxyribose-1-ylamino)methylideneamino]-1-(5-
 CC phosphoribosyl)imidazole-4-carboxamide.
 CC -!- PATHWAY: Histidine biosynthesis; fourth step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE HIS4 / HISF FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE009797; AAL63182.1; -;
 KW Isomerase; Histidine biosynthesis; Complete proteome.
 SQ SEQUENCE 229 AA; 24830 MW; F064FDBEC3B0B7FA CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 TGGGV 6
 Db 168 TGGGV 172
 |||||

 RESULT 13
 MOTB_TREPA
 ID MOTB_TREPA STANDARD; PRT; 238 AA.
 AC 007887;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chemotaxis motB protein (Motility protein B).
 GN MOTB OR TP0724.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96345631; PubMed=8755894;
 RA Limberger R.J., Slivinski L.L., El-Afandi M.C.T., Dantuono L.A.;
 RT "Organization, transcription, and expression of the 5' region of the
 RL fla operon of Treponema phagedenis and Treponema pallidum.";
 RN J. Bacteriol. 178:4628-4634(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=965876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uitterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RL spirochete";
 CC Science 281:375-388(1998).
 CC -!- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR. MIGHT
 CC BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY TO THE
 CC CELL WALL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE MOTB FAMILY.
 CC -----
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 CC -----
 CC EMBL; U28219; AAB61254.1; -.
 CC EMBL; AE001244; AAC65689.1; -.
 DR TIGR; TP0724; -.
 DR InterPro: IPR001145; Bac_OmpA.
 DR Pfam; PF00691; OmpA; 1.
 DR ProDom; PD000930; Bac_OmpA; 1.
 KW Chemotaxis; Flagella; Transmembrane; Inner membrane;
 KW Flagellar rotation; Complete proteome.
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 34 POTENTIAL.
 FT DOMAIN 35 238 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 238 AA; 26050 MW; 0AB5FCD8E9852E1F CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 238;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGGV 6
 Db 56 TGGGV 60
 RESULT 14
 PYRF-THETH STANDARD; PRT; 241 AA.
 AC P96076;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
 DE (OMPDCase) (OMPDecase) (Fragment).
 GN PYRF.
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB27;
 RX MEDLINE=96236211; PubMed=8787418;
 RA Yamagishi A., Tanimoto T., Suzuki T., Oshima T.;
 RT "Pyrimidine biosynthetic genes (pyrE and pyrF) of an extreme
 RT thermophile, Thermus thermophilus";
 RL Appl. Environ. Microbiol. 62:2191-2194(1996).
 CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
 CC -!- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
 CC -!- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY. SUBFAMILY 2.
 CC -----
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 CC -----
 CC EMBL; D83330; BAA11885.1; -.
 DR HSSP; O26232; IDVJ.
 DR InterPro: IPR001734; OMPDecase.
 DR Pfam; PF00215; OMPDecase; 1.
 DR PROSITE; PS00156; OMPDECASE; 1.
 KW Lyase; Decarboxylase; Pyrimidine biosynthesis.
 FT NON_TER 1 1
 FT ACT_SITE 70 70 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 241 AA; 25696 MW; 03AB5721A21F60F4 CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGGV 6
 Db 115 TGGGV 119
 RESULT 15
 PFLA_HAEIN STANDARD; PRT; 245 AA.
 AC P43751;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4) (PFL-
 DE activating enzyme).
 GN PFLA OR ACT OR HI0179.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: ACTIVATION OF PYRUVATE FORMATE-LYASE 1 UNDER ANAEROBIC
 CC CONDITIONS BY GENERATION OF AN ORGANIC FREE RADICAL, USING
 CC S-ADENOSYLMETHIONINE AND REDUCED FLAVODOXIN AS COSUBSTRATES TO
 CC PRODUCE 5'-DEOXY-ADENOSINE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + dihydroflavodoxin +
 CC [formate acetyltransferase]-glycine = 5'-deoxyadenosine +
 CC methionine + flavodoxin + [formate acetyltransferase]-glycine-2-yl
 CC radical.
 CC -!- COFACTOR: BINDS 1 4FE-4S CLUSTER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ORGANIC RADICAL ACTIVATING ENZYMES
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; U32703; AAC21848.1; -.

DR TIGR; H10179; -.
DR InterPro; IPR001989; Radical_activat.
DR Pfam; PF02143; Radical_activat; 1.
DR ProDom; PD004758; Radical_activat; 1.
DR PROSITE; PS01087; RADICAL_ACTIVATING; 1.
KW Oxidoreductase; Iron-sulfur; 4Fe-4S; Glucose metabolism;
KW Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
FT METAL 29 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 33 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 36 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 245 AA; 28104 MW; E868E3BD5B9BE3FD CRC64;
Query Match 41.7%; Score 5; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGGGV 6
DB 69 TGGGV 73

Search completed: March 13, 2003, 15:32:06
Job time : 6.46154 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:28:09 ; Search time 23.0769 Seconds
(without alignments)
107.144 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVMDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bactexiap:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	50.0	114	10 Q9SVK9	Q9svk9 arabidopsis
2	6	50.0	131	4 Q8WY0	Q8wy0 homo sapien
3	6	50.0	181	13 Q91665	Q91665 xenopus lae
4	6	50.0	192	5 Q9N6S3	Q9n6s3 leishmania
5	6	50.0	193	16 Q9PDE3	Q9pde3 xylella fas
6	6	50.0	381	16 Q98C19	Q98c19 rhizobium l
7	6	50.0	436	16 Q9K6F3	Q9k6f3 bacillus ha
8	6	50.0	502	16 Q8Y012	Q8y012 ralstonia s
9	6	50.0	614	16 Q98212	Q98212 rhizobium l
10	6	50.0	1068	10 Q9FF63	Q9ff63 arabidopsis
11	6	50.0	1123	10 Q41331	Q41331 lycopersico
12	5	41.7	46	15 Q80812	Q80812 human t-lym
13	5	41.7	52	12 Q98809	Q98809 yam mosaic
14	5	41.7	53	15 Q992L1	Q992l1 human t-cel
15	5	41.7	57	10 Q9SAT4	Q9sat4 nicotiana t
16	5	41.7	71	5 Q9NAJ8	Q9naj8 caenorhabdi

17	5	41.7	72	10 Q9LX10	Q9lx10 arabidopsis
18	5	41.7	75	17 Q26464	Q26464 methanobact
19	5	41.7	77	15 Q39198	Q39198 human t-lym
20	5	41.7	78	5 Q8WR25	Q8wr25 anopheles g
21	5	41.7	85	11 Q91HY3	Q91hy3 mus musculu
22	5	41.7	90	16 Q931PI	Q931pi staphylococ
23	5	41.7	94	5 Q9VM00	Q9vm00 drosophila
24	5	41.7	101	8 Q08712	Q08712 nicotiana s
25	5	41.7	102	2 Q9LCA9	Q9lca9 rhodocyclu
26	5	41.7	103	16 Q9KJ66	Q9kj66 streptomyc
27	5	41.7	107	2 Q51490	Q51490 pseudomonas
28	5	41.7	109	10 Q9FJZ0	Q9fjz0 arabidopsis
29	5	41.7	110	11 Q9D9U5	Q9d9u5 mus musculu
30	5	41.7	117	2 Q9RH52	Q9rh52 streptomyc
31	5	41.7	117	11 Q9D466	Q9d466 mus musculu
32	5	41.7	118	6 Q95JT4	Q95jt4 macaca fasc
33	5	41.7	119	16 Q9KF97	Q9kfg7 bacillus ha
34	5	41.7	122	10 Q9LW24	Q9lw24 arabidopsis
35	5	41.7	124	8 Q35862	Q35862 schistosoma
36	5	41.7	128	8 Q95AT6	Q95at6 dugesia pol
37	5	41.7	133	16 Q97ES2	Q97es2 clostridium
38	5	41.7	136	10 Q94GS2	Q94gs2 oryza sativ
39	5	41.7	139	2 Q9JMX1	Q9jmx1 bradyrhizob
40	5	41.7	140	16 Q9EWE4	Q9ewe4 streptomyc
41	5	41.7	143	10 Q944U8	Q944u8 kokia dryna
42	5	41.7	144	10 Q944V1	Q944v1 gossypium a
43	5	41.7	144	10 Q944V0	Q944v0 gossypium l
44	5	41.7	144	10 Q944U9	Q944u9 gossypium b
45	5	41.7	144	15 O41286	O41286 primate t-1

ALIGNMENTS

RESULT 1

Q9SVK9 PRELIMINARY; PRT; 114 AA.
AC Q9SVK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Hypothetical 12.9 kDa protein.
GN F18B3.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
RA Salanoubat M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049862; CAB42919.1; -
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12923 MW; F8156E1465887DBB CRC64;

Query Match 50.0%; Score 6; DB 10; Length 114;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGVWDP 9
|||||
Db 99 GGVWDP 104

RESULT 2

Q8WY0

```
ID Q8WYV0 PRELIMINARY; PRT; 131 AA.
AC Q8WYV0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 50.0%; Score 6; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVV 7
Db 29 TGGGVV 34

RESULT 3
ID Q91665 PRELIMINARY; PRT; 181 AA.
AC Q91665;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CTX (Fragment).
DE CTX (Fragment).
GN G1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PF;
RX MEDLINE=96210130; PubMed=8625968;
RA Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M.,
RA Du Pasquier L.;
RT "CTX, a novel molecule specifically expressed on the surface of
RT cortical thymocytes in Xenopus.";
RL Eur. J. Immunol. 26:780-791(1996).
DR EMBL; U43393; AAC59860.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig-like; 1.
FT NON_TER
SQ SEQUENCE 181 AA; 19380 MW; 6A558F6C824EDC16 CRC64;

Query Match 50.0%; Score 6; DB 13; Length 181;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 154 HTGGGV 159

RESULT 4
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Q9N6S3 PRELIMINARY; PRT; 192 AA.
ID Q9N6S3;
AC Q9N6S3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE L7535.14.
DE L822.2 OR L7535.14.
GN L822.2 OR L7535.14.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005893; AAF31031.1; -.
DR EMBL; AC005767; AAF27953.1; -.
DR EMBL; AC005766; AAF28379.1; -.
SQ SEQUENCE 192 AA; 19650 MW; 0CE9460B1FB5A9C4 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 129 HTGGGV 134

RESULT 5
ID Q9PDE3 PRELIMINARY; PRT; 193 AA.
AC Q9PDE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Disulfide oxidoreductase.
GN XF1436.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Artuda P., Abreu F.A., Ascencio M.,
RA Alvares J.G., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carver H.,
RA Coutinho L.L., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facchini A.P., Frasca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Fraga J.S., Frasca S.C., Franco M.C., Fröhme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Machado J.A.,
RA Lemos E.G.N., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
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RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003973; AAF84245.1; -.
DR InterPro; IPR001853; DSBA.
DR InterPro; IPR000063; ThioRed.
DR Pfam; PF01323; DSBA; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 193 AA; 21305 MW; 552DC6D86B4F555D CRC64;

Query Match 50.0%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDP 9
Db 68 GGVWDP 73
|||||

RESULT 6
Q98C19 ID Q98C19 PRELIMINARY; PRT; 381 AA.
AC Q98C19;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein mlr5331.
GN MLR5331.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF30309; PubMed=11214968;
RX MEDLINE=21089330; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Tsuchiuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003006; BAB51802.1; -.
DR InterPro; IPR000160; GGDEF.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc.C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00990; GGDEF; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 381 AA; 41817 MW; 7CDACEEF8F6E32B4 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 381;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVWDP 8
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Db 138 GGVWDP 143

RESULT 7
Q9K6F3 ID Q9K6F3 PRELIMINARY; PRT; 436 AA.
AC Q9K6F3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH oxidase (nox).
GN BH3776.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -i- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AP001519; BAB07495.1; -.
DR HSSP; P37062; 1NHP.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR001100; Pyr_redox_dim.
DR InterPro; IPR004099; Pyr_redox_dim.
DR Pfam; PF00070; Pyr_redox; 1.
DR Pfam; PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
DR PRINTS; PR00469; PNDRDTASEII.
DR ProDom; PD000139; FAD_pyr_redox; 1.
DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 436 AA; 47376 MW; 6B7997FD763FF732 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 436;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGVWDP 10
|||||
Db 424 GGVWDP 429

RESULT 8
Q8Y012 ID Q8Y012 PRELIMINARY; PRT; 502 AA.
AC Q8Y012;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable transporter transmembrane protein.
GN RSC1233 OR RS02740.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,

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RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646063; CAD14935.1; -.
DR InterPro; IPR001248; Cyt_pur_permease.
DR Pfam; PF02133; Transp_cyt_pur; 1.
DR TIGRFAMs; TIGR00800; ncs1; 1.
KW Complete proteome.
SQ SEQUENCE 502 AA; 53783 MW; 7F72D191E74030C0 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 502;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VWDPID 11
Db 304 VWDPID 309

RESULT 9
Q98212 ID Q98212 PRELIMINARY; PRT; 614 AA.
AC Q98212;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE DNA methyltransferase.
GN MLL9056.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003015; BAB5474.1; -.
DR InterPro; IPR001091; CM4_Mettransf.
DR InterPro; IPR002295; D21N6_mtfase.
DR InterPro; IPR002941; N6/N4_Mtase.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF01555; N6_N4_Mtase; 1.
DR PRINTS; PR00506; D21N6_MTFRASE.
DR PRINTS; PR00508; S21N4_MTFRASE.
DR PROSITE; PS00092; N6_MTFASE; UNKNOWN_1.
KW Transferrase; Methyltransferase; Plasmid; Complete proteome.
SQ SEQUENCE 614 AA; 69230 MW; 14507EDDAE0FBFCE CRC64;

Query Match 50.0%; Score 6; DB 16; Length 614;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 116 HTGGGV 121

RESULT 10
Q9FFF3 ID Q9FFF3 PRELIMINARY; PRT; 1068 AA.
AC Q9FFF3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Low density lipoprotein B-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsais.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT P1 clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB005242; BAB09597.1; -.
KW Lipoprotein.
SQ SEQUENCE 1068 AA; 118802 MW; D696E592DD4B991C CRC64;

Query Match 50.0%; Score 6; DB 10; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVW 7
Db 484 TGGGVW 489

RESULT 11
Q41331 ID Q41331 PRELIMINARY; PRT; 1123 AA.
AC Q41331;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE PHYA protein (Phytochrome A).
GN PHYA.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. UC82B;
RX MEDLINE=98346008; PubMed=9681030;
RA Lazarova G.I., Cordonnier-Pratt M.M., Kerckhoffs L.J.,
RA Brandstadter J., Matsui M., Pratt L.H., Kendrick R.E.;
RT "Molecular analysis of PHYA in wild-type and phytochrome A-deficient
RT mutants of tomato.";
RL Plant J. 14:653-662(1998).
RN [2]
RP SEQUENCE OF 165-277 FROM N.A.
RC STRAIN=UC-82B;
RX MEDLINE=96191281; PubMed=8616214;
RA Hauser B.A., Cordonnier-Pratt M.M., Daniel-Vedele F., Pratt L.H.;
RT "The phytochrome gene family in tomato includes a novel subfamily.";
RL Plant Mol. Biol. 29:1143-1155(1995).
DR EMBL; AJ001916; CAA05089.1; -.
DR EMBL; U32345; AAC49297.1; -.
DR EMBL; AJ001915; CAA05088.1; -.
DR EMBL; AJ001913; CAA05086.1; -.
DR EMBL; AJ001914; CAA05087.1; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.

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DR InterPro; IPR001680; WD40.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRfams; TIGR00229; sensory_box; 1.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS00046; PHYTOCHROME_2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Phytochrome.
SQ SEQUENCE 1123 AA; 124659 MW; 0432ADCCCFDF0FB1 CRC64;

Query Match 50.0%; Score 6; DB 10; Length 1123;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 1058 HTGGGV 1063
|||||

RESULT 12
Q80812 PRELIMINARY; PRT; 46 AA.
AC Q80812;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tax protein (Fragment).
GN PX.
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=93124579; PubMed=8093491;
RA Bastian I., Gardner J.F., Webb D., Gardner I.;
RT "Isolation of a human T-lymphotropic virus type I from Australian
RT Aborigines.";
RL J. Virol. 67:843-851(1993).
DR EMBL; M92819; AAA45401.1; -.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5031 MW; 52BB1E8188659FF0 CRC64;

Query Match 41.7%; Score 5; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 27 WDPID 31
|||||

RESULT 13
Q98809 PRELIMINARY; PRT; 52 AA.
AC Q98809;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Putative 6K2 protein (Fragment).
OS Yam mosaic virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=41460;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN-IVORY COAST;
RX MEDLINE=96370790; PubMed=8774686;
RA Aleman M.E., Marcos J.F., Brugidou C., Beachy R.N., Fauquet C.;
RT "The complete nucleotide sequence of yam mosaic virus (Ivory Coast
RT isolate) genomic RNA.";
RL Arch. Virol. 141:1259-1278(1996).
DR EMBL; U42596; AAC5552.1; -.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6022 MW; 43EC15F948548287 CRC64;

Query Match 41.7%; Score 5; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVW 7
Db 32 GGGVW 36
|||||

RESULT 14
Q992L1 PRELIMINARY; PRT; 53 AA.
ID Q992L1;
AC Q992L1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RC SEQUENCE FROM N.A.
RA Glaser J.B., Dube S., Polesz B.J.;
RT "HTLV-II coinfection among HIV-1 infected prison inmates.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327515; AAK19304.1; -.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 5815 MW; 416E03EF077132E7 CRC64;

Query Match 41.7%; Score 5; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 43 WDPID 47
|||||

RESULT 15
Q9SAT4 PRELIMINARY; PRT; 57 AA.
ID Q9SAT4;
AC Q9SAT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Basic beta-1,3-glucanase (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Asteridae; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=92404740; PubMed=2152343;

```

RA Neale A.D., Wahleithner J.A., Lund M., Bonnett H.T., Kelly A.,
RA Meeks-Wagner D.R., Peacock W.J., Dennis E.S.;
RT "Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in
RT tobacco explants during flower formation.";
RL Plant Cell 2:673-684(1990).
DR EMBL; S44870; AAB23376.1; -.
DR HSSP; F15737; IGHS.
DR InterPro; IPR000490; Glyco_hydro_17.
DR Pfam; PF00332; Glyco_hydro_17; 1.
FT NON_TER 1
SQ SEQUENCE 57 AA; 6401 MW; 64DFB8C1DB17E472 CRC64;

Query Match 41.7%; Score 5; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGWWD 8
Db 38 GGWWD 42

Search completed: March 13, 2003, 15:33:05
Job time : 23.0769 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 5.49231 seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	AAE12770	Human PH1 Fab anti
2	76	100.0	121	AAE12706	Human PH1 Fab anti
3	76	100.0	381	AAE12707	Human b1vPH1-IL-2
4	76	100.0	451	AAE12715	Human recombinant
5	75	98.7	14	AAE12764	Human PH1 Fab anti
6	73	96.1	14	AAE12758	Human PH1 Fab anti
7	71	93.4	14	AAE12758	Human PH1 Fab anti
8	71	93.4	14	AAE12749	Human PH1 Fab anti
9	71	93.4	14	AAE12753	Human PH1 Fab anti
10	71	93.4	14	AAE12769	Human PH1 Fab anti

11	70	92.1	14	AAE12771	Human PH1 Fab anti
12	69	90.8	14	AAE12719	Human PH1 Fab anti
13	69	90.8	14	AAE12720	Human PH1 Fab anti
14	69	90.8	14	AAE12740	Human PH1 Fab anti
15	69	90.8	14	AAE12741	Human PH1 Fab anti
16	69	90.8	14	AAE12742	Human PH1 Fab anti
17	69	90.8	14	AAE12743	Human PH1 Fab anti
18	69	90.8	14	AAE12759	Human PH1 Fab anti
19	69	90.8	14	AAE12762	Human PH1 Fab anti
20	69	90.8	14	AAE12772	Human PH1 Fab anti
21	68	89.5	14	AAE12754	Human PH1 Fab anti
22	68	89.5	14	AAE12766	Human PH1 Fab anti
23	68	89.5	14	AAE12773	Human PH1 Fab anti
24	68	89.5	16	AAE12734	Human PH1 Fab anti
25	67	88.2	14	AAE12746	Human PH1 Fab anti
26	67	88.2	14	AAE12747	Human PH1 Fab anti
27	67	88.2	14	AAE12763	Human PH1 Fab anti
28	67	88.2	14	AAE12774	Human PH1 Fab anti
29	67	88.2	16	AAE12735	Human PH1 Fab anti
30	66	86.8	14	AAE12768	Human PH1 Fab anti
31	65	85.5	14	AAE12750	Human PH1 Fab anti
32	64	84.2	14	AAE12718	Human PH1 Fab anti
33	64	84.2	14	AAE12744	Human PH1 Fab anti
34	64	84.2	14	AAE12751	Human PH1 Fab anti
35	64	84.2	14	AAE12756	Human PH1 Fab anti
36	64	84.2	16	AAE12736	Human PH1 Fab anti
37	63	82.9	14	AAE12755	Human PH1 Fab anti
38	63	82.9	14	AAE12761	Human PH1 Fab anti
39	63	82.9	14	AAE12765	Human PH1 Fab anti
40	63	82.9	14	AAE12767	Human PH1 Fab anti
41	62	81.6	14	AAE12760	Human PH1 Fab anti
42	61	80.3	14	AAE12717	Human PH1 Fab anti
43	61	80.3	14	AAE12739	Human PH1 Fab anti
44	61	80.3	16	AAE12733	Human PH1 Fab anti
45	60	78.9	14	AAE12738	Human PH1 Fab anti

ALIGNMENTS

RESULT 1

AAE12770

ID AAE12770 standard; peptide; 14 AA.

XX

AC AAE12770;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #37.

XX

KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

FH Key

FT Region

FT Location/Qualifiers

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001..

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

PA (DYAX-) DYAX CORP.

XX

PI Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Example 2; Page 125; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma,
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC region FR (framework region)3-CDR3 variant.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14
|||||
RESULT 2
ID AAE12706
XX AAE12706 standard; Protein; 121 AA.
AC AAE12706;
XX
XX 04-JAN-2002 (first entry)
DT Human PH1 Fab antibody variable heavy chain region (VH).
DE
DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT Region 97..112
FT /note= "VH domain"
FT Region 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT Region 111..112
FT /label= FR4
FT /note= "Framework region 4"
XX

PN WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
PF
XX
XX 30-MAR-2000; 2000US-0538913.
PR
XX
XX (DYAX-) DYAX CORP.
PA
XX
XX Hoogenboom HRJM, Henderikx MPG;
PI
XX WPI; 2001-626437/72.
DR
XX N-PSDB; AAD20731.
DR
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Claim 2; Page 94-95; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
CC antibody VH region.
XX
XX Sequence 121 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110
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RESULT 3
ID AAE12707
XX AAE12707 standard; Protein; 381 AA.
AC AAE12707;
XX
XX 04-JAN-2002 (first entry)
DT Human biVPH1-IL-2 immunocytokine protein.
DE
DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
KW
XX Homo sapiens.
XX
XX WO200175110-A2.
PN
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
PF
XX
XX 30-MAR-2000; 2000US-0538913.
PR
XX
XX

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 123; 126pp; English.

PS The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 98.7%; Score 75; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 2e-05;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

DB 3 HTGGGVWDPVDY 14

IIIIIIIIII

RESULT 6

AAEL12758

ID AAE12758 standard; peptide; 14 AA.

XX AC AAE12758;

XX DT 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #25.

DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX PN 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PF 30-MAR-2000; 2000US-0538913.

XX PR (DYAX-) DYAX CORP.

XX PA Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 122; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 96.1%; Score 73; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 4.3e-05;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

DB 3 HTGGGVWDPMDY 14

IIIIIIIIII

RESULT 7

AAEL12748

ID AAE12748 standard; peptide; 14 AA.

XX AC AAE12748;

XX DT 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX PN 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PF 30-MAR-2000; 2000US-0538913.

XX PR (DYAX-) DYAX CORP.

XX PA Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Example 2; Page 120; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DQ 3 HTGGGVWDPIN 14
 |||||
 |||||

RESULT 8
 AAE12749
 ID AAE12749 standard; peptide; 14 AA.
 AC AAE12749;
 XX AAE12749;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #16.
 XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 120; 126pp; English.
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DQ 3 HTGGGVWDPIN 14
 |||||
 |||||

RESULT 9
 AAE12753
 ID AAE12753 standard; peptide; 14 AA.
 AC AAE12753;
 XX AAE12753;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #20.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 121; 126pp; English.
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
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 Db 3 HTGGGVWDPIY 14

RESULT 10

AAE12769
 ID AAE12769 standard; peptide; 14 AA.

XX AC AAE12769;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #36.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..2 /label= Framework_region_3
 FT Region 3..14 /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 PS Example 2; Page 124; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 |||||
 Db 3 HTGGGVWNPIDY 14

RESULT 11

AAE12771
 ID AAE12771 standard; peptide; 14 AA.

XX AC AAE12771;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #38.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..2 /label= Framework_region_3
 FT Region 3..14 /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 PS Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PHI Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 92.1%; Score 70; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

|||||

Db 3 HTGGGVDPIDY 14

RESULT 12

AAE12719

ID AAE12719 standard; peptide; 14 AA.

XX AC AAE12719;

XX DT 04-JAN-2002 (first entry)

XX DE Human PHI Fab antibody VH region FR3-CDR3 variant #3.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytostatic; therapy; PHI antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

XX FT 1..2

XX FT /label= Framework_region_3

XX FT Region

XX FT 3..14

XX FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PD 30-MAR-2000; 2000US-0538913.

XX PD (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX DR for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX DR its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Claim 2; Page 75; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and X-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PHI Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

|||||

Db 3 HTGGGVDPIDY 14

RESULT 13

AAE12720

ID AAE12720 standard; peptide; 14 AA.

XX AC AAE12720;

XX DT 04-JAN-2002 (first entry)

XX DE Human PHI Fab antibody VH region FR3-CDR3 variant #4.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytostatic; therapy; PHI antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

XX FT 1..2

XX FT /label= Framework_region_3

XX FT Region

XX FT 3..14

XX FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PD 30-MAR-2000; 2000US-0538913.

XX PD (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX DR for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX DR its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Claim 2; Page 75; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and X-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC region FR (framework region)3-CDR3 variant.

XX

SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00018;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

|||||||

Db 3 HTGGGVDPICY 14

Search completed: March 13, 2003, 15:14:42

Job time : 6.49231 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 1.84615 seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698a-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	47	61.8	573	1	US-08-200-512-2	Sequence 2, Appli
2	43.5	57.2	774	4	US-09-346-237-8	Sequence 8, Appli
3	40	52.6	123	6	5171845-1	Patent No. 5171845
4	38	50.0	28	3	US-08-978-741-14	Sequence 14, Appl
5	38	50.0	28	4	US-09-333-729A-14	Sequence 14, Appl
6	38	50.0	109	4	US-09-134-001C-3523	Sequence 3523, Ap
7	38	50.0	328	4	US-09-300-672-2	Sequence 2, Appli
8	38	50.0	397	3	US-08-978-741-6	Sequence 6, Appli
9	38	50.0	397	4	US-09-333-729A-7	Sequence 7, Appli
10	38	50.0	447	3	US-08-508-761B-6	Sequence 6, Appli
11	38	50.0	738	1	US-07-985-458-3	Sequence 3, Appli
12	38	50.0	941	4	US-07-074-658-75	Sequence 75, Appl
13	38	50.0	944	2	US-08-867-941-23	Sequence 23, Appl
14	38	50.0	944	2	US-08-867-941-24	Sequence 24, Appl
15	38	50.0	944	4	US-09-074-658-23	Sequence 23, Appl
16	38	50.0	944	4	US-09-074-658-24	Sequence 24, Appl
17	37	48.7	848	4	US-08-976-255-10	Sequence 10, Appl
18	36	47.4	20	4	US-08-992-877-65	Sequence 65, Appl
19	36	47.4	79	2	US-08-499-676A-13	Sequence 13, Appl
20	36	47.4	152	3	US-08-916-043-2	Sequence 2, Appli
21	36	47.4	152	6	5212286-6	Patent No. 5212286
22	36	47.4	300	4	US-09-134-001C-4385	Sequence 4385, Ap
23	36	47.4	384	3	US-09-071-434-3	Sequence 3, Appli
24	36	47.4	627	2	US-08-466-589-6	Sequence 6, Appli
25	36	47.4	627	2	US-08-700-636-6	Sequence 6, Appli
26	36	47.4	627	3	US-08-467-574-6	Sequence 6, Appli
27	36	47.4	627	4	US-09-217-345-6	Sequence 6, Appli

28	36	47.4	627	4	US-08-487-596-6	Sequence 6, Appli
29	36	47.4	720	4	US-09-296-284-25	Sequence 25, Appl
30	36	47.4	754	4	US-09-296-284-4	Sequence 4, Appli
31	35.5	46.7	659	1	US-08-240-049B-16	Sequence 16, Appl
32	35.5	46.7	659	1	US-08-259-148A-20	Sequence 20, Appl
33	35.5	46.7	659	1	US-08-484-054-20	Sequence 20, Appl
34	35.5	46.7	659	2	US-07-876-941A-20	Sequence 20, Appl
35	35.5	46.7	659	4	US-08-477-232-14	Sequence 14, Appl
36	35.5	46.7	659	4	US-07-870-985A-20	Sequence 20, Appl
37	35.5	46.7	660	4	US-08-542-634-14	Sequence 14, Appl
38	35.5	46.7	660	4	US-09-462-606-48	Sequence 48, Appl
39	35.5	46.7	660	5	PCT-US95-13703-14	Sequence 14, Appl
40	35.5	46.7	970	1	US-08-375-709-7	Sequence 7, Appli
41	35.5	46.7	970	1	US-08-752-929-7	Sequence 7, Appli
42	35.5	46.7	970	4	US-09-090-793-5	Sequence 5, Appli
43	35	46.1	13	3	US-08-525-716-2	Sequence 2, Appli
44	35	46.1	95	4	US-08-928-383B-18	Sequence 18, Appl
45	35	46.1	112	4	US-08-469-260A-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-08-200-512-2
; Sequence 2, Application US/08200512
; Patent No. 5674718
; GENERAL INFORMATION:
; APPLICANT: BRIAND, MICHELLE
; TITLE OF INVENTION: DNA SEGMENTS AND TRANS-
; TITLE OF INVENTION: FORMED MICROORGANISMS COMPRISING THE DELTA'-
; TITLE OF INVENTION: DEHYDROGENASE GENE, AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,512
; FILING DATE: 17-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,660
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00094
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A.
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1116-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: (212) 661-8002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; DESCRIPTION: NO
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: PSEUDOMONAS TESTOSTERONI
; FEATURE: (R, repeat if necessary)
; NAME/KEY: PROTEIN
; LOCATION: 1..573
; OTHER INFORMATION: /note = Delta
; OTHER INFORMATION: dehydrogenase protein of Pseudomonas
; OTHER INFORMATION: testosterone1
US-08-200-512-2

Query Match 61.8%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 8.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGVWDPIDY 12
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Db 47 SGGGIWIPNY 57

RESULT 2
US-09-346-237-8
; Sequence 8, Application US/09346237A
; Patent No. 6265197
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 5629-200-US
; CURRENT APPLICATION NUMBER: US/09/346.237A
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: PA 1998 00868
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: 60/094,353
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Favobacterium odoratum
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(774)
; OTHER INFORMATION: Isoamylase
US-09-346-237-8

Query Match 57.2%; Score 43.5; DB 4; Length 774;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 HTGGGVWDPID 11
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Db 329 HTGEGGWSPTD 340

RESULT 3
5171845-1
; Patent No. 5171845
; APPLICANT: SPIK, GENEVIEVE-TARTAR, ANDRE; MONTREUIL, JEAN
; TITLE OF INVENTION: PROTEIN HOMOLOGUE OF HUMAN ANGIOGENIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392.977
; FILING DATE: 18-NOV-1988
; SEQ ID NO: 1
; LENGTH: 123
5171845-1

Query Match 52.6%; Score 40; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
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Db 85 GGSPWDPQY 94

RESULT 4
US-08-978-741-14
; Sequence 14, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
; APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Fucosyltransferase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,741
; FILING DATE: 26-No. 6100076-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792498
; FILING DATE: 31
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1041P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/223-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-978-741-14

Query Match 50.0%; Score 38; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
      | | ||| |
Db 8 HMPAGSWDPAGY 19

RESULT 5
US-09-333-729A-14
; Sequence 14, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041P1-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Plasmid insert encoded protein.

; NAME/KEY: unsure

; LOCATION: 23, 25

; OTHER INFORMATION: unknown amino acid

US-09-333-729A-14

Query Match 50.0%; Score 38; DB 4; Length 28;

Best Local Similarity 50.0%; Pred. No. 9.8;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

1 1 1 1 1 1

Db 8 HMPAGSWDPAGY 19

RESULT 6

US-09-134-001C-3523

; Sequence 3523, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3523

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3523

Query Match 50.0%; Score 38; DB 4; Length 109;

Best Local Similarity 45.5%; Pred. No. 39;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

1 1 1 1 1 1

Db 27 HTLEGHWHPVE 37

RESULT 7

US-09-300-672-2

; Sequence 2, Application US/09300672

; Patent No. 6248937

; GENERAL INFORMATION:

; APPLICANT: Finkelstein, Ruth R.

; APPLICANT: Lynch, Tim

; APPLICANT: Goodman, Howard M.

; APPLICANT: Wang, Ming-Li

; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,

; FILE REFERENCE: QUALITY AND COLD-TOLERANCE

; CURRENT APPLICATION NUMBER: US/09/300,672

; CURRENT FILING DATE: 1999-04-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Arabidopsis

US-09-300-672-2

Query Match 50.0%; Score 38; DB 4; Length 328;

Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

Db 311 HNWGSIWDFID 321

RESULT 8

US-08-978-741-6

; Sequence 6, Application US/08978741

; Patent No. 6100076

; GENERAL INFORMATION:

; APPLICANT: Yang Wang, Michael W. Spellman

; TITLE OF INVENTION: O-Fucosyltransferase

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/978,741

; FILING DATE: 26-No. 6100076-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/792498

; FILING DATE: 31

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1041P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 397 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-978-741-6

Query Match 50.0%; Score 38; DB 3; Length 397;

Best Local Similarity 50.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

1 1 1 1 1 1

Db 32 HMPAGSWDPAGY 43

RESULT 9

US-09-333-729A-7

; Sequence 7, Application US/09333729A

; Patent No. 6270987

; GENERAL INFORMATION:

; APPLICANT: Wang, Yang

; APPLICANT: Spellman, Michael W.

; TITLE OF INVENTION: O-Fucosyltransferase

; FILE REFERENCE: P1041P1D1-Substitute

; CURRENT APPLICATION NUMBER: US/09/333,729A

; CURRENT FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: US 08/798,741

; PRIOR FILING DATE: 1997-11-26

; NUMBER OF SEQ ID NOS: 21

; SEQ ID NO 7

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Plasmid insert encoded protein.
US-09-333-729A-7

Query Match 50.0%; Score 38; DB 4; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
| | | | |
Db 32 HMPAGSWDPAGY 43

RESULT 10

US-08-508-761B-6
; Sequence 6, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Arnel
; APPLICANT: Purification, Relano
; APPLICANT: Duchiron, Francis
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; TITLE OF INVENTION: Secretion Especially in Corynebacteria
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-761B-6

Query Match 50.0%; Score 38; DB 3; Length 447;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVWD 8
| | | | |
Db 304 HTDGSIMD 311

RESULT 11

US-07-985-458-3
; Sequence 3, Application US/07985458
; Patent No. 5344777

; GENERAL INFORMATION:
; APPLICANT: Tamaki, Toshihimi;
; APPLICANT: Takemura, Hiroshi;
; APPLICANT: Tayama, Kenji;
; APPLICANT: Fukaya, Masahiro;
; APPLICANT: Okumura, Hajime and
; APPLICANT: Kawamura, Yoshiya
; TITLE OF INVENTION: Structural Gene of Membrane-Bound
; TITLE OF INVENTION: Alcohol Dehydrogenase Complex, Plasmid
; TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
; TITLE OF INVENTION: Bacteria
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frischauf, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72 mb
; COMPUTER: IBM PC compatible (NEC PC-9801 ES)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/985,458
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,221
; FILING DATE: 20-FEB-1991
; APPLICATION NUMBER: 73440/1990
; FILING DATE: 26-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910134/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MATURE PEPTIDE
; LOCATION: 36 to 738
; IDENTIFICATION METHOD: N-terminal sequences of the
; IDENTIFICATION METHOD: purified protein having a molecular weight of about
; IDENTIFICATION METHOD: 72,000
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter altoacetigenes
; STRAIN: MH-24
; PUBLICATION INFORMATION:
; AUTHORS: Tamaki, Toshihimi;
; AUTHORS: Fukaya, Masahiro;
; AUTHORS: Takemura, Hiroshi;
; AUTHORS: Tayama, Kenji;
; AUTHORS: Okumura, Hajime;
; AUTHORS: Kawamura, Yoshiya;
; AUTHORS: Nishiyama, Makoto;
; AUTHORS: Horinouchi, Sueharu and
; AUTHORS: Beppu, Teruhiko
; TITLE: Cloning and Sequencing of the Gene Cluster
; TITLE: Encoding Two Subunits of Membrane-Bound
; TITLE: Alcohol Dehydrogenase from Acetobacter
; TITLE: polyoxogenes
; JOURNAL: Biochimica et Biophysica Acta.
; VOLUME: 1088
; PAGES: 292-300

;
US-07-985-458-3

Query Match 50.0%; Score 38; DB 1; Length 738;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
|| ||| ||
Db 276 GGTWDSIVY 285

RESULT 12

US-09-074-658-75
Sequence 75, Application US/09074658

Patent No. 6184371

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,658

FILING DATE: 08-MAY-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-795

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 75:

SEQUENCE CHARACTERISTICS:

LENGTH: 941 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-074-658-75

Query Match 50.0%; Score 38; DB 4; Length 941;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 HTGGG--VWDPIDY 12
:|||| : ||:|
Db 326 YTGGRILPDPMDY 339

RESULT 13

US-08-867-941-23

Sequence 23, Application US/08867941

Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Du, Run-Pan

APPLICANT: Wang, Quijun

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,941

FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-867-941-23

Query Match 50.0%; Score 38; DB 2; Length 944;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 HTGGG--VWDPIDY 12
:|||| : ||:|
Db 331 YTGGRILPDPMDY 344

RESULT 14

US-08-867-941-24

Sequence 24, Application US/08867941

Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Du, Run-Pan

APPLICANT: Wang, Quijun

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,941

FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

Search completed: March 13, 2003, 15:18:42
Job time : 2.84615 secs

REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-24

Query Match 50.0%; Score 38; DB 2; Length 944;
Best Local Similarity 57.1%; Pred. No. 3 6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HTGGG--VWDPIDY 12
:||||:||||
Db 330 YTGGRILPDPMDY 343

RESULT 15

US-09-074-658-23
; Sequence 23, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 944 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-23

Query Match 50.0%; Score 38; DB 4; Length 944;
Best Local Similarity 57.1%; Pred. No. 3 6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HTGGG--VWDPIDY 12
:||||:||||
Db 331 YTGGRILPDPMDY 344

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 1.70769 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVNDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	76	100.0	14	10	US-09-822-698A-105	Sequence 105, App
2	76	100.0	121	10	US-09-822-698A-3	Sequence 3, Appli
3	76	100.0	381	10	US-09-822-698A-5	Sequence 5, Appli
4	76	100.0	451	10	US-09-822-698A-26	Sequence 26, Appl
5	75	98.7	14	10	US-09-822-698A-99	Sequence 99, Appl
6	73	96.1	14	10	US-09-822-698A-93	Sequence 93, Appl
7	71	93.4	14	10	US-09-822-698A-83	Sequence 83, Appl
8	71	93.4	14	10	US-09-822-698A-84	Sequence 84, Appl
9	71	93.4	14	10	US-09-822-698A-88	Sequence 88, Appl
10	71	93.4	14	10	US-09-822-698A-104	Sequence 104, App
11	70	92.1	14	10	US-09-822-698A-106	Sequence 106, App
12	69	90.8	14	10	US-09-822-698A-31	Sequence 31, Appl
13	69	90.8	14	10	US-09-822-698A-32	Sequence 32, Appl
14	69	90.8	14	10	US-09-822-698A-75	Sequence 75, Appl
15	69	90.8	14	10	US-09-822-698A-76	Sequence 76, Appl
16	69	90.8	14	10	US-09-822-698A-77	Sequence 77, Appl
17	69	90.8	14	10	US-09-822-698A-78	Sequence 78, Appl
18	69	90.8	14	10	US-09-822-698A-94	Sequence 94, Appl
19	69	90.8	14	10	US-09-822-698A-97	Sequence 97, Appl

20	69	90.8	14	10	US-09-822-698A-107	Sequence 107, App
21	68	89.5	14	10	US-09-822-698A-89	Sequence 89, Appl
22	68	89.5	14	10	US-09-822-698A-101	Sequence 101, App
23	68	89.5	14	10	US-09-822-698A-108	Sequence 108, App
24	68	89.5	16	10	US-09-822-698A-65	Sequence 65, Appl
25	67	88.2	14	10	US-09-822-698A-81	Sequence 81, Appl
26	67	88.2	14	10	US-09-822-698A-82	Sequence 82, Appl
27	67	88.2	14	10	US-09-822-698A-98	Sequence 98, Appl
28	67	88.2	14	10	US-09-822-698A-109	Sequence 109, App
29	67	88.2	16	10	US-09-822-698A-67	Sequence 67, Appl
30	66	86.8	14	10	US-09-822-698A-103	Sequence 103, App
31	65	85.5	14	10	US-09-822-698A-85	Sequence 85, Appl
32	64	84.2	14	10	US-09-822-698A-30	Sequence 30, Appl
33	64	84.2	14	10	US-09-822-698A-79	Sequence 79, Appl
34	64	84.2	14	10	US-09-822-698A-86	Sequence 86, Appl
35	64	84.2	14	10	US-09-822-698A-91	Sequence 91, Appl
36	64	84.2	16	10	US-09-822-698A-69	Sequence 69, Appl
37	63	82.9	14	10	US-09-822-698A-90	Sequence 90, Appl
38	63	82.9	14	10	US-09-822-698A-96	Sequence 96, Appl
39	63	82.9	14	10	US-09-822-698A-100	Sequence 100, App
40	63	82.9	14	10	US-09-822-698A-102	Sequence 102, App
41	62	81.6	14	10	US-09-822-698A-95	Sequence 95, Appl
42	61	80.3	14	10	US-09-822-698A-29	Sequence 29, Appl
43	61	80.3	14	10	US-09-822-698A-74	Sequence 74, Appl
44	61	80.3	16	10	US-09-822-698A-63	Sequence 63, Appl
45	60	78.9	14	10	US-09-822-698A-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-09-822-698A-105

; Sequence 105, Application US/098222698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Henderikx, Hendricus R.J.M.

; APPLICANT: Hooogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DXN-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 105

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 100.0%; Score 76; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPIDY 12

Db 3 HTGGGVNDPIDY 14

RESULT 2

US-09-822-698A-3

; Sequence 3, Application US/098222698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hooogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DXN-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

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; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 76; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 76; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-1gG1
US-09-822-698A-26

Query Match      100.0%; Score 76; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99

Query Match      98.7%; Score 75; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 1.6e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

RESULT 6
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match      96.1%; Score 73; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPMDY 14

US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

US-09-822-698A-84
; Sequence 84, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-84

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

US-09-822-698A-88
; Sequence 88, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-88

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

US-09-822-698A-104
; Sequence 104, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 104
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-104

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

US-09-822-698A-106
; Sequence 106, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14
```

```

; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106

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```

Query Match          92.1%; Score 70; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 HTGGGVWDPIDY 12
   ||| |||||
Db 3 HTGAGVWDPIGY 14

```

```

RESULT 12
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

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```

Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 HTGGGVWDPIDY 12
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Db 3 HTGGGVWDPIGY 14

```

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RESULT 13
US-09-822-698A-32
; Sequence 32, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

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```

Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 HTGGGVWDPIDY 12
   ||| |||||
Db 3 HTGGGVWDPIKY 14

```

```

RESULT 14
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

```

```

Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HTGGGVWDPID 11
   ||| |||||
Db 3 HTGGGVWDPID 13

```

```

RESULT 15
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

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```

Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 HTGGGVWDPIDY 12
   ||| |||||
Db 3 HTGGGVWDPIGY 14

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Fri Mar 14 09:40:02 2003

us-09-822-698a-3_copy_99_110_1.rapb

Page 5

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Job time : 1.70769 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 25.5692 Seconds
(without alignments)
302.582 Million cell updates/sec

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Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
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- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
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- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
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- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	22	US-09-822-698A-105
2	76	100.0	121	19	US-09-538-913-3
3	76	100.0	121	22	US-09-822-698A-3
4	76	100.0	381	19	US-09-538-913-5
5	76	100.0	381	22	US-09-822-698A-5
6	76	100.0	451	22	US-09-822-698A-26

7	75	98.7	14	22	US-09-822-698A-99	Sequence 99, Appl
8	73	96.1	14	22	US-09-822-698A-93	Sequence 93, Appl
9	71	93.4	14	22	US-09-822-698A-83	Sequence 83, Appl
10	71	93.4	14	22	US-09-822-698A-84	Sequence 84, Appl
11	71	93.4	14	22	US-09-822-698A-88	Sequence 88, Appl
12	71	93.4	14	22	US-09-822-698A-104	Sequence 104, App
13	70	92.1	14	22	US-09-822-698A-106	Sequence 106, App
14	69	90.8	14	22	US-09-822-698A-31	Sequence 31, Appl
15	69	90.8	14	22	US-09-822-698A-32	Sequence 32, Appl
16	69	90.8	14	22	US-09-822-698A-75	Sequence 75, Appl
17	69	90.8	14	22	US-09-822-698A-76	Sequence 76, Appl
18	69	90.8	14	22	US-09-822-698A-77	Sequence 77, Appl
19	69	90.8	14	22	US-09-822-698A-78	Sequence 78, Appl
20	69	90.8	14	22	US-09-822-698A-94	Sequence 94, Appl
21	69	90.8	14	22	US-09-822-698A-97	Sequence 97, Appl
22	68	89.5	14	22	US-09-822-698A-107	Sequence 107, App
23	68	89.5	14	22	US-09-822-698A-89	Sequence 89, Appl
24	68	89.5	14	22	US-09-822-698A-101	Sequence 101, App
25	68	89.5	14	22	US-09-822-698A-108	Sequence 108, App
26	68	89.5	16	22	US-09-822-698A-65	Sequence 65, Appl
27	67	88.2	14	22	US-09-822-698A-81	Sequence 81, Appl
28	67	88.2	14	22	US-09-822-698A-82	Sequence 82, Appl
29	67	88.2	14	22	US-09-822-698A-98	Sequence 98, Appl
30	67	88.2	14	22	US-09-822-698A-109	Sequence 109, App
31	67	88.2	16	22	US-09-822-698A-67	Sequence 67, Appl
32	66	86.8	14	22	US-09-822-698A-103	Sequence 103, App
33	65	85.5	14	22	US-09-822-698A-85	Sequence 85, Appl
34	64	84.2	14	22	US-09-822-698A-30	Sequence 30, Appl
35	64	84.2	14	22	US-09-822-698A-79	Sequence 79, Appl
36	64	84.2	14	22	US-09-822-698A-86	Sequence 86, Appl
37	64	84.2	14	22	US-09-822-698A-91	Sequence 91, Appl
38	64	84.2	16	22	US-09-822-698A-69	Sequence 69, Appl
39	63	82.9	14	22	US-09-822-698A-90	Sequence 90, Appl
40	63	82.9	14	22	US-09-822-698A-96	Sequence 96, Appl
41	63	82.9	14	22	US-09-822-698A-100	Sequence 100, App
42	63	82.9	14	22	US-09-822-698A-102	Sequence 102, App
43	62	81.6	14	22	US-09-822-698A-95	Sequence 95, Appl
44	61	80.3	14	22	US-09-822-698A-29	Sequence 29, Appl
45	61	80.3	14	22	US-09-822-698A-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DXX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 100.0%; Score 76; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
|||||
Db 3 HTGGGVWDPIDY 14

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RESULT 2
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match      100.0%; Score 76; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHL Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 76; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 76; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 76; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
   |||||
Db 99 HTGGGVWDPIDY 110

RESULT 6
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHL-IgG1
US-09-822-698A-26
```



```

Query Match          100.0%; Score 76; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 99 HTGGGVDPIDY 110

RESULT 7
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99

Query Match          98.7%; Score 75; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPVDY 14

RESULT 8
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match          96.1%; Score 73; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPMDY 14

RESULT 9

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US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIN 14

RESULT 10
US-09-822-698A-84
; Sequence 84, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-84

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIN 14

RESULT 11
US-09-822-698A-88
; Sequence 88, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

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; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 88
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
 US-09-822-698A-88

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00043;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWDPIN 14

RESULT 12
 US-09-822-698A-104
 ; Sequence 104, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 104
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
 US-09-822-698A-104

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00043;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWNPIDY 14

RESULT 13
 US-09-822-698A-106
 ; Sequence 106, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 106
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
 US-09-822-698A-106

Query Match 92.1%; Score 70; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00063;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWDPIDY 14
 RESULT 14
 US-09-822-698A-31
 ; Sequence 31, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 31
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: region of a MUC1-specific binding member
 US-09-822-698A-31

Query Match 90.8%; Score 69; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00091;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWDPIDY 14

RESULT 15
 US-09-822-698A-32
 ; Sequence 32, Application US/09822698A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoogenboom, Hendricus R.J.M.
 ; APPLICANT: Henderikx, Maria P.G.
 ; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 ; FILE REFERENCE: DYX-015.1 US
 ; CURRENT APPLICATION NUMBER: US/09/822,698A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 09/538,913
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 32
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
 US-09-822-698A-32

Query Match 90.8%; Score 69; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00091;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
 Db 3 HTGGGVWDPIDY 14

Search completed: March 13, 2003, 15:28:04
 Job time : 25.8192 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 4.38462 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	57.9	218	6	US-10-282-122A-50009
2	44	57.9	330	6	US-10-366-683-23794
3	41	53.9	57	1	PCT-US02-32727-17567
4	41	53.9	57	5	US-09-978-825-17567
5	41	53.9	57	6	US-10-057-498-17567
6	41	53.9	251	6	US-10-282-122A-46525
7	41	53.9	264	1	PCT-US02-40225-3079
8	41	53.9	264	6	US-10-320-797-3079
9	41	53.9	300	6	US-10-282-122A-46309
10	41	53.9	710	6	US-10-156-761-14284
11	40	52.6	34	6	US-10-203-138A-13646
12	40	52.6	93	1	PCT-US02-32727-9150
13	40	52.6	93	5	US-09-978-825-9150
14	40	52.6	93	6	US-10-057-498-9150
15	40	52.6	152	6	US-10-156-761-10926
16	40	52.6	158	6	US-10-282-122A-54884
17	40	52.6	717	6	US-10-369-493-10840
18	40	52.6	799	6	US-10-282-122A-49879
19	39.5	52.0	473	1	PCT-US02-32727-17396
20	39.5	52.0	473	6	US-09-978-825-17396
21	39.5	52.0	473	6	US-10-057-498-17396
22	39	51.3	351	6	US-10-156-761-12617
23	39	51.3	480	6	US-10-369-493-9063
24	39	51.3	687	6	US-10-369-493-7152
25	39	51.3	692	6	US-10-369-493-4397
26	39	51.3	807	6	US-10-369-493-22143

27	39	51.3	1583	1	PCT-US02-32727-15149
28	39	51.3	1583	5	US-09-978-825-15149
29	39	51.3	1583	6	US-10-057-498-15149
30	38.5	50.7	101	1	PCT-US02-32727-5698
31	38.5	50.7	101	5	US-09-978-825-5698
32	38.5	50.7	101	6	US-10-057-498-5698
33	38.5	50.7	327	6	US-10-369-493-634
34	38	50.0	76	1	PCT-US02-32727-2924
35	38	50.0	76	5	US-09-978-825-2924
36	38	50.0	76	6	US-10-057-498-2924
37	38	50.0	108	6	US-10-366-683-19965
38	38	50.0	109	6	US-10-092-411A-3523
39	38	50.0	217	6	US-10-282-122A-47986
40	38	50.0	250	5	US-09-724-676-96838
41	38	50.0	250	5	US-09-724-676A-96838
42	38	50.0	304	1	PCT-US03-01363-179
43	38	50.0	327	6	US-10-156-761-12586
44	38	50.0	328	1	PCT-US02-25805A-542
45	38	50.0	328	6	US-10-171-404A-32

ALIGNMENTS

RESULT 1
US-10-282-122A-50009
; Sequence 50009, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50009
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50009

Query Match 57.9%; Score 44; DB 6; Length 218;
Best Local Similarity 63.6%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVNDP 11
| | | | | | | |
Db 80 HGGGLYQPID 90

RESULT 2
US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 57.9%; Score 44; DB 6; Length 330;
Best Local Similarity 87.5%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGVNDP 11
| | | | | | | |
Db 101 GSVNDP 108

RESULT 3
PCT-US02-32727-17567
; Sequence 17567, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiyang
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514cl
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-17567

Query Match 53.9%; Score 41; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVNDP 9
| | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 4
US-09-978-825-17567
; Sequence 17567, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiyang
; APPLICANT: Jen, Shiyang
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514cl
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-17567

Query Match 53.9%; Score 41; DB 5; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVNDP 9
| | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 5
US-10-057-498-17567
; Sequence 17567, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-17567

Query Match 53.9%; Score 41; DB 6; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVNDP 9
| | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 6
US-10-282-122A-46525
; Sequence 46525, Application US/10282122A

```
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46525
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46525

Query Match      53.9%; Score 41; DB 6; Length 251;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGGWDPI 10
        |||||
Db      152 TGGGWDGPI 160

RESULT 7
PCT-US02-40225-3079
; Sequence 3079, Application PC/TUS0240225
; GENERAL INFORMATION:
; APPLICANT: Eroskin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-228
; CURRENT APPLICATION NUMBER: PCT/US02/40225
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
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```
; ORGANISM: Cryptococcus neoformans
PCT-US02-40225-3079

Query Match      53.9%; Score 41; DB 1; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 HTGGGVWDPI 11
        :| ||| | |
Db      233 YKGTGVWTPVD 243

RESULT 8
US-10-320-797-3079
; Sequence 3079, Application US/10320797
; GENERAL INFORMATION:
; APPLICANT: Eroskin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS A
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3079

Query Match      53.9%; Score 41; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 HTGGGVWDPI 11
        :| ||| | |
Db      233 YKGTGVWTPVD 243

RESULT 9
US-10-282-122A-46309
; Sequence 46309, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
```

```

; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46309
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46309

Query Match          53.9%; Score 41; DB 6; Length 300;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 10
    |||||
Db 149 TGGGGWGPI 157

RESULT 10
US-10-156-761-14284
; Sequence 14284, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14284
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14284

Query Match          53.9%; Score 41; DB 6; Length 710;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
    |||||
Db 600 HTGGGSWSVED 610

RESULT 11
US-10-203-138A-13646
; Sequence 13646, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

```

; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 13646
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007247.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.2
US-10-203-138A-13646

Query Match          52.6%; Score 40; DB 6; Length 34;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDPI 10
    |||||
Db 5 GGVWDPI 11

RESULT 12
PCT-US02-32727-9150
; Sequence 9150, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-9150

Query Match          52.6%; Score 40; DB 1; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGVWDPI 10
```

Db 10 GGGWDSL 17
|||||:

RESULT 13

US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Sigang
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: US/09/978,825

; CURRENT FILING DATE: 2003-01-29

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 9150

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Propioni acnes

US-09-978-825-9150

Query Match 52.6%; Score 40; DB 5; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGWDP1 10
|||||:
Db 10 GGGWDSL 17

RESULT 14

US-10-057-498-9150

; Sequence 9150, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 9150

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-9150

Query Match 52.6%; Score 40; DB 6; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGWDP1 10
|||||:
Db 10 GGGWDSL 17

RESULT 15

US-10-156-761-10926

; Sequence 10926, Application US/10156761

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 10926

; LENGTH: 152

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-10926

Query Match 52.6%; Score 40; DB 6; Length 152;

Best Local Similarity 33.3%; Pred. No. 2e+02;

Matches 9; Conservative 1; Mismatches 1; Indels 16; Gaps 1;

QY 1 HTG-----GGWDPID 11
||| | :|||
Db 105 HTGGEWTTGGDHWVTPDGRWDPID 131

Search completed: March 13, 2003, 15:29:47
Job time : 5.38462 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 2.07692 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_l10

Perfect score: 76

Sequence: 1 HTGGVWDPIDY 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	61.8	573	2 A41319	3-oxosteroid 1-deh
2	45	59.2	381	2 B97182	acyl-protein synth
3	43	56.6	71	2 A34768	ORF1 protein - Orf
4	43	56.6	304	2 H82984	hypothetical prote
5	43	56.6	435	2 B87412	conserved hypothet
6	43	56.6	536	2 T08241	gas-vesicle operon
7	43	56.6	536	2 S15183	hypothetical prote
8	42.5	55.9	597	2 G75070	hypothetical prote
9	42.5	55.9	598	2 B71095	cytochrome-c oxida
10	42	55.3	255	2 S26020	peptide pheromone
11	41	53.9	42	2 E95061	ATF1 protein - yea
12	41	53.9	182	2 S17005	hypothetical prote
13	40	52.6	114	2 T08411	pts iIA protein [i
14	40	52.6	158	2 B8498	pts iIA protein -
15	40	52.6	158	2 E72124	disulfide oxidore
16	40	52.6	193	2 C82683	probable geranyl t
17	40	52.6	291	2 E71491	hypothetical prote
18	40	52.6	300	2 F69997	hypothetical prote
19	40	52.6	338	2 H84173	acetoin utilizatio
20	40	52.6	345	2 E90817	hypothetical prote
21	40	52.6	345	2 C90974	hypothetical prote
22	40	52.6	345	2 A85677	unknown protein en
23	40	52.6	345	2 E95821	unknown protein en
24	40	52.6	347	2 F90904	hypothetical prote
25	40	52.6	347	2 G85712	unknown protein en
26	40	52.6	478	1 I47154	transcription fact
27	39	51.3	125	1 B43825	angiogenin - rabbi
28	39	51.3	237	2 A82607	hypothetical prote
29	39	51.3	260	2 C75454	hypothetical prote

30 39 51.3 312 2 T36986 probable ribosylgl
31 39 51.3 370 2 F86338 protein F2D10.2 [i
32 39 51.3 386 2 S74778 hypothetical prote
33 39 51.3 418 2 S42031 LbJ2 protein - lee
34 39 51.3 518 2 S42387 MIPP protein homol
35 39 51.3 524 2 S30575 glycoprotein precu
36 39 51.3 579 2 H88478 protein F47D12.7 [i
37 39 51.3 807 2 A32582 protein kinase YAK
38 39 51.3 886 2 T10890 cysteine proteinas
39 39 51.3 1276 2 T02711 probable calmoduli
40 38.5 50.7 265 2 B90506 oxidoreductase, al
41 38.5 50.7 327 2 B75341 probable oxidoredu
42 38.5 50.7 610 2 T24352 hypothetical prote
43 38.5 50.7 1077 2 T01474 hypothetical prote
44 38 50.0 97 2 E83584 hypothetical prote
45 38 50.0 131 2 E75550 probable transposa

ALIGNMENTS

RESULT 1

A41319
3-oxosteroid 1-dehydrogenase (EC 1.3.99.4) - Comamonas testosteroni
C:Species: Comamonas testosteroni
C:Date: 05-Jun-1992 #sequence_revision 28-Apr-1993 #text_change 29-Sep-1999
C:Accession: A41319
R:Plesiat, P.; Grandguillot, M.; Harayama, S.; Vragar, S.; Michel-Briand, Y.
J. Bacteriol. 173, 7219-7227, 1991
A:Title: Cloning, sequencing, and expression of the Pseudomonas testosteroni gene enc
A:Reference number: A41319; MUID:92041619; PMID:1657885
A:Accession: A41319
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <PLE>
A:Cross-references: GB:M68488; NID:G485378; PID:AAA25679.1; PID:G485379
A:Note: The authors translated the codon ACC for residue 497 as Tyr
... C:Superfamily: 3-oxosteroid 1-dehydrogenase; 3-oxosteroid 1-dehydrogenase homology
C:Keywords: Oxidoreductase
F:450-548/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match 61.8%; Score 47; DB 2; Length 573;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPIDY 12

Db :|||:|:|

47 SGGGIWIPLY 57

RESULT 2

B97182
acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: B97182
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; J
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97182
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <KUR>
A:Cross-references: GB:AE001437; PID:AAK80245.1; PID:g15025293; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2288

Query Match 59.2%; Score 45; DB 2; Length 381;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 HTGGGVWD 8
      |||||
Db 223 HTGGGWD 230

RESULT 3
A34768
ORF1 protein - Orf virus (strain N22)
C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C:Accession: A34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the para
A:Reference number: A34768; MUID:90266454; PMID:2129563
A:Accession: A34768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <FRA>
A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46787.1; PID:g332563

Query Match 56.6%; Score 43; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 5.3;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPID 11
      :|||:
Db .32 SGGIWDGPLE 41

RESULT 4
H82984
hypothetical protein PA5284 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H82984
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H82984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004941; GB:AE004091; NID:g9951596; PIDN:AAG08669.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5284

Query Match 56.6%; Score 43; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGVWDPID 11
      |
Db 75 GSVWDPEVD 82

RESULT 5
B87412
conserved hypothetical protein CCI313 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87412
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
```

```
A:Accession: B87412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <STO>
A:Cross-references: GB:AE005673; NID:g13422654; PIDN:AAK23294.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCI313
```

```
Query Match 56.6%; Score 43; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 HTGGGVWDPI 10
      |
Db 372 HNPGGFWDPL 381
```

```
RESULT 6
T08241
gas-vesicle operon protein gvpD - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N:Alternate names: hypothetical protein H0263
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
R:Ng, W.V.; Ciufu, S.A.; Smith, T.M.; Bungarner, R.E.; Baskin, D.; Faust, J.; Hall, B
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid o
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08241
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-536 <NGW>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822302; HALOSP:H0263
C:Experimental source: strain NRC-1
C:Genetics:
A:Gene: gvpD; HALOSP:H0263
A:Genome: Plasmid pNRC100
```

```
Query Match 56.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 TGGGVWDPI 10
      ||
Db 247 TGNGTWDPL 255
```

```
RESULT 7
S15183
gas-vesicle operon protein gvpD - Halobacterium salinarum plasmids pHH1 and pNRC100
C:Species: Halobacterium salinarum
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C:Accession: S15183; S06185
R:Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A:Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis
A:Reference number: S15183; MUID:92065812; PMID:1956294
A:Accession: S15183
A:Molecule type: DNA
A:Residues: 1-536 <HOR>
A:Cross-references: EMBL:X55648; NID:g43516; PID:g43517
A:Experimental source: plasmid pHH1
A:Genetics: pHH
A:Note: the authors translated the codon ACG for residue 531 as Ile
R:Jones, J.G.; Hackett, N.R.; Halladay, J.T.; Scothorn, D.J.; Yang, C.F.; Ng, W.L.; D
Nucleic Acids Res. 17, 7785-7793, 1989
A:Title: Analysis of insertion mutants reveals two new genes in the pNRC100 gas vesic
A:Reference number: S06184; MUID:90016863; PMID:2552415
A:Accession: S06185
A:Molecule type: DNA
A:Residues: 1-536 <JON>
```


Db 22 TGGGLWEDLLY 32
||||:|:|

RESULT 12

S17005

AHT1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: activator of hexose transport; protein H9332.3; protein YHR093w

C:Species: Saccharomyces cerevisiae

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 29-Oct-1999

C:Accession: S17005; S46717

R:Oezcan, S.; Cirliacy, M.

submitted to the EMBL Data Library, May 1991

A:Reference number: S17005

A:Accession: S17005

A:Molecule type: DNA

A:Residues: 1-182 <OEZ>

A:Cross-references: EMBL:X59464; NID:g3354; PIDN:CA42071.1; PID:g663230

A:Experimental source: strain MC 971 B

R:Vaadin, M.

submitted to the EMBL Data Library, May 1994

A:Description: The sequence of S. cerevisiae cosmid 9332.

A:Reference number: S46715

A:Accession: S46717

A:Molecule type: DNA

A:Residues: 1-182 <VAU>

A:Cross-references: EMBL:U00060; NID:g487928; PIDN:AAB68925.1; PID:g487931; MIPS:YHR093w

C:Genetics:

A:Gene: SGD:AHT1

A:Cross-references: SGD:S0001135; MIPS:YHR093w

A:Map position: 8R

C:Superfamily: Saccharomyces AHT1 protein

Query Match 53.9%; Score 41; DB 2; Length 182;

Best Local Similarity 55.6%; Pred. No. 28;

Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

QY 3 GGGVWDPID 11

|||||

Db 44 GGGIWGPM 52

RESULT 13

T08411

hypothetical protein F18B3.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T08411

R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16409

A:Accession: T08411

A:Molecule type: DNA

A:Residues: 1-114 <QUE>

A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180

A:Experimental source: cultivar Columbia; BAC clone F18B3

C:Genetics:

A:Gene: ATSP:F18B3.180

A:Map position: 3

C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match

Best Local Similarity 52.6%; Score 40; DB 2; Length 114;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDP 9

|||||

Db 99 GGVWDP 104

RESULT 14

E86498

Pts IIA Protein [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86498
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: E86498

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-158 <STO>

A:Cross-references: GB:BA000008; NID:g8578434; PIDN:BAA98271.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: ptsN_1

C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

Query Match 52.6%; Score 40; DB 2; Length 158;

Best Local Similarity 63.6%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

|||:|:|

Db 92 HTQGILWDAID 102

RESULT 15

E72124

pts iia protein - Chlamydomophila pneumoniae (strain CWL029)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000

C:Accession: E72124

R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: E72124

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-158 <ARN>

A:Cross-references: GB:AE001591; GB:AE001363; NID:g4376311; PIDN:AAD18213.1; PID:g437

A:Experimental source: strain CWL029

C:Genetics:

A:Gene: ptsN_1

C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III hom

Query Match 52.6%; Score 40; DB 2; Length 158;

Best Local Similarity 63.6%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

|||:|:|

Db 92 HTQGILWDAID 102

Search completed: March 13, 2003, 15:17:53

Job time : 3.07692 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 1.2 seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698a-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	61.8	573	1	301D_COMTE
2	43	56.6	536	1	GVDL_HALN1
3	43	56.6	1371	1	PUR2_CHITE
4	42	55.3	255	1	COX3_ASCSU
5	41	53.9	182	1	AHT1_YEAST
6	40	52.6	478	1	OCT2_PIG
7	39	51.3	125	1	ANG1_RABIT
8	39	51.3	418	1	DNJ2_ALLPO
9	39	51.3	518	1	YNV6_CAEEL
10	39	51.3	579	1	YK47_CAEEL
11	39	51.3	807	1	YAK1_YEAST
12	39	51.3	868	1	PRTT_PORGI
13	38	50.0	185	1	EPF_DEIRA
14	38	50.0	256	1	YM56_YEAST
15	38	50.0	272	1	COX3_PYLII
16	38	50.0	387	1	YB96_YEAST
17	38	50.0	420	1	TABA_PSESZ
18	38	50.0	447	1	DHE4_CORGL
19	38	50.0	521	1	GLGA_METJA
20	38	50.0	643	1	YKQ9_CAEEL
21	38	50.0	738	1	DHET_ACEPU
22	38	50.0	739	1	DHET_ACEPU
23	38	50.0	943	1	LRPA_NEIMB
24	38	50.0	944	1	LRPA_NEIMA
25	37.5	49.3	637	1	TRGS_ECOLI
26	37	48.7	32	1	GHR4_RAT
27	37	48.7	238	1	PRRC_RAT
28	37	48.7	242	1	Y252_MVCGE
29	37	48.7	344	1	PUR5_ECOLI
30	37	48.7	344	1	PUR5_HAEIN
31	37	48.7	357	1	YFQ8_SCHFO
32	37	48.7	382	1	SUCL_ARCFU
33	37	48.7	497	1	ACCD_CUSRE

34	37	48.7	512	1	ACCD_TOBAC
35	37	48.7	628	1	BGAL_LACAC
36	37	48.7	1014	1	BGAL_BACHD
37	37	48.7	1101	1	GUNC_CELFI
38	37	48.7	1403	1	VG22_HSVI1
39	36.5	48.0	1025	1	HIRA_FUGRU
40	36	47.4	87	1	SODC_ACTAC
41	36	47.4	115	1	YIDD_MYCPA
42	36	47.4	120	1	Y3C2_MYCTU
43	36	47.4	152	1	ANF_RAT
44	36	47.4	211	1	NADD_MYCTU
45	36	47.4	214	1	NADD_MYCLE

p12219	nicotiana t
O07684	lactobacill
O9K9C6	bacillus ha
P14090	cellulomona
Q00105	ictalurid h
Q02611	fugu rubrip
Q59081	actinobacil
Q917M0	mycobacteri
O53600	mycobacteri
P01161	rattus norv
O86328	mycobacteri
Q9CBZ8	mycobacteri

ALIGNMENTS

RESULT 1
301D_COMTE
ID 301D_COMTE STANDARD; PRT; 573 AA.
AC Q06401;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxosteroid 1-dehydrogenase (EC 1.3.99.4).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17410;
RX MEDLINE=92041619; PubMed=1657885;
RA Plesiat P., Grandquillot M., Harayama S., Vragar S., Michel-Briand Y.;
RT "Cloning, sequencing, and expression of the pseudomonas testosteroni
gene encoding 3-oxosteroid delta 1-dehydrogenase.";
RL J. Bacteriol. 173:7219-7227(1991).
CC -!- FUNCTION: DEHYDROGENATES STEROIDS BY INTRODUCING A DOUBLE
BOND IN STEROID RING A.
CC -!- CATALYTIC ACTIVITY: A 3-oxosteroid + acceptor = a 3-oxo-delta(1)-
steroid + reduced acceptor.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: FIRST STEP IN STEROID CATABOLISM.
CC -!- SUBCELLULAR LOCATION: Inner membrane.
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CC -----
CC EMBL; M68488; AAA25679.1; -;
CC EMBL; A22347; CAA01596.1; -;
CC PIR; A41319; A41319.
KW Oxidoreductase; Flavoprotein; Inner membrane; Steroid metabolism;
KW FAD.
FT NP_BIND 7 36 FAD (BY SIMILARITY).
SQ SEQUENCE 573 AA; 62672 MW; 8E941AF569897734 CRC64;
Query Match 61.8%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 4.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGGGVWDPIDY 12
:||||:|
Db 47 SGGGIWIPLYN 57
RESULT 2
GVDL_HALN1 STANDARD; PRT; 536 AA.
ID GVDL_HALN1
AC P13043; Q9H119;

DT	01-JAN-1990 (Rel. 13, Created)	DR	EMBL; AF016485; AAC82808.1; -;
DT	01-JAN-1990 (Rel. 13, Last sequence update)	DR	EMBL; AE005141; AAG20725.1; -;
DT	16-OCT-2001 (Rel. 40, Last annotation update)	DR	EMBL; X55648; CAA39171.1; -;
DE	GvpD protein 1.	DR	PIR; S06185; S06185.
GN	(GVPD11 OR GVPD OR VNG5029G) AND (GVPD12 OR VNG6028G).	DR	PIR; S15183; S15183.
OS	Halobacterium sp. (strain NRC-1), and	KW	Gas vesicle; Plasmid; ATP-binding; Complete proteome.
OS	Halobacterium sp. (strain NRC-817).	FT	NP_BIND 39 46 ATP (POTENTIAL).
OG	Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1.	SQ	SEQUENCE 536 AA; 59342 MW; 3FC4E4F8F129F9CD CRC64;
OC	Archaea; Euryarchaeota; Halobacteria; Halobacteriales;		
OC	Halobacteriaceae; Halobacterium.		
OX	NCBI_TaxID=64091, 148370;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NRC-1; PLASMID=pNRC100;		
RX	MEDLINE=90016863; PubMed=2352415;		
RA	Jones J.G., Hackett N.R., Halladay J.T., Scothorn D.J.,		
RA	Yang C.-F., Ng W.-L., Dassarma S.;		
RT	"Analysis of insertion mutants reveals two new genes in the pNRC100		
RT	gas vesicle gene cluster of Halobacterium halobium.";		
RL	Nucleic Acids Res. 17:7785-7794(1989).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NRC-1; PLASMID=pNRC100;		
RX	MEDLINE=91323716; PubMed=1864501;		
RA	Jones J.G., Young D.C., Dassarma S.;		
RT	"Structure and organization of the gas vesicle gene cluster on the		
RT	Halobacterium halobium plasmid pNRC100.";		
RL	Gene 102:117-122(1991).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NRC-1; PLASMID=pNRC100;		
RX	MEDLINE=99063795; PubMed=9847077;		
RA	Ng W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,		
RA	Hall B., Loretz C., Seto J., Slagel J., Hood L., Dassarma S.;		
RT	"Snapshot of a large dynamic replicon in a halophilic archaean:		
RT	megaplasmid or minichromosome?";		
RL	Genome Res. 8:1131-1141(1998).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NRC-1; PLASMID=pNRC200;		
RX	MEDLINE=20504483; PubMed=11016950;		
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,		
RA	Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,		
RA	Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,		
RA	Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,		
RA	Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,		
RA	Isenbarger T.A., Feck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,		
RA	Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,		
RA	Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;		
RT	"Genome sequence of Halobacterium species NRC-1.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NRC-817; PLASMID=pHH1;		
RX	MEDLINE=92065812; PubMed=1956294;		
RA	Horne M., Englert C., Wimmer C., Pfeifer F.;		
RT	"A DNA region of 9 kbp contains all genes necessary for gas vesicle		
RT	synthesis in halophilic archaeobacteria.";		
RL	Mol. Microbiol. 5:1159-1174(1991).		
CC	-1- FUNCTION: MAY PLAY A ROLE IN AN ENERGY REQUIRING PROCESS SUCH AS		
CC	ASSEMBLY OF GAS VESICLES IN ADDITION TO A POSSIBLE STRUCTURAL OR		
CC	REGULATORY FUNCTION.		
CC	-----		
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CC	-----		
DR	EMBL; X15374; CAA33435.1; -;		
DR	EMBL; M58557; AAA98195.1; -;		

DR InterPro: IPR002376; formyl_transf.
DR Pfam: PF00551; formyl_transf; 1.
DR Pfam: PF00586; AIRS; 2.
DR Pfam: PF01071; GARS; 1.
DR Pfam: PF02769; AIRS_C; 2.
DR Pfam: PF02842; GARS_B; 1.
DR Pfam: PF02843; GARS_C; 1.
DR Pfam: PF02844; GARS_N; 1.
DR TIGRFAMs: TIGR00639; PurN; 1.
DR TIGRFAMs: TIGR00877; purD; 1.
DR TIGRFAMs: TIGR00878; purM; 2.
DR TIGRFAMs: TIGR00879; purM; 2.
DR PROSITE: PS00184; GARS; 1.
DR PROSITE: PS00373; GART; 1.
DR PROSITE: PS00373; GART; 1.

KW Multifunctional enzyme; Purine biosynthesis; Ligase; Transferase.
FT DOMAIN 1 433 GARS.
FT DOMAIN 434 1171 AIRS.
FT DOMAIN 1172 1371 GART.
FT ACT_SITE 1315 1315 BY SIMILARITY.
SQ SEQUENCE 1371 AA; 149103 MW; 7BF4664DB1538946 CRC64;

Query Match 56.6%; Score 43; DB 1; Length 1371;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 10
||||:|
Db 1057 TGGGLWDNI 1065

RESULT 4

ID COX3_ASCSU STANDARD; PRT; 255 AA.
AC P24879;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COIII.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OG Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body wall muscle, and Egg;
RX MEDLINE=92201635; PubMed=1551572;
RA Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial genomes of two nematodes, *Caenorhabditis elegans*
and *Ascaris suum*,";
RL Genetics 130:471-498(1992).
CC -!- FUNCTION: Subunits I, II and III form the functional core of
the enzyme complex.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
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or send an email to license@isb-sib.ch).
CC EMBL; X54253; CAA38169.1; -
DR PIR; S26020; S26020.
DR InterPro: IPR000298; Cytc_oxdse_III.
DR Pfam: PF00510; COX3; 1.
DR ProDom: PD000382; Cytc_oxdse_III; 1.
DR PROSITE: PS00253; COX3; 1.
KW Oxidoreductase; Mitochondrion; Transmembrane.
SQ SEQUENCE 255 AA; 29094 MW; 05A992684AC92755 CRC64;

Query Match 55.3%; Score 42; DB 1; Length 255;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
| | | | | |
Db 106 HDVGGVWSPi 115

RESULT 5

ID AHT1_YEAST STANDARD; PRT; 182 AA.
AC P29589; P38807;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hexose transport activator protein.
GN AHT1 OR YHR093W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC 971 B;
RA Oezcan S., Ciriacy M.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
Vaudin M.;
RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
VIII,";
RL Science 265:2077-2082(1994).
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CC EMBL; X59464; CAA42071.1; -
DR EMBL; U00060; AAB68925.1; -
DR PIR; S17005; S17005.
DR PIR; S46717; S46717.
DR SGD: S0001135; AHT1.
SQ SEQUENCE 182 AA; 19776 MW; 7B0723BAA1066713 CRC64;

Query Match 53.9%; Score 41; DB 1; Length 182;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPI 11
| | | | | |
Db 44 GGGVWPM 52

RESULT 6

ID OCT2_PIG STANDARD; PRT; 478 AA.
AC Q29013; Q29089;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Octamer-binding transcription factor 2 (OTF-2) (Lymphoid-restricted
Immunoglobulin octamer binding protein NF-A2) (OTF-2 factor).
POU2F2 OR OTF2 OR OCT2.
Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Splice;
RC MEDLINE=95030552; PubMed=7943947;
RA Tuggle C.K., Helm J., Rothschild M.F.;
RT "Cloning, sequencing and restriction fragment length polymorphism
analysis of a porcine cDNA for OCT2.";
RL Anim. Genet. 25:141-145(1994).
[2]
SEQUENCE OF 210-350 FROM N.A.
RP STRAIN=Duroc;
RC MEDLINE=94095558; PubMed=8270542;
RA Tuggle C.K.;
RT "Cloning and sequence analysis of the swine Oct-2 POU-domain genomic
region.";
RL J. Anim. Sci. 71:3172-3172(1993).
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR THAT SPECIFICALLY
BINDS TO THE OCTAMER MOTIF ('ATTGTCAT') AND PLAYS AN IMPORTANT
ROLE IN REGULATING TRANSCRIPTION IN A NUMBER OF TISSUES IN
ADDITION TO ACTIVATING IMMUNOGLOBULIN GENE EXPRESSION (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN B-CELLS (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC -1- CLASS-2 SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.

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EMBL; U00794; AAA80148.1; -;
DR EMBL; L03842; AAA74657.1; -;
DR HSP; P09086; 1HDP.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000972; Octamer-bind_TF.
DR InterPro; IPR000327; POU_domain.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00157; pou; 1.
DR PRINTS; PR00029; OCTAMER.
DR PRINTS; PR00028; POU_DOMAIN.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000583; POU_domain; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
KW Homeobox; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein.
FT DOMAIN 199 269 POU.
FT DNA_BIND 297 356 HOMEBOX.
FT DOMAIN 389 410 LEUCINE-ZIPPER.
FT DOMAIN 77 80 POLY-PRO.
FT DOMAIN 417 424 GLY-RICH.
FT DOMAIN 437 440 POLY-PRO.
FT DOMAIN 437 440 POLY-PRO.
FT CONFLICT 212 215 Q -> V (IN REF. 2).
FT CONFLICT 215 215 I -> M (IN REF. 2).
FT CONFLICT 222 222 G -> V (IN REF. 2).

FT CONFLICT 233 233 G -> A (IN REF. 2).
FT CONFLICT 238 238 Q -> K (IN REF. 2).
FT CONFLICT 285 285 R -> S (IN REF. 2).
SQ SEQUENCE 478 AA; 51098 MW; FD196758B603B718 CRC64;
Query Match 52.6%; Score 40; DB 1; Length 478;
Best Local Similarity 54.5%; Pred. No. 47; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 3;
QY 2 TGGGVWDPIDY 12
| | | | | | | | | |
Db 466 TGPGLWNPAPY 476
| | | | | | | | | |
RESULT 7
ANGI_RABIT STANDARD; PRT; 125 AA.
AC P31347; 1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 41, Last annotation update)
DE Angiogenin (EC 3.1.1.27.-).
GN ANG.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiotensins: discernment of functionally important residues and
regions".
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
HYDROLYZING CELLULAR TRNAs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR; B43825; B43825.
DR PIR; S29833; S29833.
DR HSP; P03950; 1A4Y.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 13 13 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 114 114 BY SIMILARITY.
FT DISULFID 26 81 BY SIMILARITY.
FT DISULFID 39 92 BY SIMILARITY.
FT DISULFID 57 107 BY SIMILARITY.
SQ SEQUENCE 125 AA; 14361 MW; 3A737E595D767B04 CRC64;
Query Match 51.3%; Score 39; DB 1; Length 125;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
| | | | | | | | | |
Db 83 HVGGSPPPCRY 94
| | | | | | | | | |


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RESULT 8
DNJ2_ALLPO STANDARD; PRT; 418 AA.
AC P42824;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ protein homolog 2.
GN LDJ2.
OS Allium porrum (Leek).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4681;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessoule J.J., Testet E., Cassagne C.;
RT "Cloning of a new isoform of a DnaJ protein from Allium porrum
RT epidermal cells.";
RL Plant Physiol. Biochem. 32:723-727(1994).
CC -!- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
CC IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC -----
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CC -----
EMBL: X77632; CAA54720.1; -.
DR HSSP; P25685; IHDJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
KW Chaperone; Repeat; Prenylation; Lipoprotein; Multigene family.
FT DOMAIN 11 76 J-DOMAIN.
FT DOMAIN 83 88 POLY-GLY.
FT DOMAIN 81 108 GLY-RICH.
FT REPEAT 148 155 CXXCXGKG MOTIF.
FT REPEAT 164 171 CXXCXGKG MOTIF.
FT REPEAT 191 198 CXXCXGKG MOTIF.
FT REPEAT 207 214 CXXCXGKG MOTIF.
FT Lipid 415 415 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 418 AA; 46584 MW; DCE2A4DF192329E6 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 418;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGVWDPTD 11
DB 85 GGGVHDPFD 93

RESULT 9
YNV6_CAEL STANDARD; PRT; 518 AA.
AC P34569; P34570;

Query Match 51.3%; Score 39; DB 1; Length 518;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
DB 368 HGGGEVYDPV 377

RESULT 10
YR47_CAEL STANDARD; PRT; 579 AA.
AC Q09563;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 66.0 kDa protein F47D12.7 in chromosome III.
GN F47D12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Taich A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.

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DR EMBL; U22831; AAK20068.1; -;
 DR WormPep; F47D12.7; CE01951.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR001798; Kelch.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.
 DR SMART; SM00225; BTB; 1.
 DR PROSITE; PSS0097; BTB; 1.
 KW Hypothetical protein; Repeat.
 FT DOMAIN 51 119
 FT REPEAT 266 316
 FT REPEAT 317 363
 FT REPEAT 369 415
 FT REPEAT 417 463
 FT REPEAT 465 511
 FT REPEAT 513 559
 SQ SEQUENCE 579 AA; 66042 MW; 3FE770B5E4C2D32F CRC64;

Query Match 51.3%; Score 39; DB 1; Length 579;

Best Local Similarity 60.0%; Pred. No. 81; Length 579;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
 I I I I I
 Db 429 HOGGEVYDPV 438

RESULT 11

YAKI_YEAST
 ID YAKI_YEAST STANDARD; PRT; 807 AA.
 AC P14680;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase YAKI (EC 2.7.1.-).
 GN YAKI OR YJL141C OR J0652.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90108683; PubMed=2558053;
 RA Garrett S., Broach J.;
 RT "Loss of Ras activity in Saccharomyces cerevisiae is suppressed by
 RT disruptions of a new kinase gene, YAKI, whose product may act
 RT downstream of the cAMP-dependent protein kinase.";
 RL Genes Dev. 3:1336-1348(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / FY1679;
 RX MEDLINE=96408771; PubMed=8813765;
 RA Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.;
 RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast
 RT chromosome X reveals 14 known genes and 13 new open reading frames
 RT including homologues of genes clustered on the right arm of
 RT chromosome XI".
 RL Yeast 12:787-797(1996).
 CC -1- FUNCTION: THIS PROTEIN OCCURS IN REVERTANT RAS/CAMP MUTANTS
 CC YEAST AND MAY BE INVOLVED IN CELL-CYCLE REGULATION.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MNB/DYRK SUBFAMILY.
 CC -----

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DR EMBL; X16056; CAA34192.1; -;
 DR EMBL; X87371; CAA60814.1; -;
 DR EMBL; Z49417; CAA89437.1; -;
 DR PIR; A32582; A32582.
 DR HSP; P24941; 1A01.
 DR SGD; S0003677; YAKI.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 56 85 GLN-RICH.
 FT DOMAIN 369 704 PROTEIN KINASE.
 FT NP_BIND 375 383 ATP (BY SIMILARITY).
 FT BINDING 398 398 ATP (BY SIMILARITY).
 FT ACT_SITE 496 496 BY SIMILARITY.
 FT MOD_RES 127 127 PHOSPHORYLATION (PROBABLE).
 FT MOD_RES 206 206 PHOSPHORYLATION (PROBABLE).
 FT MOD_RES 240 240 PHOSPHORYLATION (PROBABLE).
 FT MOD_RES 295 295 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 807 AA; 91245 MW; E0B7C56FAA35E056 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 807;

Best Local Similarity 55.6%; Pred. No. 11e+02; Length 807;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 9
 I I I I I
 Db 43 HMGGRWNP 51

RESULT 12

PRTT_PORGI
 ID PRTT_PORGI STANDARD; PRT; 868 AA.
 AC P43158;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Thiol protease/hemagglutinin prt precursor (EC 3.4.22.-).
 GN PRTT.
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 53977;
 RX MEDLINE=93114862; PubMed=8093357;
 RA Ologoto J.-I., Kuramitsu H.K.;
 RT "Isolation and characterization of the Porphyromonas gingivalis prt
 RT gene, coding for protease activity.";
 RL Infect. Immun. 61:117-123(1993).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RC STRAIN=ATCC 53977;
 RX MEDLINE=95105001; PubMed=7806362;
 RA Madden T.E., Clark V.L., Kuramitsu H.K.;
 RT "Revised sequence of the Porphyromonas gingivalis prt cysteine
 RT protease/hemagglutinin gene: homology with streptococcal pyrogenic
 RT exotoxin B/streptococcal proteinase.";
 RT

RL Infect. Immun. 63:238-247(1995).
 CC -!- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGinine-CONTAINING PEPTIDE
 CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
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 CC
 CC EMBL; M83096; ; NOT_ANNOTATED_CDS.
 CC MEROPS; C10.002;
 CC InterPro; IPR000200; Peptidase_C10.
 CC InterPro; IPR001230; Prenyl_site.
 CC Pfam; PF01640; Peptidase_C10; 1.
 CC PRINTS; PR00797; STREPTOPAIN.
 CC HYDROLASE; Thiol protease; Signal; Hemagglutinin.
 CC SIGNAL 1 27 POTENTIAL.
 CC PROPEP 28 ? POTENTIAL.
 CC CHAIN ? 868 THIOLE PROTEASE/HEMAGGLUTININ PRPT.
 CC ACT_SITE 184 184 BY SIMILARITY.
 CC ACT_SITE 327 327 BY SIMILARITY.
 CC SEQUENCE 868 AA; 96444 MW; 45436EP32779323 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 868;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGVWDPID 11
 DB 736 GGVWDPID 742

RESULT 13
 EFP_DEIRA STANDARD; PRT; 185 AA.
 AC Q9RY32;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Elongation factor P (EFP-P).
 GN EFP OR DR0119.
 OS Deinococcus radiodurans.
 CC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 CC Deinococcaceae; Deinococcus.
 CC NCBI_TaxID=1299;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=RL;
 CC MEDLINE=20036896; PubMed=10567266;
 CC White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 CC Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 CC Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 CC Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 CC Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 CC Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 CC Fraser C.M.;
 CC "Genome sequence of the radioresistant bacterium Deinococcus
 CC radiodurans R1.";
 CC Science 286:1571-1577(1999).
 CC -!- FUNCTION: Involved in peptide bond synthesis. Stimulates efficient
 CC translation and peptide-bond synthesis on native or reconstituted
 CC 70S ribosomes in vitro. Probably functions indirectly by altering
 CC the affinity of the ribosome for aminoacyl-tRNA, thus increasing
 CC their reactivity as acceptors for peptidyl transferase (By
 CC similarity).
 CC -!- PATHWAY: Protein biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.

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 CC
 CC EMBL; AE001874; RAF09709.1; -
 CC TIGR; DR01119; -
 CC InterPro; IPR001059; EF-P.
 CC Pfam; PF01132; EFP; 1.
 CC TIGRFAMs; TIGR00038; efp; 1.
 CC PROSITE; PS01275; EFP; 1.
 CC Protein biosynthesis; Elongation factor; Complete proteome.
 CC SEQUENCE 185 AA; 20475 MW; 893FD0850AC102D3 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 185;
 Best Local Similarity 55.6%; Pred. No. 38;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGVWDPID 12
 DB 17 GGVWDPID 25

RESULT 14
 YM56_YEAST STANDARD; PRT; 256 AA.
 AC Q03691;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Hypothetical 28.9 kDa protein in CLN1-RAD14 intergenic region.
 GN YMR200W OR YMR325.01.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CC [1]
 CC SEQUENCE OF 39-256 FROM N.A.

QY 4 GGVWDPID 12
 DB 17 GGVWDPID 25

RESULT 15
 COX3_PYLII STANDARD; PRT; 272 AA.
 ID COX3_PYLII
 AC Q37600;

Query Match 50.0%; Score 38; DB 1; Length 256;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGGVWDPID 11
 DB 44 TCGGVWDPID 53

RESULT 15
 COX3_PYLII STANDARD; PRT; 272 AA.
 ID COX3_PYLII
 AC Q37600;

Query Match 50.0%; Score 38; DB 1; Length 256;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGGVWDPID 11
 DB 44 TCGGVWDPID 53

RESULT 15
 COX3_PYLII STANDARD; PRT; 272 AA.
 ID COX3_PYLII
 AC Q37600;

Query Match 50.0%; Score 38; DB 1; Length 256;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGGVWDPID 11
 DB 44 TCGGVWDPID 53

RESULT 15
 COX3_PYLII STANDARD; PRT; 272 AA.
 ID COX3_PYLII
 AC Q37600;

Query Match 50.0%; Score 38; DB 1; Length 256;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGGVWDPID 11
 DB 44 TCGGVWDPID 53

RESULT 15
 COX3_PYLII STANDARD; PRT; 272 AA.
 ID COX3_PYLII
 AC Q37600;

```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COX3.
OS Pylaiella littoralis.
OG Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pylaiella.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RA Fontaine J.-M., Rousvoal S., Delaroque N., Loiseaux-De Goer S.;
RT "Characterisation of the cox3, nad7 and atp6 genes from the
RT mitochondrial genome of the brown alga Pylaiella littoralis.";
RL Plant Physiol. Biochem. 33:605-609(1995).
CC -!- FUNCTION: Subunits I, II and III form the functional core of
CC the enzyme complex.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z37967; CAA86022.1; -.
DR InterPro; IPR000298; CytC_oxdse_III.
DR Pfam; PF0510; COX3; 1.
DR ProDom; PD000382; CytC_oxdse_III; 1.
DR PROSITE; PS0253; COX3; 1.
KW Oxidoreductase; Mitochondrion; Transmembrane.
SQ SEQUENCE 272 AA; 30628 MW; B9EFF7803A08E8DD CRC64;

Query Match 50.0%; Score 38; DB 1; Length 272;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGWDPID 11
Db 120 GGWPPPTD 127

Search completed: March 13, 2003, 15:15:16
Job time : 2.2 secs

```

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:11:14 ; Search time 4.33846 Seconds
(without alignments)
569.918 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_l10
Perfect score: 76
Sequence: 1 HTGGVWDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	60.5	171	13 Q98U44	Q98U44 mantidactyl
2	46	60.5	177	13 Q98U43	Q98U43 aglyptodact
3	46	60.5	177	13 Q98U41	Q98U41 boophis tep
4	46	60.5	177	13 Q98U33	Q98U33 nyctibatrac
5	46	60.5	177	13 Q98U32	Q98U32 nyctibatrac
6	46	60.5	177	13 Q98U26	Q98U26 micrixalus
7	46	60.5	177	13 Q98U25	Q98U25 micrixalus
8	46	60.5	177	13 Q98U24	Q98U24 indirana sp
9	46	60.5	177	13 Q98U20	Q98U20 philautus m
10	46	60.5	177	13 Q98U19	Q98U19 philautus w
11	45	59.2	131	4 Q8WYX0	Q8WYX0 homo sapien
12	45	59.2	177	13 Q98U42	Q98U42 boophis xer
13	45	59.2	177	13 Q98U21	Q98U21 rhacophorus
14	45	59.2	381	16 Q97GS7	Q97GS7 clostridium
15	44	57.9	489	2 P72455	P72455 streptomyce
16	43.5	57.2	762	2 Q9RM63	Q9RM63 myroides od

17	43	56.6	51	2	Q9F2F8	Q9F2F8 streptococc
18	43	56.6	71	12	Q85298	Q85298 orf virus.
19	43	56.6	102	2	Q9LCA9	Q9LCA9 rhodocyclus
20	43	56.6	304	16	Q9HTS0	Q9HTS0 pseudomonas
21	43	56.6	435	16	Q9A8P0	Q9A8P0 caulobacter
22	43	56.6	762	2	Q9RQ15	Q9RQ15 neisseria d
23	42.5	55.9	597	17	Q9V038	Q9V038 pyrococcus
24	42.5	55.9	597	17	Q8U2G5	Q8U2G5 pyrococcus
25	42.5	55.9	598	17	O58774	O58774 pyrococcus
26	42	55.3	174	13	Q98U45	Q98U45 mantella ma
27	42	55.3	458	10	Q8RU64	Q8RU64 oryza sativ
28	42	55.3	502	16	Q8Y012	Q8Y012 raietonia s
29	41	53.9	42	16	Q9ETQ9	Q9ETQ9 streptococc
30	41	53.9	324	10	Q9LVW5	Q9LVW5 arabidopsis
31	41	53.9	801	16	Q8XV55	Q8XV55 raietonia s
32	41	53.9	1456	2	Q9F636	Q9F636 stigmatella
33	40.5	53.3	181	10	Q9C5D5	Q9C5D5 arabidopsis
34	40.5	53.3	388	10	Q9M8R4	Q9M8R4 arabidopsis
35	40	52.6	114	10	Q9SVK9	Q9SVK9 arabidopsis
36	40	52.6	158	16	Q9Z9C1	Q9Z9C1 chlamydia p
37	40	52.6	176	13	Q98U40	Q98U40 laliostoma
38	40	52.6	177	13	Q98U31	Q98U31 limonectes
39	40	52.6	177	13	Q98U23	Q98U23 indirana sp
40	40	52.6	177	13	Q98U18	Q98U18 philautus c
41	40	52.6	193	16	Q9PDE3	Q9PDE3 xylella fas
42	40	52.6	197	2	Q8VNU8	Q8VNU8 chromatium m
43	40	52.6	259	16	Q9ZQ67	Q9ZQ67 rhizobium m
44	40	52.6	291	16	O84633	O84633 chlamydia t
45	40	52.6	300	16	O34430	O34430 bacillus su

ALIGNMENTS

RESULT 1

ID	Q98U44	PRELIMINARY;	PRT;	171 AA.
AC	Q98U44:			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Tyrosinase (Fragment).			
OS	Mantidactylus cf. ulcerosus.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;			
OC	Mantidactylus.			
OX	NCBI_TaxID=129014;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bossuyt F.; Milinkovitch M.C.;			
RT	"Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs			
RT	Reveal Co-variation between Larval and Adult Traits.";			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF249165; AAG49808.1; -			
DR	InterPro; IPR000561; EGF-like.			
DR	InterPro; IPR002049; Laminin_EGF.			
DR	InterPro; IPR002227; Tyrosinase.			
DR	Pfam; PF00264; tyrosinase; 1.			
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.			
DR	PROSITE; PS00497; TYROSINASE_1; 1.			
FT	NON_TER	1		
FT	NON_TER	171		
SQ	SEQUENCE	171 AA; 19816 MW; 50CEFA8130D2A7B CRC64;		

Query Match 60.5%; Score 46; DB 13; Length 171;
Best Local Similarity 70.0%; Pred. No. 9.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
|||||
Db 133 GGGVWENIDF 142

```
RESULT 2
Q98043 ID Q98043 PRELIMINARY; PRT; 177 AA.
AC Q98043;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tyrosinase (Fragment).
OS Aglyptodactylus madagascariensis (Madagascar jumping frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Aglyptodactylus
OX NCBI_TaxID=68424;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249166; AAG49809.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20410 MW; A4E5A34F90563FF1 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGWENIDF 142
||||: ||:

RESULT 3
Q98041 ID Q98041 PRELIMINARY; PRT; 177 AA.
AC Q98041;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Boophis tephraeomystax.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=68440;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249168; AAG49811.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20542 MW; 22C28DBB1217467B CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
```

```
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGWENIDF 142
||||: ||:

RESULT 4
Q98033 ID Q98033 PRELIMINARY; PRT; 177 AA.
AC Q98033;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus major.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129023;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249176; AAG49819.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20589 MW; 1B647613316D7C42 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGWENIDF 142
||||: ||:

RESULT 5
Q98032 ID Q98032 PRELIMINARY; PRT; 177 AA.
AC Q98032;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus aliciae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129021;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249177; AAG49820.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
```

DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20556 MW; 2C67161CDF6FB392 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142
 |||||: ||:

RESULT 6
 ID Q98U26 PRELIMINARY; PRT; 177 AA.

AC Q98U26;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus fuscus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OC NCBI_TaxID=129016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF249183; AAG49828.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20560 MW; A76738DA4102C9CE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142
 |||||: ||:

RESULT 7
 ID Q98U25 PRELIMINARY; PRT; 177 AA.

AC Q98U25;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus kottigeharensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OC NCBI_TaxID=130786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs

RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF249184; AAG49827.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20574 MW; 05A658678D3BF9D4 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142
 |||||: ||:

RESULT 8
 ID Q98U24 PRELIMINARY; PRT; 177 AA.

AC Q98U24;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Indirana sp. 1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Indirana.
 OC NCBI_TaxID=147865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF249185; AAG49828.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 177
 SQ SEQUENCE 177 AA; 20434 MW; 29EB35222BA6D60B CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142
 |||||: ||:

RESULT 9
 ID Q98U20 PRELIMINARY; PRT; 177 AA.

AC Q98U20;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Philautus microtypanum.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=129024;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249189; AAG49832.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20464 MW; 4E2C1654EA212ADE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 10
Q98U19 PRELIMINARY; PRT; 177 AA.
AC Q98U19;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Philautus wynaadensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=130794;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249190; AAG49833.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20516 MW; 51214062A983B9DE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 11
Q8WYU PRELIMINARY; PRT; 177 AA.
```

```
ID Q8WYU PRELIMINARY; PRT; 131 AA.
AC Q8WYU;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
DR Hypothetical protein.
RW K
SQ SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 59.2%; Score 45; DB 4; Length 131;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGVWDP 9
Db 40 TGGGVWQP 47
|||||: |

RESULT 12
Q98U42 PRELIMINARY; PRT; 177 AA.
AC Q98U42;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Boophis xerophilus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=128996;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249167; AAG49810.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20587 MW; DB6493AF16D0F020 CRC64;

Query Match 59.2%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 13
Q98U21 PRELIMINARY; PRT; 177 AA.
ID Q98U21
```



```

AC Q98U21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Rhacophorus malabaricus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Rhacophorus.
OX NCBI_TaxID=129031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF249188; AAG49831.1; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR002227; Tyrosinase.
DR Pfam: PF00264; tyrosinase; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE: PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20426 MW; 16A9E9F4F1BE2035 CRC64;

Query Match 59.2%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
|||||:|:
DB 133 GGGVWVDF 142

RESULT 14
Q97GS7
ID Q97GS7 PRELIMINARY; PRT; 381 AA.
AC Q97GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Acyl-protein synthetase, luxE.
GN CAC2288.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007729; AAK80245.1; -.
KW Complete proteome.
SQ SEQUENCE 381 AA; 43104 MW; 68D07900AC06AA70 CRC64;

Query Match 59.2%; Score 45; DB 16; Length 381;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVWD 8
|||||
DB 223 HTGGGVWD 230

```

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RESULT 15
P72455
ID P72455 PRELIMINARY; PRT; 489 AA.
AC P72455;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH:N-amidino-scylo-inosamine oxidoreductase.
GN STSB.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=97385085; PubMed=9238101;
RA Ahlert J., Distler J., Mansouri K., Piepersberg W.;
RT "Identification of stsc, the gene encoding the L-glutamine:scyllo-
RT inosose aminotransferase from streptomycin-producing Streptomycetes.";
RL Arch. Microbiol. 168:102-113(1997).
DR EMBL: Y08763; CA70011.1; -.
DR InterPro: IPR000205; NAD_binding.
SQ SEQUENCE 489 AA; 51576 MW; 73B6863C3FAA3C93 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 489;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDP 9
|||||
DB 166 SGGGLWDP 173

Search completed: March 13, 2003, 15:17:01
Job time : 5.33846 secs

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 20.076 Seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-24
Perfect score: 1146
Sequence: 1 EIVLQPSLSLPTPEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
A_Geneseq_101002.*			
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4:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*		
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6:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*		
7:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*		
8:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*		
9:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*		
10:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*		
11:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*		
12:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*		
13:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*		
14:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*		
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23:	/SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1146	100.0	220	AAE12714	Human recombinant
2	1073.5	93.7	239	AA82615	Human PTHrP monocl
3	1069.5	93.3	239	AA82616	Human PTHrP monocl
4	1065.5	93.0	239	AA82617	Human PTHrP monocl
5	1058.5	92.4	239	AA82611	Human PTHrP monocl
6	1053.5	91.9	239	AA82610	Human PTHrP monocl
7	1048.5	91.5	239	AA82614	Human PTHrP monocl
8	1034.5	90.3	239	AA82612	Human PTHrP monocl
9	1034.5	90.3	239	AA82613	Human PTHrP monocl
10	1031.5	90.0	239	AA82619	Human PTHrP monocl

11	1021.5	89.1	239	21	AA82618	Human PTHrP monocl
12	1015.5	88.6	238	22	AA82617	Humanised 323/A3 (
13	1015.5	88.6	238	22	AA82616	Humanised 323/A3 (
14	1015.5	88.6	238	22	AA82615	Humanised 323/A3 (
15	1015.5	88.6	238	22	AA82614	Humanised 323/A3 (
16	992.5	86.6	239	18	AAW01819	Primate anti-hu
17	992.5	86.6	239	19	AAW18786	Anti-human Fas hum
18	992.5	86.6	239	19	AAW18787	Anti-human Fas hum
19	992.5	86.6	239	19	AAW63762	Macaque primatized
20	992.5	86.6	239	21	AA812913	Anti-human Fas imm
21	992.5	86.6	239	21	AA812915	Anti-human Fas imm
22	992.5	86.6	239	23	AA811540	Protein sequence o
23	988.5	86.3	239	19	AAW18777	Anti-human Fas hum
24	988.5	86.3	239	19	AAW18779	Anti-human Fas hum
25	988.5	86.3	239	21	AA812914	Anti-human Fas imm
26	988.5	86.3	239	21	AA812916	Anti-human Fas imm
27	987.5	86.2	238	22	AAU07744	Humanised monoclon
28	987	86.1	238	17	AA893554	Monoclonal antibod
29	986.5	86.1	238	18	AAW14942	3P4 Human IgG4 exp
30	986.5	86.1	238	18	AAW14937	Murine anti-porcine
31	978.5	85.4	238	22	AAE03754	Chimeric 2403 IgG
32	974.5	85.0	239	21	AAU77288	Protein #1 in inve
33	971	84.7	228	23	AAE20274	Human lung specifi
34	963.5	84.1	241	21	AA896303	Human IGFAM-15 imm
35	952.5	83.1	242	16	AA86323	Chimeric 6G4.2.5 l
36	952.5	83.1	242	18	AAW42323	Murine variable re
37	952.5	83.1	242	18	AAW31580	Chimeric anti IL-8
38	952.5	83.1	242	18	AAW23790	Chimeric monoclon
39	952.5	83.1	242	19	AAW69311	Anti-IL-8 mouse-hu
40	952.5	83.1	242	19	AAW40126	Chimeric Mab 6G4.2
41	952.5	83.1	242	19	AAW3745	Chimeric anti IL-8
42	952.5	83.1	242	20	AAW29442	Chimeric 6G4.2.5 l
43	952.5	83.1	242	21	AA830305	Murine 6G4-2.5 ant
44	952.5	83.1	242	21	AAW77748	Chimeric 6G4.2.5 a
45	929	81.1	218	22	AAE03756	Chimeric antibody

ALIGNMENTS

RESULT 1	
AAE12714	AAE12714 standard; Protein; 220 AA.
ID	AAE12714 standard; Protein; 220 AA.
XX	AAE12714;
AC	AAE12714;
XX	04-JAN-2002 (first entry)
DT	04-JAN-2002 (first entry)
XX	Human recombinant immunoglobulin (Ig) light chain region.
DE	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX	light chain region; cancer; breast; ovary; lung; bladder;
KW	cytostatic; therapy; immunoglobulin; Ig.
KW	
XX	Homo sapiens.
OS	
XX	WO200175110-A2.
FN	
XX	11-OCT-2001.
PD	
XX	30-MAR-2001; 2001WO-US10589.
PF	
XX	30-MAR-2000; 2000US-0538913.
PR	
XX	(DYAX-) DYAX CORP.
FA	
XX	Hoogenboom HRJM, Henderikx MPG;
PI	
XX	WPI: 2001-626437/72.
DR	
XX	N-PSDB; AAD20744.
DR	
XX	Novel isolated tumor-associated antigen mucin-1-specific binding member
PT	for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT	

its portion for binding to an epitope of the protein core of mucin-1 -

Claim 12; Page 103; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1 (MUC-1)-specific binding member comprising an antigen binding domain region having an antibody variable light (VL) or heavy (VH) region, or a complementarity determining region (CDR) of VL or VH. MUC1-specific binding member is useful for diagnosing cancer, preferably adenocarcinoma. The binding of MUC1-specific binding member to MUC1 is detected by a detection method selected from enzyme-linked immunosorbent assay, magnetic resonance imaging, scintillation counting, and x-ray film.

MUC1-specific binding member is useful for treating cancer, preferably adenocarcinoma, in an individual, where the cancer is present in tissue of the breast, ovary, lung, or bladder of the individual. MUC1-specific binding member is useful for diagnosing and imaging MUC1-expressing cancer cells and tissues, for purifying or isolating non-glycosylated, underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-containing molecules, and for therapeutically or prophylactically treating cancer. The present sequence is human recombinant immunoglobulin (Ig) light chain region (variable VL and CL constant kappa light chain).

Sequence 220 AA;

Query Match 100.0%; Score 1146; DB 22; Length 220;

Best Local Similarity 100.0%; Pred. No. 3e-70;

Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

DB 1 EIVLTQSPVLPVTPGPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSVSGTDFTLIRISVEAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 120

DB 61 SGVPDRFSGSVSGTDFTLIRISVEAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 120

QY 121 VFIFPPSDEQLKSGTASVYVCLLNNEFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180

DB 121 VFIFPPSDEQLKSGTASVYVCLLNNEFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180

QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

DB 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 2

AA82615

ID AAY82615 standard; Protein; 239 AA.

XX AAY82615;

XX 02-AUG-2000 (first entry)

XX Human pTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.

XX Human; parathyroid hormone related protein; pTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 155

XX /note= "possible Ala"

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

17-JUN-1998; 98JP-0188196.

26-JUN-1998; 98JP-0196729.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX N-PSDB; AAA13925.

XX A human monoclonal antibody to parathyroid hormone related protein. -

XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, and pain

XX Claim 31; Page 45-46; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to parathyroid hormone related protein (pTHrP). The monoclonal antibody or its fragments, following the stimulation of pTHrP has the following properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and hypophosphataemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human pTHrP monoclonal antibody clone protein sequence from the present invention.

Query Match 93.7%; Score 1073.5; DB 21; Length 239;

Best Local Similarity 94.1%; Pred. No. 2.7e-65;

Matches 207; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLPVTPGPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

DB 21 DIVMTQSPVLPVTPGPASISCRSSQSLHNSGNVLDWYLQKPGQSPQLLIYLSGNRA 80

QY 61 SGVPDRFSGSVSGTDFTLIRISVEAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 120

DB 81 SGVPDRFSGSVSGTDFTLIRISVEAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 139

QY 121 VFIFPPSDEQLKSGTASVYVCLLNNEFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180

DB 140 VFIFPPSDEQLKSGTASVYVCLLNNEFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 199

QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

DB 200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3

AA82616

ID AAY82616 standard; Protein; 239 AA.

XX AAY82616;

XX 02-AUG-2000 (first entry)

XX Human pTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.

XX Human; parathyroid hormone related protein; pTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 5

XX /label= Val, Ala, Asp, Gly

XX Misc-difference 13

```
FT FT      /note= "possibly Leu"
FT Misc-difference 25
FT /label= Ile, Thr, Asn, Ser
FT Misc-difference 27
FT /label= Phe, Ser, Tyr, Cys
FT Misc-difference 216
FT /note= "possible Val"
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISR ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13926.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 48-49; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingivitis, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 93.3%; Score 1069.5; DB 21; Length 239;
XX Best Local Similarity 93.6%; Pred. No. 4.9e-65;
XX Matches 206; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
XX
XX QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPQLLIYSGSHRA 60
XX DB 21 DIVMXQXPLSLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPQLLIYLSNRA 80
XX
XX QY 61 SGVPRFSGSGVSGTDFTLRISVEAEADVGVYCMQGLQSPFTFGTKVDIKRGTVAAPS 120
XX DB 81 SGVPRFSGSGSGTDFTLRISVEAEADVGVYCMQALQTPFTFGTKVDIKR-TVAAPS 139
XX
XX QY 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
XX DB 140 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 199
XX
XX QY 181 LSSTLTLSKADYEKKHKVACEVTHOGLSSPVTKSFNRGEC 220
XX DB 200 LSSTLTLSKADYEKKHKVACEVTHOGLSSPVTKSFNRGEC 239
XX
XX RESULT 4
XX ID AAY82617
XX AC AAY82617;
XX DT 02-AUG-2000 (first entry)
XX
```

```
DE XX      Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
KW KW      Human: parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingivitis;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 3 /label= Phe, Leu, Ile, Val
XX FT Misc-difference 4 /label= Leu, Pro, His, Arg
XX FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
XX FT Misc-difference 117 /label= Leu, Ile, Val
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISR ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13927.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 51-52; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingivitis, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 93.0%; Score 1065.5; DB 21; Length 239;
XX Best Local Similarity 93.6%; Pred. No. 9.2e-65;
XX Matches 206; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
XX
XX QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPQLLIYSGSHRA 60
XX DB 21 DIVMTQXPLSLPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGSPQLLIYLSNRA 80
XX
XX QY 61 SGVPRFSGSGVSGTDFTLRISVEAEADVGVYCMQGLQSPFTFGTKVDIKRGTVAAPS 120
XX DB 81 SGVPRFSGSGSGTDFTLRISVEAEADVGVYCMQAXQTPFTFGTKVDIKR-TVAAPS 139
XX
XX QY 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
XX DB 140 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 199
XX
XX QY 181 LSSTLTLSKADYEKKHKVACEVTHOGLSSPVTKSFNRGEC 220
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|||||
Db 200 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
AAY82611
ID AAY82611 standard; Protein; 239 AA.
XX
AC AAY82611;
DT
XX 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
PN JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX WPI: 2000-286723/25.
XX
XX N-PSDB; AAA13921.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Claim 31; Page 34-35; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 92.4%; Score 1058.5; DB 21; Length 239;
XX Best Local Similarity 92.7%; Pred. No. 2,7e-64;
XX Matches 204; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIVLTQSPSLPVTGPEPASTICRSSQSLHNSGYTYLDWYLRKPGSQPOLLYSGSHRA 60
Db 21 DIVMTQSPSLPVTGPEPATISCRSSQSLHNRNNTLDWFLQKPGSQPOLLYLGSNRA 80

Qy 61 SGVPRFSGSVGDTFTLRISRVRAEDGVVYCMQGLQSPETFGTGKVDIKRGTVAAPS 120
Db 81 SGVPRFSGSGGDTFTLKLRSRVAEDVGLYCMQALQIPFTFGTKVDIKR-TVAAPS 139

Qy 121 VFIFPPSDEQLKSGTASVVVCLNLFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180
Db 140 VFIFPPSDEQLKSGTASVVVCLNLFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 199
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|||||
Qy 181 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSLTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6
AAY82610
ID AAY82610 standard; Protein; 239 AA.
XX
AC AAY82610;
DT
XX 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 156
FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 164
FT Misc-difference 164 /label= Phe, Leu
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX WPI: 2000-286723/25.
XX
XX N-PSDB; AAA13920.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Claim 31; Page 33; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 91.9%; Score 1053.5; DB 21; Length 239;
XX Best Local Similarity 92.7%; Pred. No. 6e-64;
XX Matches 204; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 EIVLTQSPSLPVTGPEPASICRSSQSLHNSGYTYLDWYLRKPGSQPOLLYSGSHRA 60
```

Db	21	DIWVQAPLSUPTVGPASISCRFSQSLHSGNNYLDWLQKPGSQPFLIYLGSNRA	80
QY	61	SGVPDRFSGSVSGTDFTLRISRVEAEDGVYCYMOGLQSPFTFGPTGKVDIKRGTTVAAPS	120
Db	81	SGVPDRFSGSVSGTDFTLKISRVEAEDGVYCYMOALQTPFTFGPTGKVDIKR-TVAAPS	139
QY	121	VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180
Db	140	VFIFPPDEQLKSGTAVVVCLLNNXYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	199
QY	181	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	200	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	239
RESULT 7			
AY82614			
ID	AA82614	standard; Protein; 239 AA.	
AC	AA82614;		
DT	02-AUG-2000	(first entry)	
DE	Human PTHR protein monoclonal antibody clone 2F8-10-3	protein SEQ ID NO:12.	
KW	Human; parathyroid hormone related protein; PTHR; monoclonal antibody		
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;		
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;		
KW	sepsis; systemic inflammatory response syndrome; SIRS;		
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Misc-difference 25	/label= Ile, Thr, Asn, Ser	
FT	Misc-difference 27	/label= Phe, Ser, Tyr, Cys	
FT	Misc-difference 117	/label= Leu, Ile, Val	
FT	Misc-difference 146	/label= Phe, Ser, Tyr, Cys	
FT	Misc-difference 216	/note= "possible Val"	
PN	JP2000080100-A.		
PD	21-MAR-2000.		
PF	12-OCT-1998; 98JP-0304793.		
PR	17-JUN-1998; 98JP-0188198.		
PR	26-JUN-1998; 98JP-0196729.		
PA	(NISR) JAPAN TOBACCO INC.		
DR	WPI; 2000-286723/25.		
DR	N-PSDB; AAA13924.		
PT	A human monoclonal antibody to parathyroid hormone related protein.		
PT	useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone		
PT	including metastasis, and pain		
PS	Claim 31; Page 43; 88pp; Japanese.		
CC	The present invention describes a human monoclonal antibody to		
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or		
CC	its fragments, following the stimulation of PTHrP has the following		
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits		
CC	the release of calcium from bone; or (c) inhibits elevation of blood		
CC	calcium content. The monoclonal antibody can be used in the treatment		
CC	of hypercalcaemia, rheumatoid arthritis, cancer of bone including		

Db	140	VFIFPSBQDKSGTASVVCLLNIFYPREAKVQWVDNALQSGNQSVEEDSKDSTYS	199
Qy	181	LSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	200	LSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC	239
RESULT 11			
ID	AY82618	standard; Protein; 239 AA.	
XX	AC	AC	
XX	AY82618;		
DT	02-AUG-2000	(first entry)	
XX			
DE	Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:20.		
XX			
KW	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;		
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;		
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;		
KW	sepsis; systemic inflammatory response syndrome; SIRS;		
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 25	/label= Ile, Thr, Asn, Ser	
FT	Misc-difference 27	/label= Phe, Ser, Tyr, Cys	
FT	Misc-difference 213	/label= Gln, Lys, Glu	
FT	Misc-difference 215	/label= Gln, Lys, Glu	
FT	Misc-difference 219	/label= Cys, Trp	
FT	Misc-difference 220	/label= Val, Ala, Glu, Gly	
FT	Misc-difference 222	/label= Ile, Thr, Asn, Ser	
XX			
PN	JP2000080100-A.		
XX			
PD	21-MAR-2000.		
XX			
PF	12-OCT-1998;	98JP-0304793.	
XX			
PR	17-JUN-1998;	98JP-0188196.	
PR	26-JUN-1998;	98JP-0196729.	
XX			
PA	(NISE) JAPAN TOBACCO INC.		
XX			
WI	WPI; 2000-286723/25.		
DR	N-PSDB; AAA13928.		
XX			
PT	A human monoclonal antibody to parathyroid hormone related protein.		
PT	useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone		
PT	including metastasis, and pain		
XX			
PS	Claim 31; Page 55; 88pp; Japanese.		
XX			
CC	The present invention describes a human monoclonal antibody to		
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or		
CC	its fragments, following the stimulation of PTHrP has the following		
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits		
CC	the release of calcium from bone; or (c) inhibits elevation of blood		
CC	calcium content. The monoclonal antibody can be used in the treatment		
CC	of hypercalcaemia, rheumatoid arthritis, cancer of bone including		
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal		
CC	diseases and gingiva, sepsis, systemic inflammatory response syndrome		
CC	(SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and		
CC	antiinflammatory activities. The present sequence represents a		
CC	human PTHrP monoclonal antibody clone protein sequence from the		

CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the kappa light chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be
 CC used in the combination of the invention.

XX Sequence 238 AA;

Query Match 88.6%; Score 1015.5; DB 22; Length 238;
 Best Local Similarity 90.5%; Pred. No. 2.2e-61;
 Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
 20 DIVMTQSPVLPVTPGEPASISCRSSKNLLHNSGITYLYWYLOKPGQSPQLLIYQMSNLA 79
 Qy 61 SGVPDRFSGVSGTDFTLIRSRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 80 SGVPDRFSSSGSGTDFTLKISRVEAEDVGYVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138
 Qy 121 VFIPPSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 139 VFIPPSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 198
 Qy 181 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 220
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 199 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 14

AAB72233
 ID AAB72233 standard; Protein; 238 AA.

XX AAB72233;

XX 10-MAY-2001 (first entry)

XX Humanised 323/A3 (IgG4cys) antibody kappa light chain amino acid.

XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW light chain.

XX Mus sp.

XX Homo sapiens.

XX WO200107082-A1.

XX 01-FEB-2001.

XX 23-JUL-1999; 99WO-EP05271.

XX 23-JUL-1999; 99WO-EP05271.

XX (GLAX) GLAXO GROUP LTD.

XX Knick VC, Stimmel JB, Thurmond LM;

XX WPI; 2001-182729/18.

XX Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -

XX Example 7; Fig 11; 103pp; English.

XX This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)

CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the kappa light chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG4cys) which can be
 CC used in the combination of the invention.

XX Sequence 238 AA;

Query Match 88.6%; Score 1015.5; DB 22; Length 238;
 Best Local Similarity 90.5%; Pred. No. 2.2e-61;
 Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
 20 DIVMTQSPVLPVTPGEPASISCRSSKNLLHNSGITYLYWYLOKPGQSPQLLIYQMSNLA 79
 Qy 61 SGVPDRFSGVSGTDFTLIRSRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 80 SGVPDRFSSSGSGTDFTLKISRVEAEDVGYVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138
 Qy 121 VFIPPSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 139 VFIPPSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 198
 Qy 181 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 220
 Db |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 199 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 15

AAB72235
 ID AAB72235 standard; Protein; 238 AA.

XX AAB72235;

XX 10-MAY-2001 (first entry)

XX Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.

XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW light chain.

XX Mus sp.

XX Homo sapiens.

XX WO200107082-A1.

XX 01-FEB-2001.

XX 23-JUL-1999; 99WO-EP05271.

XX 23-JUL-1999; 99WO-EP05271.

XX (GLAX) GLAXO GROUP LTD.

XX Knick VC, Stimmel JB, Thurmond LM;

XX WPI; 2001-182729/18.

XX Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -

XX Example 8; Fig 13; 103pp; English.

CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy.
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents the kappa light chain of
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be
CC used in the combination of the invention.

xx	Sequence	238	AA;
sq	Query Match	88.6%	Score 1015.5; DB 22; Length 238;
	Best Local Similarity	90.5%	Pred. No. 2.2e-61;
	Matches 199;	Conservative 8;	Mismatches 12; Indels 1; Gaps 1;
QY	1	EIVLTQSPVLSPLPTGCEPASISCRSSQSLHSHNGYTYLDWYLQKPGQSPQLLIYSGSHRA	60
Db	20	DIWMTQSPVLSPLPTGCEPASISCRSSKLLHSHNGITYLYWYLQKPGSPQLLIYQMSNLA	79
QY	61	SGVPDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS	120
Db	80	SGVPDRFSSSGSGTDFTLKISRVEAEDGVYYCAQNLEIPRTFGGQTKVEIKR-TVAAPS	138
QY	121	VFIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS	180
Db	139	VFIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS	198
QY	181	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	199	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	238

Search completed: March 14, 2003, 11:47:38
Job time : 22.076 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	992.5	86.6	239	3	US-08-487-550-6	Sequence 6, Appl
2	952.5	83.1	242	1	US-08-398-613A-56	Sequence 56, Appl
3	952.5	83.1	242	1	US-08-398-612A-56	Sequence 56, Appl
4	952.5	83.1	242	1	US-08-398-611A-56	Sequence 56, Appl
5	952.5	83.1	242	2	US-08-491-334A-56	Sequence 56, Appl
6	952.5	83.1	242	3	US-09-027-449-42	Sequence 42, Appl
7	952.5	83.1	242	3	US-08-804-444A-42	Sequence 42, Appl
8	952.5	83.1	242	4	US-09-026-985-42	Sequence 42, Appl
9	952.5	83.1	242	4	US-09-121-952A-42	Sequence 42, Appl
10	952.5	83.1	242	4	US-09-234-340A-42	Sequence 42, Appl
11	899	78.0	240	4	US-09-301-593-36	Sequence 36, Appl
12	893.5	78.0	219	3	US-09-027-449-72	Sequence 36, Appl
13	893.5	78.0	219	4	US-09-026-985-72	Sequence 72, Appl
14	893.5	78.0	219	4	US-09-121-952A-72	Sequence 72, Appl
15	893.5	78.0	219	4	US-09-234-340A-72	Sequence 72, Appl
16	893.5	78.0	242	3	US-09-027-449-51	Sequence 51, Appl
17	893.5	78.0	242	3	US-09-027-449-56	Sequence 51, Appl
18	893.5	78.0	242	3	US-09-027-449-62	Sequence 56, Appl
19	893.5	78.0	242	3	US-08-804-444A-51	Sequence 62, Appl
20	893.5	78.0	242	3	US-08-804-444A-56	Sequence 51, Appl
21	893.5	78.0	242	4	US-09-026-985-51	Sequence 56, Appl
22	893.5	78.0	242	4	US-09-026-985-56	Sequence 51, Appl
23	893.5	78.0	242	4	US-09-026-985-62	Sequence 56, Appl
24	893.5	78.0	242	4	US-09-121-952A-51	Sequence 62, Appl
25	893.5	78.0	242	4	US-09-121-952A-56	Sequence 51, Appl
26	893.5	78.0	242	4	US-09-121-952A-62	Sequence 56, Appl
27	893.5	78.0	242	4	US-09-234-340A-51	Sequence 51, Appl

```
QY 61 SGVPDRFSGSGTDFTLRLISRVEAEDGVVYCMQGLSPFTFGPTKVDIKRGTVAAAPS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVPDRFSGSGTDFTLRLISAVEAEDGVYFCGGTPTPTFGGKTVEIKR-TVAAPS 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VFIFPPSDQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 VFIFPPSDQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 199
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 2
US-08-398-613A-56
; Sequence 56, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,613A
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 874P1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1489
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-398-613A-56
Query Match 83.1%; Score 952.5; DB 1; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 DIVMTQTPSLPVSIGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKSNRF 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGTDFTLRLISRVEAEDGVVYCMQGLSPFTFGPTKVDIKRGTVAAAPS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 SGVPDRFSGSGTDFTLRLISRVEAEDGLYFCQSOSTHVPLTFGAGTKLELKR-AVAAPT 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 202
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 3
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-398-612A-56
Query Match 83.1%; Score 952.5; DB 1; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 DIVMTQTPSLPVSIGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKSNRF 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGTDFTLRLISRVEAEDGVVYCMQGLSPFTFGGTVKVDIKRGTVAAAPS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 SGVPDRFSGSGTDFTLRLISRVEAEDGLYFCQSOSTHVPLTFGAGTKLELKR-AVAAPT 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYS 202
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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db 203 LSSTLTSKADYEKHKVACEVTHQGLSSPVTKSFNRGEC 242

RESULT 4

US-08-398-611A-56
 : Sequence 56, Application US/08398611a
 : Patent No. 5702946
 : GENERAL INFORMATION:
 : APPLICANT: Doershuk, Claire M.
 : APPLICANT: Fong, Sherman
 : APPLICANT: Hebert, Caroline Alice
 : APPLICANT: Kim, Kyung Jin
 : APPLICANT: Leong, Steven R.
 : TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
 : OF INFLAMMATORY DISORDERS
 : NUMBER OF SEQUENCES: 58
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/398,611A
 : FILING DATE: 01-Mar-1995
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/205864
 : FILING DATE: 03-MAR-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Love, Richard B.
 : REGISTRATION NUMBER: 34,659
 : REFERENCE/DOCKET NUMBER: P0874P1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/225-5530
 : TELEFAX: 415/952-9881
 : TELEX: 910/371-7168
 : INFORMATION FOR SEQ ID NO: 56:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 242 amino acids
 : TYPE: Amino Acid
 : TOPOLOGY: Linear
 : US-08-398-611A-56

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Query Match      83.1%; Score 952.5; DB 1; Length 242;
Best local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY   1 EIVLTQSPLSPVTPCEPASISCRSSQSLLHSNGTYTLDWYLKPGQSPOLLIIYSGSHRA 60
      :|||:|||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db    24 DIVMTQTPLSPVLGDQAASICRSSQSGLVHGIGNTVLHWYLKPGQSPKLIIYKVSNRF 83

QY   61 SGVPDFRSGSVGTDTLIRSRVEAEDGVYYCMQGLSQSPFTGPGTKVDIKRGITVAAPS 120
      |||||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db    84 SGVPDFRSGSGGTDTTLIRSRVEAEDUGLVFCQSQTHVTPLTGAGTKUELKR-AVAAPT 142

QY   121 VFIFPPSDQLKSGTASVVCLLNPNYPREAKVOMKNVDNALQSGNSQESVTEQDSKDSTYS 180
      |||||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db    143 VFIFPPSSQLKSGTASVVCLLNPNYPREAKVOMKNVDNALQSGNSQESVTEQDSKDSTYS 202

QY   181 LSSTLTLSRADYEKKHKVACEVTHOGLSPVTKSFNRGEC 220
      |||||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db    203 LSSTLTLSRADYEKKHKVACEVTHOGLSPVTKSFNRGEC 242

RESULT 5
US-08-491-334A-56
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```

: Sequence 56, Application US/08491334A
: Patent No. 5874080
: GENERAL INFORMATION:
: APPLICANT: Hebert, Caroline A.
: APPLICANT: Kabakoff, Rhona C.
: APPLICANT: Moore, Mark W.
: TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
: TITLE OF INVENTION: Disorders and Asthma
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/491,334A
: FILING DATE: 27-Jun-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/398611
: FILING DATE: 01-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/205864
: FILING DATE: 03-MAR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0874P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 56:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 242 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-491-334A-56

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[illegible]

RESULT 6

RESOL 6
US-09-037-449-42
; Sequence 42, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/026,985
;; FILING DATE: 20-Feb-1998
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P1085R3-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 42:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 242 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-09-026-985-42

Query Match 83.1%; Score 952.5; DB 4; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||:|||||:|:|||||:|||||:|:|||||:|||||:|||||:|||||:|:|
Db 24 DIVMTQTLPLSVLSGDAQSISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 SGVPRFSGSVSGDTFLRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 84 SGVPRFSGSGGDTFLRISRVEAEDGLGYFCQSQSTHVPITFGAGTKLELKR-AVAAPT 142
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYTS 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 143 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYTS 202
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 181 LSSITLTKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 203 LSSITLTKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 242
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 9
US-09-121-952A-42
; Sequence 42, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 60/075467
;; FILING DATE: 20-FEB-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P1085R4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 42:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 242 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-09-121-952A-42

Query Match 83.1%; Score 952.5; DB 4; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||:|||||:|:|||||:|||||:|:|||||:|||||:|||||:|||||:|:|
Db 24 DIVMTQTLPLSVLSGDAQSISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 SGVPRFSGSVSGDTFLRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 84 SGVPRFSGSGGDTFLRISRVEAEDGLGYFCQSQSTHVPITFGAGTKLELKR-AVAAPT 142
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYTS 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 143 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYTS 202
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 181 LSSITLTKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 203 LSSITLTKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 242
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 10
US-09-234-340A-42
; Sequence 42, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-234-340A-42
Query Match 83.1%; Score 952.5; DB 4; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 24 DIVMTQTPSLPVSLGDSASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSRRF 83
QY 61 SGVPDRFSGSGVSGTDFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 84 SGVPDRFSGSGVSGTDFTLRISRVEAEDGLYFCQSQSTHVLPTFGAGTKLEKRAVAAPT 142
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKSDTYS 180
Db 143 VFIFPPSDEQLKSGTASVVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKSDTYS 202
QY 181 LSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 220
Db 203 LSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 242

RESULT 11
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-301-593-36
Query Match 78.4%; Score 899; DB 4; Length 240;
Best Local Similarity 81.9%; Pred. No. 2e-72;
Matches 181; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSH-NGYTYLDWYLOKPGQSPQLLIYSGSHR 59
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQLLYSRNKNYLAWYQKPGQPKLLIFWASTR 80
QY 60 ASGVDPDRFSGSGVSGTDFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
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Db 81 ESGVPDRFSGSGVSGTDFTLTSSQLAEDVAVYTCQYFSYPLTFGGGTKEIKR-TVAAP 139
QY 120 SVFIFPPSDEQLKSGTASVVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKSDTYS 179
Db 140 SVFIFPPSDEQLKSGTASVVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKSDTYS 199
QY 180 SLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 220
Db 200 SLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 240

RESULT 12
US-09-027-449-72
; Sequence 72, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Presta, Steven R.
; APPLICANT: Leong, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-027-449-72
Query Match 78.0%; Score 893.5; DB 3; Length 219;
Best Local Similarity 79.5%; Pred. No. 5.4e-72;
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIQMTQSPSLASVSGDRVTITCRSSQSLVHGIGATYLDWYLOKPGKAPKLLIYKVSRRF 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGLYFCQSQSTHVLPTFGGTKEIKR-TVAAPS 119
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKSDTYS 180
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RESULT 15
US-09-234-340A-72
; Sequence 72, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa

Db 180 LSSTLTKADYERHKVACEVTHQGLSSPVTKSNRGEC 219

RESULT 14
US-09-121-952A-72
; Sequence 72, Application US/09121952A
; Patent No. 6458355

APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-72
Query Match 78.0%; Score 893.5; DB 4; Length 219;
Best Local Similarity 79.5%; Pred. No. 5.4e-72;
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
QY 1 EIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIQMTQSPFSLASVGRVITTCSSQSLVHGIGATYLVHWYQKPGKAPKLLIYKYSNRF 60
QY 61 SGVPDRFSGVSGPDFTLRLISRVEAEDVGYCYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 61 SGVPSRFSGSGSGDFTLTISLQPEDFATYYCSQSTHVPFLTEFGQGTKEIKR-TVAAPS 119
QY 121 VFIPPPDEQLKSTASVWCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 180
Db 120 VFIPPPDEQLKSTASVWCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 179
QY 181 LSSTLTSLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
Db 180 LSSTLTSLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 219

Search completed: March 14, 2003, 11:50:17
Job time : 7.90114 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 ; Search time 6.69202 Seconds
(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPSLPLVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	1146	100.0	220	US-09-822-698A-24
2	1050.5	91.7	239	US-09-924-340-8
3	1050.5	91.7	239	US-09-992-600A-8
4	992.5	86.6	239	US-10-124-905-6
5	992.5	86.6	239	US-09-948-429B-6
6	971	84.7	228	US-09-909-567B-50
7	952.5	83.1	242	US-09-728-238-42
8	898	78.4	240	US-09-799-514-8
9	893.5	78.0	219	US-09-726-258-72
10	893.5	78.0	239	US-09-249-011A-22
11	893.5	78.0	242	US-09-726-258-51
12	893.5	78.0	242	US-09-726-258-56
13	893.5	78.0	242	US-09-728-238-62
14	889	77.6	220	US-09-995-693-1
15	889	77.6	236	US-09-859-053-34
16	882	77.0	236	US-09-859-053-38
17	879	76.7	218	US-09-925-179-67
18	872	76.1	218	US-09-925-179-9
19	872	76.1	218	US-09-802-077-9

20	872	76.1	218	10	US-09-802-096-9	Sequence 9, Appl
21	872	76.1	218	10	US-09-920-171-13	Sequence 13, Appl
22	869	75.8	239	10	US-09-825-012-9	Sequence 9, Appl
23	865	75.5	218	10	US-09-920-171-15	Sequence 15, Appl
24	865	75.5	218	10	US-09-920-171-17	Sequence 17, Appl
25	865	75.5	218	10	US-09-920-171-19	Sequence 19, Appl
26	865	75.5	218	10	US-09-920-171-24	Sequence 24, Appl
27	865	75.5	220	10	US-09-917-410-5	Sequence 5, Appl
28	863	75.3	218	10	US-09-917-410-2	Sequence 2, Appl
29	854.5	74.6	235	10	US-09-910-059-97	Sequence 97, Appl
30	853	74.4	234	10	US-09-740-002-24	Sequence 24, Appl
31	848.5	74.0	235	10	US-09-910-059-17	Sequence 17, Appl
32	846.5	73.9	235	10	US-09-910-059-52	Sequence 52, Appl
33	846	73.8	212	12	US-10-011-125-5	Sequence 5, Appl
34	843.5	73.6	669	9	US-09-807-721-2	Sequence 2, Appl
35	843	73.6	214	10	US-09-940-166A-2	Sequence 2, Appl
36	843	73.6	214	10	US-09-811-384-11	Sequence 11, Appl
37	843	73.6	237	10	US-09-940-166A-6	Sequence 6, Appl
38	841.5	73.4	213	9	US-09-996-288-231	Sequence 231, App
39	840.5	73.3	235	10	US-09-910-059-99	Sequence 99, Appl
40	839	73.2	237	10	US-09-056-160B-100	Sequence 100, App
41	839	73.2	491	12	US-10-011-125-2	Sequence 2, Appl
42	838	73.1	237	9	US-09-726-258-25	Sequence 25, Appl
43	836.5	73.0	213	9	US-09-996-288-209	Sequence 209, App
44	836.5	73.0	213	9	US-09-996-288-237	Sequence 237, App
45	836.5	73.0	213	9	US-09-996-288-247	Sequence 247, App

ALIGNMENTS

RESULT 1
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24

Query Match	100.0%;	Score 1146;	DB 10;	Length 220;
Best Local Similarity	100.0%;	Pred. No. 3.7e-50;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EIVLTQSPSLPLVTPGEPASISCRSSQLHNSGTYLDWYLRKPGSQPLLIIYSGSHRA	60	
Db	1	EIVLTQSPSLPLVTPGEPASISCRSSQLHNSGTYLDWYLRKPGSQPLLIIYSGSHRA	60	
Qy	61	SGVPDRSGSGVSGDFTLRISRVAEADVGVYCMQGLSPFTFGPGTKVDIKRGTVAAPS	120	
Db	61	SGVPDRSGSGVSGDFTLRISRVAEADVGVYCMQGLSPFTFGPGTKVDIKRGTVAAPS	120	
Qy	121	VFIFPPDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180	
Db	121	VFIFPPDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180	
Qy	181	LSSTLTLSKADYERHKHYACEVTHQGLSSPVTKSFNRGEC	220	
Db	181	LSSTLTLSKADYERHKHYACEVTHQGLSSPVTKSFNRGEC	220	

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RESULT 2
US-09-924-340-8
; Sequence 8, Application US/09924340
; Publication NO. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-924-340-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1  EIVLTQSPLSLPVTGCEPASISCRSSQSLLSHNSGYTYLDWYLOKPGSQSPOLLIIYSGSHRA 60
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 21  DIVMTQSPFLPVTGCEPASISCRSSQSLLSHNSGYTYLDWYLOKPGSQSPOLLIIYLSGNSRA 80
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 61  SGVPDRFSGSGVSGTFTLIRISVEAEDGVVYCYMQLSPFTFGPGTKVDIKRGTTVAAPS 120
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 81  SGVPDRFSGSGSGTFTLIRISVEAEDGVVYCYMQLAQTFTFGPGTRVDIKR-TYVAAPS 139
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 121 VFIFPPSDQLKSGTASVVYCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITYS 180
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 140 VFIFPPSDQLKSGTASVVYCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITYS 199
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 181 LSSTLTLSKADYEKKHVACEVTHQGLSSPVTKSFNRGEC 220
      :||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 200 LSSTLTLSKADYEKKHVACEVTHQGLSSPVTKSFNRGEC 239
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RESULT 3
US-09-992-600A-8
; Sequence 8, Application US/09992600A
; Publication NO. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698

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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-905-6

Query Match 86.6%; Score 992.5; DB 9; Length 239;
Best Local Similarity 87.7%; Pred. No. 1.3e-42;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
QY 61 SGVPDRFSGSVGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 81 SGVPDRFSGSGAGDTFTLKISAVEAEDGVYFCGQGTPTPTFGGKVEIKR-TVAAPS 139
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
QY 181 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
US-09-948-429B-6
Sequence 6, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-6

Query Match 86.6%; Score 992.5; DB 9; Length 239;
Best Local Similarity 87.7%; Pred. No. 1.3e-42;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
QY 61 SGVPDRFSGSVGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 81 SGVPDRFSGSGAGDTFTLKISAVEAEDGVYFCGQGTPTPTFGGKVEIKR-TVAAPS 139
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
QY 181 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6
US-09-909-567B-50
Sequence 50, Application US/09909567B
Publication No. US2003002257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nair, Manoj
APPLICANT: Chen, Seiyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapien
US-09-909-567B-50

Query Match 84.7%; Score 971; DB 9; Length 228;
Best Local Similarity 86.4%; Pred. No. 1.4e-41;
Matches 191; Conservative 14; Mismatches 14; Indels 2; Gaps 2;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 9 EIVMTQTPUSLTITGGEQASMSCRSSQSLHSDGYTYLWFLQKPGQSPQLLIYEVSNRF 68
QY 61 SGV-PDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAP 119
Db 69 SGVSPIRFSGSGGREFTLRISRVEADAGVYVYCMQTQTPTPTFGGKVEIKR-TVAAP 127
QY 120 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 179
Db 128 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 187
QY 180 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 188 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 228

RESULT 7
US-09-726-258-42
Sequence 42, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-726-258-42

Query Match 83.1%; Score 952.5; DB 9; Length 242;
Best Local Similarity 84.1%; Pred. No. 1.2e-40;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 1 EIVLTQSPVLPVTPGPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIYSGSHRA 60
Db 24 DIVMTQTPSLPVSLGLDQASISCRSSQSLVHGIGNTYLVHLYLQKPGQSPKLLIYKYSNRF 83
Qy 61 SGVPDRFSGVSGDFTFLRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 84 SGVPDRFSGVSGDFTFLRISRVEAEADGLYFCQSQSTHVLPLTFGAGTKLELKR-AVAAPT 142
Qy 121 VFIPPPDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 143 VFIPPPSEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 202
Qy 181 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 203 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 8
US-09-799-514-8
Sequence 8, Application US/09799514
Patent No. US20020065220A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An

FILE REFERENCE: PT015P1
CURRENT APPLICATION NUMBER: US/09/799,514
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/US00/23662
PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/152,248
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-514-8
Query Match 78.4%; Score 898; DB 10; Length 240;
Best Local Similarity 80.5%; Pred. No. 5.9e-38;
Matches 178; Conservative 18; Mismatches 23; Indels 2; Gaps 2;
Qy 1 EIVLTQSPVLPVTPGPASISCRSSQSLH-SNGYTYLDWYLQKPGQSPOLLIYSGSHR 59
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSDNKNYLAWYQKPGPPKLLIYWASTR 80
Qy 60 ASGVDPDRFSGVSGDFTFLRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
Db 81 ESGVPDRFSGVSGDFTFLTISLQAEDVAVYVYQQYVSTPYSEFGQGTKLKIKR-TVAAP 139
Qy 120 SVFIPTPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTY 179
Db 140 SVFIPTPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTY 199
Qy 180 SLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 SLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 9
US-09-726-258-72
Sequence 72, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:

Qy	121	VFIFPSDEQLKSGTASVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSIYS	180
Db	143	VFIFPSDEQLKSGTASVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSIYS	202
Qy	181	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	203	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	242

RESULT 12
US-09-726-258-56
; Sequence 56, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS: ;

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (GenesTech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726.258

```

1 CLASSIFICATION:
2
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 09/234,182
5
6 FILING DATE:
7
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 60/094003
10 FILING DATE: 24-JUL-1998
11
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Love, Richard B.
14
15 REGISTRATION NUMBER: 34,659
16 REFERENCE/DOCKET NUMBER: P1085R4-
17
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 650/225-5530
20
21 TELEFAX: 650/952-9881
22
23 INFORMATION FOR SEQ ID NO: 56:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 242 amino acids
27 TYPE: Amino Acid
28
29 TOPOLOGY: Linear
30
31 US-09-726-56

```

	Query Match	78.0%;	Score 893.5;	DB 9;	Length 242;
	Best Local Similarity	79.5%;	Pred. No.	9.3e-38;	
Matches	175; Conservative	14;	Mismatches	30;	Indels 1; Gaps 1;
QY	1	EVLVTQSPLSLPVTGEPASICRSQSLLHNSGYTYLDWYLQKPGSQPLLIIYGSHRA	60		
Dy	24	DIQMTOQPSSLSASVGDRTYTICRSSQLVHGIGATYLEHWYQQKGAKPLLIYKVSNRF	83	:	: :: :
		:: :	:	:: :	:
		:: :	:	:: :	:
QY	61	SGVPDRFSGSVSGDTFTLIRISAEVDGVGYCMOGLSOPSTFFGGTKVDIKRGTVAAPS	120	:	:
Dy	84	SGVPSRFGSGSGGTDFLTILTSLOPEDFATYYCSOSTHVPLTFGGTGKVEIKR--TVAAPS	142	:	:
		:: :	:	:: :	:
		:: :	:	:: :	:
		:: :	:	:: :	:
QY	121	VFIETPPSDRLKSQTAVVVCLNNPYTPREARKVOWKDVALOSGNDSQESVTEODSKDSTYS	180	:	:

Db	143	VFIFFPDSDEQLKSGTASVWCLLNFFYPREAKYQWKVDNALQSGNSQESVTEQDSKOSTYS	202
QY	181	LSSTLTLSKADYEKKHYACEVTHTQGLSSPVTKSFNRGEC	220
Dh	203	TSSSTTTISKADYEKKHYACEVTHTQGLSSPVTKSFNRGEC	242

RESULT 13
US-09-726-258-62
; Sequence 62, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726.258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-726-258-62

Query Match	78.0%;	Score 893.5;	DB 9;	Length 242;
Best Local Similarity	79.5%;	Pred. No. 9.3e-38;		
Matches 175: Conservative	14;	Mismatches 30;	Indels 1;	Gaps 1;

QY	1	EIVLTQSP ^{LS} LPV ^{TP} GP ^{EP} ASIS ^{CS} RSS ^{SS} OS ^{LS} LA ^{HS} NG ^{TY} TL ^{DW} LV ^{LK} PK ^{QS} PO ^{LLI} Y ^{SG} SH ^{RA} 60
DB	24	DIQMTQSP ^{SS} LS ^{AS} VG ^{DR} VT ^{IT} CR ^{SS} OS ^{SL} LV ^{HG} TE ^{TL} L ^{HW} Y ^{QK} PK ^{AK} PL ^{LI} Y ^{KY} SN ^{RF} 83
QY	61	SGV ^{PD} RF ^{SG} SV ^{SD} FT ^{LR} IS ^{RV} EA ^{ED} GV ^{YV} Y ^{QM} GL ^{QS} PF ^{TE} GP ^{TK} VD ^{IK} KG ^{TV} AA ^{PS} 120
DB	84	SGV ^{PS} RF ^{SG} SG ^{SD} FT ^{LT} IS ^{LS} LP ^{ED} FA ^{YV} Y ^{QS} TH ^{VL} TE ^{CG} Q ^{TK} VEI ^{KR} -TV ^{AA} PS 142
QY	121	VFIP ^{PD} DE ^{QL} KG ^{TA} SV ^{VV} CL ^{LN} NF ^Y PR ^{EAK} VO ^{WK} V ^D NA ^{LQ} SN ^{GS} PS ^{EV} TE ^{QD} SK ST YS 180
DB	143	V ^{TI} PP ^{SD} FO ^Y KG ^{CT} SA ^{SV} CI ^L NF ^Y PR ^{EAK} VO ^{WK} V ^D NA ^{LQ} SN ^{GS} PS ^{EV} TE ^{QD} SK ST YS 202

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:54 ; Search time 8.9924 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPPLSLPVTGPGEAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893.5	78.0	215	2 JE0242	Ig kappa chain NIG
2	877.5	76.6	215	2 JE0244	Ig kappa chain NIG
3	869.5	75.9	215	2 JE0243	Ig kappa chain NIG
4	847.5	74.0	215	2 A23746	Ig kappa chain V-I
5	823	71.8	216	2 JE0241	Ig kappa chain Am3
6	785.5	68.5	219	2 S52028	Ig kappa chain - m
7	782.5	68.3	219	2 PC4203	Ig kappa chain (mc)
8	777.5	67.8	217	2 S42772	Ig kappa chain - m
9	777.5	67.8	219	2 S16112	Ig kappa chain V r
10	769.5	67.1	219	2 S38865	Ig kappa chain - m
11	750.5	65.5	225	2 JL0029	Ig kappa chain pre
12	725	63.3	240	2 S06084	Ig kappa chain pre
13	690	60.2	220	2 A31790	Ig kappa chain V r
14	677	59.1	218	2 S68241	Ig kappa chain V r
15	671	58.6	218	2 JC5810	Ig kappa chain V r
16	662	57.8	214	2 S68212	monoclonal antibod
17	651.5	56.8	197	2 S29593	Ig kappa chain (Ma
18	640	55.8	210	2 A56169	Ig kappa chain (WM
19	640	55.8	234	2 S14237	Ig kappa chain V r
20	636	55.5	234	2 S01320	Ig kappa chain pre
21	634.5	55.4	225	2 S37484	Ig kappa chain pre
22	627	54.7	230	2 S33161	Ig kappa chain - m
23	621.5	54.2	235	2 S25058	Ig kappa chain - s
24	611.5	53.4	178	2 PT0219	Ig kappa chain - m
25	587.5	51.3	135	2 S52059	Ig kappa chain V-C
26	549.5	47.9	121	2 S40371	JC-kappa protein -
27	548	47.8	106	1 K3HU	Ig kappa chain - h
28	546.5	47.7	135	2 S40342	Ig kappa chain C r
29	535.5	46.7	136	2 S40357	Ig kappa chain V-J

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 893.5; DB 2; Length 215;

Best Local Similarity 81.4%; Pred. No. 2.4e-56;

Matches 179; Conservative 14; Mismatches 22; Indels 5; Gaps 3;

QY 1 EIVLTQSPPLSLPVTGPGEASISCRSSQLLHNSGTYTLDWYLRKPGQSPQLLIYSGSHRA 60

Db 1 EIVLTQSPGTSLSLSPGERATLSCRASQSV--SN--NYLAWYQQKPGQAPSLIYDASSRA 56

QY 61 SGVPDRFSSVSGTDFTLRISRVEADGVYVCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120

Db 57 TGIPDRFSSGSGTDFILTISGLEPDEFAYVYCCQYDRPPWTFGGTKVEIKR--TVAAPS 115

QY 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 180

Db 116 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 175

QY 181 LSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 176 LSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yanaki, S.; Kazi, H.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 785.5; DB 2; Length 219;
Best Local Similarity 67.7%; Pred. No. 1.7e-48;
Matches 149; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRA 60
Db 1 DVVMTQTPSLPLSVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSPKVIYKVSNR 60
QY 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 119
QY 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDY 179
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTDKDEYRHSNYTCEATHKTSPIVKSFNREC 219

RESULT 7
PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 68.3%; Score 782.5; DB 2; Length 219;
Best Local Similarity 66.8%; Pred. No. 1.7e-48;
Matches 147; Conservative 32; Mismatches 40; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRA 60
Db 1 DVLMTQTPSLPLSVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSPKVIYKVSNR 60
QY 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 119
QY 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDY 179
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTDKDEYRHSNYTCEATHKTSPIVKSFNREC 219

RESULT 8
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 777.5; DB 2; Length 217;
Best Local Similarity 67.9%; Pred. No. 3.9e-48;
Matches 148; Conservative 27; Mismatches 42; Indels 1; Gaps 1;

QY 3 VLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRAS 62
Db 1 VMTQSPSLPLSVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSPKVIYKVSNR 60
QY 63 VPDREFSGSVGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 122
Db 61 VPDREFSGSGGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 119
QY 123 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 182
Db 120 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDY 179
QY 183 SLTTLTSLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 SLTTLTSLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 217

RESULT 9
S16112
Ig kappa chain V region (G2a) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16112
R:Vaesen, M.; Froesch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
A:Reference number: S16112; MUID:92000313; PMID:1910583
A:Accession: S16112
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-219 <BIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 777.5; DB 2; Length 219;
Best Local Similarity 66.8%; Pred. No. 3.9e-48;
Matches 147; Conservative 31; Mismatches 41; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRA 60
Db 1 DVVMTQTPSLPLSVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSPKVIYKVSNR 60
QY 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 119
QY 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDY 179
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTDKDEYRHSNYTCEATHKTSPIVKSFNREC 219

RESULT 10

S38865

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001

C:Accession: S38865

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of an

A:Reference number: S38864

A:Accession: S38865

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <KIP>

A:Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 67.1%; Score 769.5; DB 2; Length 219;

Best Local Similarity 67.3%; Pred. No. 1.4e-47;

Matches 148; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

DQ 1 ELVMTQSPISLSVSLGDAQASISCRSSQSLVHTNGNTLHWYLOKPGQSPQLLIYVSNR 60

QY 61 SGVPDRFSGSVSGTDTLRLSRVEADGVVYCMQGLQSPFTFGCTKVDIKRGTVAAAPS 120

DQ 61 SGVPDRFSGSVSGTDTLRLSRVEADGVVYCMQGLQSPFTFGCTKVDIKRGTVAAAPS 119

QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180

DQ 120 VSIFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 179

QY 181 LSSTLTLSKADYEKKHYKVVACEVTHOGLSSPVTKSFNRGEC 220

DQ 180 MSSTLTLSKADYEKKHYKVVACEVTHOGLSSPVTKSFNRGEC 219

RESULT 11

JL0029

Ig kappa chain precursor (RP93) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000

C:Accession: JL0029

R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.

J. Exp. Med. 167, 954-973, 1988

A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor

A:Reference number: JL0029; MUID:88171315; PMID:3127529

A:Accession: JL0029

A:Molecule type: mRNA

A:Residues: 1-225 <CHI>

A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell

A:Note: the authors translated the codon CCG for residue 106 as Pro, ACC for residue 132

A:Note: the nucleotide sequence shown is inconsistent with authors' translation because

ect except for four positions shown above

C:Comment: The protein is an anti-phosphorylcholine antibody.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:7-225/Product: Ig kappa chain #status predicted <IIC>

F:7-106/Domain: V region #status predicted <VAR>

F:107-119/Domain: J region #status predicted <JIR>

F:120-225/Domain: C region #status predicted <COR>

Query Match 65.5%; Score 750.5; DB 2; Length 225;

Best Local Similarity 64.5%; Pred. No. 3.3e-46;

Matches 142; Conservative 31; Mismatches 46; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

DQ 7 DVLMTQIPSLPVSLGDAQASISCRSSQSLVHTNGNTLHWYLOKPGQSPQLLIYKISNR 66

Best Local Similarity 60.6%; Pred. No. 6e-42;
Matches 134; Conservative 29; Mismatches 56; Indels 2; Gaps 2;

QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGY-TYLDWYLQKPGQSPOLLIIYSGSHR 59
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 1 DIVMTQSPSSLTVTAGIEKHYKRVYACEVTHOGLSSPVTKSFNRGEC 60
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 60 ASGYDPDFSGSVSGTDFTLIRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 61 ESGVPDRFTGSGGSDFTLLISSVQAEDLAVYYCQNDYSNPLTFGGGTKLELRAD-AAP 119
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 120 SVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 179
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 120 TVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDYSL 179
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 180 SLSTLTLSKADYEKKHYKRVYACEVTHOGLSSPVTKSFNRGEC 220
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 180 SMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNREC 220
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

RESULT 14
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takaqi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:g473962; PID:BAA06141.1; PID:g473963
R:Takaqi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'NI', 3-212 <TAW>
A:Cross-references: EMBL:D29670
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 59.1%; Score 677; DB 2; Length 218;
Best Local Similarity 59.5%; Pred. No. 5e-41; Mismatches 55; Indels 2; Gaps 2;

QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYSGSHRA 60
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 1 ELVLTQSPASLAVSLGQRATISCRASKS-VSASGYIYMHYQKPGQPKLLISLATNLE 59
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 60 SGVPARFSGSGGSDFTLLNIHPVEEDVATYYCQHSRELPLTFGAGTKLELRAD-AAPT 118
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 119 VSIFPPSSQELTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDYSL 178
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 181 LSSTLTLSKADYEKKHYKRVYACEVTHOGLSSPVTKSFNRGEC 220
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 179 MSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNREC 218
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

RESULT 15
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamauchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p
F:16-94/Domain: immunoglobulin homology; immunoglobulin homology <IMM>

Query Match 58.6%; Score 671; DB 2; Length 218;
Best Local Similarity 59.8%; Pred. No. 1.3e-40; Mismatches 131; Conservative 30; Mismatches 56; Indels 2; Gaps 2;

QY 2 IVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYSGSHRAS 61
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 2 IVLTQSPASLAVSLGQRATISCRASKS-VSASGYIYMHYQKPGQPKLLISLASNLES 60
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 62 GVPDRFSGSVSGTDFTLIRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPSV 121
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 61 GVPARFSGSGGSDFTLLNIHPVEEDVATYYCQHSRELPLTFGAGTKLELRAD-AAPT 119
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 122 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 181
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 120 SIFPPSSQELTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDYSL 179
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

QY 182 SSTLTLSKADYEKKHYKRVYACEVTHOGLSSPVTKSFNRGEC 220
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |
Db 180 SSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNREC 218
:|||||:| | | | | :||| :||| :| | | | | :||| :| | | | | :||| :| | | | |

Search completed: March 14, 2003, 11:51:08
Job time : 9.9924 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 5.01901 seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSLPLPVTGPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	47.8	106	1	KAC_HUMAN
2	527	46.0	117	1	KV2E_HUMAN
3	500	43.6	113	1	KV2D_HUMAN
4	478.5	41.8	112	1	KV2C_HUMAN
5	467.5	40.8	115	1	KV2A_HUMAN
6	455	39.7	113	1	KV2B_HUMAN
7	444	38.7	133	1	KV2F_HUMAN
8	432	37.7	113	1	KV2E_MOUSE
9	429	37.4	113	1	KV2G_MOUSE
10	423	36.9	113	1	KV2F_MOUSE
11	402	35.1	112	1	KV2D_MOUSE
12	394.5	34.4	108	1	KV1_CANFA
13	394	34.4	113	1	KV2C_MOUSE
14	387	33.8	112	1	KV2A_MOUSE
15	370	32.3	129	1	KV3L_HUMAN
16	369	32.2	129	1	KV3M_HUMAN
17	368.5	32.2	114	1	KV4A_HUMAN
18	367	32.0	106	1	KACB_RAT
19	366.5	32.0	134	1	KV4C_HUMAN
20	366	31.9	109	1	KV3B_HUMAN
21	366	31.9	109	1	KV3D_HUMAN
22	362	31.6	120	1	KV2B_MOUSE
23	359	31.3	106	1	KACA_RAT
24	357	31.2	109	1	KV3E_HUMAN
25	357	31.2	109	1	KV3G_HUMAN
26	354	30.9	133	1	KV4B_HUMAN
27	351	30.6	108	1	KV3A_HUMAN
28	350	30.5	106	1	KAC_MOUSE
29	349.5	30.5	128	1	KV3K_HUMAN
30	343.5	30.0	111	1	KV3M_MOUSE
31	340.5	29.7	111	1	KV3L_MOUSE
32	340	29.7	109	1	KV3F_HUMAN
33	338.5	29.5	111	1	KV3O_MOUSE

34	338.5	29.5	111	1	KV3U_MOUSE	P01673 mus musculu
35	338	29.5	129	1	KV3H_HUMAN	P04207 homo sapien
36	336.5	29.4	111	1	KV3S_MOUSE	P01671 mus musculu
37	335.5	29.3	111	1	KV3N_MOUSE	P01666 mus musculu
38	334.5	29.2	111	1	KV3R_MOUSE	P01670 mus musculu
39	333.5	29.1	111	1	KV3H_MOUSE	P01660 mus musculu
40	332	29.0	110	1	KV3P_MOUSE	P01668 mus musculu
41	331.5	28.9	111	1	KV3Q_MOUSE	P01669 mus musculu
42	326.5	28.5	111	1	KV3J_MOUSE	P01662 mus musculu
43	326.5	28.5	111	1	KV3T_MOUSE	P01672 mus musculu
44	324.5	28.3	111	1	KV3C_MOUSE	P01656 mus musculu
45	324.5	28.3	131	1	KV3I_MOUSE	P01661 mus musculu

ALIGNMENTS

RESULT 1				
ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Fraenkel F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

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RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RX SEQUENCE (BENCE-JONES PROTEIN AG).
RP MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RX SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RP MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1.2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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DR EMBL; V00557; CAA23823.1; -.
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR Genew; HGNC:5716; IGKC.
DR MIM; 147200; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1.2) MARKER).
FT /FTid=VAR_003897.
FT CONFLICT 14 14
FT CONFLICT 57 57
FT CONFLICT E -> Q (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 47.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.9e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPPSDEQLKSGTASVVCLLNNFPRAKQVQKVDNALQSGNSQESVTEQDS 174
D 1 TVAAPSVFIPPSDEQLKSGTASVVCLLNNFPRAKQVQKVDNALQSGNSQESVTEQDS 60
QY 175 KDSTYLSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
D 61 KDSTYLSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

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RN SEQUENCE FROM N.A.
RP MEDLINE=84191506; PubMed=6325927;
RX Klobeck H.G., Solomon A., Zachau H.G.;
RA "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RT Nature 309:73-76(1984).
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CC -----
CC EMBL; Z00009; -. NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
SQ
Query Match 46.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 3.4e-38;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHSGNYVLDWYLOKPGQSPOLLIYSGSHRA 60
D 5 DIVMTQSLPLSPVTPGEPASISCRSSQSLHSGNYVLDWYLOKPGQSPOLLIYSGSRA 64
QY 61 SGVPDRFSGSGVDFTLRISRAEDVGVYCMQGLQSPFTFGPGTKVDIKR 113
D 65 SGVPDRFSGSGVDFTLRISRAEDVGVYCMQGLQSPFTFGPGTKVDIKR 117

RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE (BENCE-JONES PROTEIN TEW).
RP MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
[2]
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RP MEDLINE=73166638; PubMed=4700495;

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RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RL patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR: A01888; K2HUTW.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 43.68; Score 500; DB 1; Length 113;
Best Local Similarity 82.38; Pred. No. 6.4e-36;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSDGFDLWYLYLQKPGQSPZLLIYALSRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSGVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGSGTDFTLKISRVAEDGVVYCMZALQAPITFGGQTRLEIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
KV2C_HUMAN
ID KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.88; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.88; Pred. No. 3.8e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHR 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTGPEPASISCRSSQSLDSDGNTLNWYLYLQKAGQSPOLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVPDRFSGSGVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVPDRFSGSGSGTDFTLKISRVAEDGVVYCMQRLQLEIPYTFGGQTKLEIRR 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN

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FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 41.88; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.88; Pred. No. 4.2e-34;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVLTQSPSLPVTGPEPASISCRSSQSLZSBG-DYLDWYLYLQKPGZSPZLLIYLGSNRA 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSGVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 SGVPDRFSGSGSGTDFTLKISRVAZABGVYVCMQALQPLTFGGGTNVEIKR 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.88; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.88; Pred. No. 3.8e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHR 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTGPEPASISCRSSQSLDSDGNTLNWYLYLQKAGQSPOLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVPDRFSGSGVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVPDRFSGSGSGTDFTLKISRVAEDGVVYCMQRLQLEIPYTFGGQTKLEIRR 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN

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ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms Igm
RL with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
CC PIR; A01886; K2HUPR.
DR HSSP; P01607; 1REL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT CHAIN 1 20
FT SIGNAL 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 38.7%; Score 444; DB 1; Length 133;
Best Local Similarity 75.2%; Pred. No. 4.5e-31;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPLEPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DVVMTQSPLEPVTLGQSPASISCRSSQSLVYSDGNTYLNMFQRPQSPRLIYKVSNRD 80
QY 61 SGVPDRSGSGVSGTDFLTRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
Db 81 SGVPDRSGSGVSGTDFLTRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 133

RESULT 8
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57BL/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -I- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR HSSP; P01607; 1REL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 39.7%; Score 455; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 4.2e-32;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPLEPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DVVMTQSPLEPVTLGQSPASISCRSSQSLVYREGTYLWYLOKPGQSPQLLIYSSYRD 60
QY 61 SGVPDRSGSGVSGTDFLTRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
Db 61 SGVPDRSGSGVSGTDFLTRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113

RESULT 7
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Weindl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human Immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match
Best Local Similarity 37.7%; Score 432; DB 1; Length 113;
Matches 85; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHNSNGTYILDWYLRQPGSQPOLLIYSGSHRA 60
Db 1 DIVMTQTAPSAVLTGTSASISCRSSKSLHNSNGTYILWYLRQPGSQPOLLIYQMSNLA 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVIYCMQGLQSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADVGVIYCAINLELPYTFGGTKLEIKR 113

RESULT 9
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=83178921; PubMed=6404298;
RC STRAIN=A/J;
RA Novotny J., Margolles M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVM526.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 37.4%; Score 429; DB 1; Length 113;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHNSNGTYILDWYLRQPGSQPOLLIYSGSHRA 60
Db 1 DVMTQTAPSAVLSVSGTSASISCRSSQSLHNSNGTYILNWLQKAGQSKLLIYKVSNRF 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVIYCMQGLQSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADLGIYFCQSTHTVPTFGGTKLEIKR 113

RESULT 10
KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
light chains from a mouse hybridoma-derived anti-(streptococcal group
A polysaccharide) antibody containing an additional cysteine residue.
Application of the dimethylaminobenzene isothiocyanate technique
for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match
Best Local Similarity 36.9%; Score 423; DB 1; Length 113;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHNSNGTYILDWYLRQPGSQPOLLIYSGSHRA 60
Db 1 DIVMTQTAPSAVLTGTSASISCRSSKSLHNSNGTYILWYLRQPGSQPOLLIYRMSNLA 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVIYCMQGLQSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADVGVIYCMQREYPTFGGTKLEIKR 113

RESULT 11
KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=83055101; PubMed=7141411;
RA Herbst H., Chang J.-Y., Aebersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
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CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC PIR: A01911; KVM51.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;

Query Match 35.1%; Score 402; DB 1; Length 112;
Best Local Similarity 72.3%; Pred. No. 1.3e-27;
Matches 81; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQAATFNPVTLGTSASFCSKSLQSKGITYLYWYLQKPGQSPQLLIYQMSNLA 60

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 112
DB 61 SGVPDRFSGSGGTDFTLIRISRVEAEDGVVYCANLQELPYTFGGGKLEIK 112

RESULT 12
KV1_CANFA
ID KV1_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunochimistry 15:303-305(1978).
CC -!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC PIR: A01907; K2DGGM.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
```

```
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 34.4%; Score 394.5; DB 1; Length 108;
Best Local Similarity 69.0%; Pred. No. 5.5e-27;
Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQTPLSLSVSPGEPASISCRSSQSNL----DYLNMVYLQKAGOSPRLLPEQDSQRA 55

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 56 SGVPDRFSGSGGTDFTLIRIGRVEAEDAGIYCMQRGSFYPTFGQGRLEVRR 108

RESULT 13
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A01910; KVM551.
DR INTERPRO: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 34.4%; Score 394; DB 1; Length 113;
Best Local Similarity 69.0%; Pred. No. 6.4e-27;
Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVITQDELSPVTSGESVLSICRSSLKLDKGTLYLNMFLQGPQSPRLIYLMSTRA 60

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVSDRFSGSGGTDFTLIRISRVEAEDGVVYCOQLVEYPLTFGAGTKLEIKR 113

RESULT 14
KV2A_MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```


15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region MOPC 167.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE
MEDLINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding myeloma protein.";
Biochemistry 17:2703-2707(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN HAS ALSO BEEN DETERMINED.

PTR; A01908; KVM516.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SK00406; IGV; 1.
KW Immunoglobulin v region.

	DOMAIN	1	23
FT	DOMAIN	24	39
FT	DOMAIN	40	54
FT	DOMAIN	55	61
FT	DOMAIN	62	93
FT	DOMAIN	94	102
FT	DOMAIN	103	112
FT	DISULFID	23	93
FT	NON_TER	112	112
SQ	SEQUENCE	112 AA;	12349 MW; A58EDFD640AB9726 CRC64;

Query Match 33.8%; Score 387; DB 1; Length 112;
Best_Local_Similarity 68.8%; Pred.No. 2.5e-26;
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps

QY 1 EVLTQSPLSLPTPGEPASISCRSSSQSLISSGTYILDWLKPQGSPOLLIVSGSHRA 60
::||| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIVITQDELNSNPVTGSSEVSISCRSSSKLLYKDGTLYNLFWRFGSPQLTSLMSTRA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :: ||| ||| :::
QY 61 SGVPDFRGSGVSGDTFTLRISRVAEDVGVIYCMOGLQSPETFGGPKVDIK 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| :::
Db 61 SGVSDFRGSGGRDFTLEISRKAEDGVIIYCOVLVEYLTFAGATKLELK 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 15
KV3L_HUMAN ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC F18135;
AD 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
ES Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."; J. Exp. Med. 167:840-852(1988).
RL CC -I- DISASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
CC CC PIR; PLO022; K3HUHA.
CC DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:09 ; Search time 16.3118 seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSLPLPVTGPAS.....EVTHQGLSPVTKSENRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	973.5	84.9	239	4	Q8TCD0	Q8tcd0 homo sapien
2	795.5	69.4	238	11	Q99M37	Q99m37 mus musculu
3	782.5	68.3	239	11	Q8VC55	Q8vc55 mus musculu
4	776.5	67.8	238	11	Q8VC16	Q8vc16 mus musculu
5	648	56.5	234	11	Q8VCF0	Q8vcp0 mus musculu
6	635	55.4	214	11	Q91A5	Q91a5 mus musculu
7	624.5	54.5	235	11	Q91W12	Q91w12 mus musculu
8	621	54.2	234	11	Q91WF8	Q91wf8 mus musculu
9	615	53.7	234	11	Q8R062	Q8r062 mus musculu
10	609	53.1	233	11	Q91WS9	Q91ws9 mus musculu
11	590	51.5	234	11	Q8R028	Q8r028 mus musculu
12	437.5	38.2	233	4	Q8TBC9	Q8tbc9 homo sapien
13	433.5	37.8	237	4	Q8WTU6	Q8wtu6 homo sapien
14	431.5	37.7	237	4	Q8WUK4	Q8wuk4 homo sapien
15	428.5	37.4	114	4	Q9UL80	Q9ul80 homo sapien
16	407	35.5	236	4	Q96E61	Q9ee61 homo sapien

17	406	35.4	104	11	Q9JL82	Q9jl82 mus musculu
18	377	32.9	240	4	Q8WUK3	Q8wuk3 homo sapien
19	376.5	32.9	235	11	Q99M11	Q99m11 mus musculu
20	373	32.5	109	4	Q9UL78	Q9ul78 homo sapien
21	369	32.2	109	4	Q9UL86	Q9ul86 homo sapien
22	364.5	31.8	233	4	Q96I69	Q96i69 homo sapien
23	351.5	30.7	108	4	Q9UL83	Q9ul83 homo sapien
24	340.5	29.7	111	11	Q920E9	Q920e9 mus musculu
25	325.5	28.4	107	11	Q9ER29	Q9er29 mus musculu
26	322	28.1	107	4	Q9UL81	Q9ul81 homo sapien
27	322	28.1	109	4	Q9UL85	Q9ul85 homo sapien
28	316.5	27.6	108	4	Q9UL77	Q9ul77 homo sapien
29	316	27.6	116	4	Q96PF6	Q96pf6 homo sapien
30	313	27.3	106	5	Q904I0	Q904i0 schistosoma
31	309.5	27.0	108	4	Q9UL79	Q9ul79 homo sapien
32	308	26.9	107	4	Q96SA9	Q96sa9 homo sapien
33	307.5	26.8	298	11	Q9QXF0	Q9qyf0 mus musculu
34	306.5	26.7	108	4	Q9UL70	Q9ul70 homo sapien
35	299.5	26.1	134	11	Q8VDD0	Q8vdd0 mus musculu
36	295.5	25.8	108	11	Q8VIJ0	Q8vij0 mus musculu
37	293.5	25.6	109	11	Q920E6	Q920e6 mus musculu
38	284.5	24.8	103	11	Q9JL80	Q9jl80 mus musculu
39	283.5	24.7	99	11	Q9JL74	Q9jl74 mus musculu
40	276.5	24.1	101	11	Q9JL78	Q9jl78 mus musculu
41	265.5	23.2	97	11	Q9JL76	Q9jl76 mus musculu
42	255.5	22.3	127	11	Q925S9	Q925s9 mus musculu
43	249.5	21.8	109	6	Q9N0W5	Q9n0w5 oryctolagus
44	240.5	21.0	107	11	Q9JL84	Q9jl84 mus musculu
45	234	20.4	130	11	Q9D8W4	Q9d8w4 mus musculu

ALIGNMENTS

RESULT 1

Q8TCD0	PRELIMINARY;	PRT;	239	AA.
ID	Q8TCD0			
AC	Q8TCD0;			
DT	01-JUN-2002 (TReMBLrel. 21, Created)			
DT	01-JUN-2002 (TReMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	Hypothetical 26.2 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LUNG;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC022362; AAH22362.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;			

Query Match	84.9%	Score 973.5;	DB 4;	Length 239;
Best Local Similarity	85.5%	Pred. No. 1.5e-84;		
Matches	188;	Conservative	18;	Mismatches 13;
Indels	1;	Gaps	1;	
Qy	1	EIVLTQSLPLPVTGPASISCRSSQSLLSNGYTLDWYLRKPGQSPQLLIYSGSHR	60	
Db	21	DVWMTQSPSLPVTLGQSPASISCRSTQSLVSDGNTVLNNFQQRPGQSPRELIYKVNRD	80	
Qy	61	SGVPRDRSGVSGDFTLIRSRVEAEADVGYCYMGQLQSPFTFGPGTKVDIKRGTVAAPS	120	
Db	81	SGVPRDRSGVSGDFTLIRSRVEAEADVGYCYMGQLQSPFTFGPGTKVDIKRGTVAAPS	139	
Qy	121	VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYS	180	
Db	140	VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYS	199	
Qy	181	LSSTLTLSKADYEKHKH YACEVTHQGLSSPVTKSFNRGEC	220	

Db	200	LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC	239
RESULT 2			
Q99M37	Q99M37	PRELIMINARY;	PRT; 238 AA.
AC	Q99M37;		
DT	01-JUN-2001 (Tremblrel. 17, Created)		
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	Hypothetical 26.3 kDa protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Strausberg R.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC002035; AA02035.1; -		
DR	HSSP; P01679; 2FBJ		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR003597; Ig_c1.		
DR	InterPro; IPR003600; Ig_like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 2.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;		
Query Match 69.4%; Score 795.5; DB 11; Length 238;			
Best Local Similarity 67.7%; Pred. No. 1.3e-67;			
Matches 149; Conservative 31; Mismatches 39; Indels 1; Gaps 1;			
Qy	1	EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA	60
Db	20	DVWMTQTPLSLPVSLGDAQSISCRSSQIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRF	79
Qy	61	SGVPDRFSGVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAFS	120
Db	80	SGVPDRFSGSGSDTFTLKISRVEAEDLGVYCFQGSHPVYTFGSGTKLEIKRAD-AAPT	138
Qy	121	VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS	180
Db	139	VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVVKWIDGSEKQNGVLSNWTDDQDSKDS	198
Qy	181	LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC	220
Db	199	MSSTLTLTQDEYERHNSYTCATHKTSPIVKSFNREC	238
Qy	181	LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC	220
Db	199	MSSTLTLTQDEYERHNSYTCATHKTSPIVKSFNREC	238
RESULT 3			
Q8VC55	Q8VC55	PRELIMINARY;	PRT; 239 AA.
AC	Q8VC55;		
DT	01-MAR-2002 (Tremblrel. 20, Created)		
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)		
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)		
DE	Hypothetical 26.3 kDa protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-COLON;		
RA	Strausberg R.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		

RESULT	6
ID	Q9RIA5
AC	PRELIMINARY;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	kappa light chain of Mab7 (fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

```
Query Match      54.5% Score 624.5 DB 11 Length 235;
Best Local Similarity 55.0%; Pred. No. 2.3e-51;
Matches 121 Conservative 33 Mismatches 59 Indels 7 Gaps 2;

QY 1 EIVLTQSPLSPVTGEPASISCRSSSQSLLSNGTYLDWYLKQPQQSPLLIIYSGRHA 60
||||| : ||| ::||| : | | | | | | | | | |
Db 23 QIVLTSQAIMGSGERVTVTTCAGSSSVH-----MHMYQKGSTGPKRVITDYDFKL 76
```



```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020233; AAH20233.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 37.7%; Score 431.5; DB 4; Length 237;
Best Local Similarity 43.2%; Pred. No. 5.3e-33;
Matches 96; Conservative 42; Mismatches 73; Indels 11; Gaps 7;

QY 3 VLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRASG 62
DB 22 VLTQPP-SVSGAPGQGVITISCTGSSNIGA-GYD-VHVIQQLPGTAPKLLIYGNSNRPSG 78
QY 63 VPDFSGSVSGDFTLRISRVEAEDVGYYVYCM--QGLOSPFTFGPGTKVDIKRGTVAAP 119
DB 79 VPDFSGSKSGTFSASIAITGLQAEADYCYQSYDSSLGFWFGGKTLVLGPKAAP 138
QY 120 SVFIPTPSDEQLKSTASVWCLLNFPYREAKVQWKVDNA-LQSGNSQESVTEQDSKDS 178
DB 139 SVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVKAG--VETTTPSKQSNK 196
QY 179 YSLSTLTLSKADYKHKVYACENVTHOGLSSPVTKSFNRGEC 220
DB 197 YAASSYLSLTPEQWKSRSYSCQVTHEG--STVEKTVAPTEC 236

RESULT 15
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSP; F80362; 1WTU.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
```

```
Query Match 37.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 3.7e-33;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 DVVMTQSPVLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQORPGQSPRLIYKVSNRD 60
QY 61 SGVPDRFSGSVSGDFTLRISRVEAEDVGYYVYCMQGLQ-SPTEFGPTKVDIKR 113
DB 61 SGVPDRFSGSGSDFTLKRISRVEAEDVGYYVYCMQGTHTWPPWTFGGTKVEIKR 114
```

Search completed: March 14, 2003, 11:49:36
Job time : 17.3118 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 41.1559 seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-26
Perfect score: 2411
Sequence: 1 QVQLVSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 908470

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	100.0	451	22	AAE12715 Human recombinant
2	2270	94.2	449	21	AAE12715 A rat heavy chain
3	2257	93.6	474	23	AAO14065 Heavy chain protei
4	2236.5	92.8	461	22	AAU07745 Humanised monoclon
5	2229.5	92.5	477	22	AAU14288 Human novel protei
6	2228.5	92.4	475	13	AAE20057 Heavy chain of 3D6
7	2216	91.9	582	22	AAE1987 Ganglioside GD3 sp
8	2211.5	91.7	452	20	AAE1987 Recombinant immuno
9	2211.5	91.7	452	21	AAE1987 Humanised anti-IL-
10	2211.5	91.7	452	21	AAE1987 Humanised anti-IL-

11	2207.5	91.6	459	14	AAE12715 Human anti-HBs hea
12	2202.5	91.4	452	19	AAE12715 Anti-IL-8 humanise
13	2190	90.8	477	15	AAE12715 chiT84.12 H3 heavy
14	2186	90.7	466	13	AAE12715 Sequence encoded b
15	2177	90.3	453	14	AAE12715 Humanised MaE11 ve
16	2177	90.3	453	21	AAE12715 Heavy chain amino
17	2174	90.2	461	14	AAE12715 Anti-HIV-1 recombi
18	2172.5	90.1	444	21	AAE12715 Humanised anti-CD2
19	2171	90.0	582	22	AAE12715 Ganglioside GD3 sp
20	2169	90.0	451	20	AAE12715 Mus musculus anti-
21	2169	90.0	451	20	AAE12715 Mus musculus anti-
22	2169	90.0	451	21	AAE12715 Light chain amino
23	2169	90.0	451	22	AAE12715 Anti-IgE antibody,
24	2169	90.0	451	22	AAE12715 Full length heavy
25	2169	90.0	451	22	AAE12715 Full length heavy
26	2168	89.9	451	20	AAE12715 Human E27 anti-IgE
27	2168	89.9	451	20	AAE12715 Mus musculus anti-
28	2168	89.9	451	21	AAE12715 Amino acid sequenc
29	2168	89.9	451	22	AAE12715 E27 anti-IgE antib
30	2168	89.9	451	22	AAE12715 Full length heavy
31	2165.5	89.8	470	7	AAE12715 Chimeric human-mou
32	2165.5	89.8	470	8	AAE12715 Sequence of novel
33	2160	89.6	478	19	AAE12715 Macaque primatized
34	2160	89.6	478	23	AAE12715 Protein sequence o
35	2154	89.3	478	18	AAE12715 Primatized anti-hu
36	2118	87.8	481	13	AAE12715 Sequence of antibo
37	2116	87.8	449	14	AAE12715 Completely humanis
38	2116	87.8	449	19	AAE12715 Amino acid sequenc
39	2114.5	87.7	519	23	AAE12715 Human secreted pro
40	2113.5	87.7	731	22	AAE12715 Humanised HMFG-1 h
41	2113.5	87.7	741	22	AAE12715 Humanised HMFG-1 h
42	2112.5	87.6	581	22	AAE12715 Ganglioside GD2 sp
43	2109.5	87.5	465	22	AAE12715 Humanised 323/A3 (
44	2109.5	87.5	467	13	AAE12715 Reshaped CD4 antib
45	2109.5	87.5	467	13	AAE12715 Reshaped CD4 antib

ALIGNMENTS

RESULT 1
AAE12715
ID AAE12715 standard; Protein; 451 AA.

XX AAE12715;

AC AC

DT 04-JAN-2002 (first entry)

XX Human recombinant immunoglobulin (Ig) heavy chain region.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;

XX heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; immunoglobulin; Ig.

OS Homo sapiens.

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20745.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

XX for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -
XX Claim 12; Page 106-108; 126pp; English.
PS
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human recombinant immunoglobulin
CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX
SQ Sequence 451 AA;

Query Match 100.0%; Score 2411; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 6.3e-136;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 120
DB 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 120
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180
DB 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180
QY 181 SGLYSLSVTVVPSSSLGTTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 240
DB 181 SGLYSLSVTVVPSSSLGTTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 240
QY 241 GPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTKPREEQY 300
DB 241 GPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTKPREEQY 300
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
DB 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
DB 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
QY 421 WQOQNVFSCVMHEALHNHYTQKSLSLSPGK 451
DB 421 WQOQNVFSCVMHEALHNHYTQKSLSLSPGK 451
RESULT 2
ID AAY68810
XX AAY68810 standard; Protein; 449 AA.
AC AAY68810;
XX
XX 16-MAY-2000 (first entry)
XX
XX A rat heavy chain region and a human hinge region.
XX
XX CD3 antigen complex; chimeric antibody; immunosuppression; heavy chain;
KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.

XX Synthetic.
OS Rattus sp.
OS Homo sapiens.
XX WO200005268-A1.
XX 03-FEB-2000.
XX 21-JUL-1999; 99WO-GB02380.
XX 21-JUL-1998; 98GB-0015909.
XX (BTGI-) BTG INT LTD.
XX Waldmann H, Frewin M;
XX WPI; 2000-182655/16.
XX N-PSDB; AAZ60599.
XX New humanized anti-CD3 antibodies, used for treating cancer or for
PT immunosuppression and preventing graft rejection -
XX Disclosure; Page 45-47; 56pp; English.
XX The present sequence represents the heavy chain variable region of a rat
CC immunoglobulin G (IgG) antibody which is specific for the CD3 antigen
CC complex, and the human CHI-hinge-aglycosylCH2CH3. The specification
CC describes chimeric human/rodent anti-CD3 antibodies, which have a
CC rodent CD3 light chain variable region and a human heavy chain variable
CC region. The anti-CD3 antibodies can render T-cells non-functional by
CC antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex.
CC They can be used for immunosuppression, particularly for the control
CC of graft rejection. The antibodies can also enhance or re-direct T-cell
CC responses to antigens. They can be used in the treatment of cancer.
XX
SQ Sequence 449 AA;
Query Match 94.2%; Score 2270; DB 21; Length 449;
Best Local Similarity 94.9%; Pred. No. 1.6e-127;
Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
DB 1 EQVLESGLVQPGGSLRLSCAASGFTFSPMAVWRQAPGKLEWVSTISTSGRTYY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYCAK---HTGGGVWDPIDYWGQGLTV 117
DB 61 RDSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYCAKFRQYSGG----FDYWGQGLTV 115
QY 118 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177
DB 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
QY 178 LQSSGLYSLSVTVVPSSSLGTTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPE 237
DB 176 LQSSGLYSLSVTVVPSSSLGTTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPE 235
QY 238 LLGGPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTKPRE 297
DB 236 LLGGPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTKPRE 295
QY 298 EOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 357
DB 296 EOYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
QY 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 417
DB 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 415
QY 418 KSRWQOQNVFSCVMHEALHNHYTQKSLSLSPGK 451
DB 416 KSRWQOQNVFSCVMHEALHNHYTQKSLSLSPGK 449

Db	196	TFPAVLQSSGLSLSSVTVVPSSSSLGTQYIICNVNHNKPSNTKVDKRVKPSCKDKTHTCPP	255		
Qy	233	CPAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	292		
Db	256	CPAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	315		
Qy	293	TKPREQYNSTRYVYSVLTVLHODWLNCKEYKCKVSNKALPAPAEKTIISKAKGQPREPOV	352		
Db	316	TKPREQYNSTRYVYSVLTVLHODWLNCKEYKCKVSNKALPAPAEKTIISKAKGQPREQV	375		
Qy	353	YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYS	412		
Db	376	YTLPPSRDEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYS	435		
Qy	413	KLIVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	451		
Db	436	KLIVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	474		
RESULT 4					
ID	AAU07745	standard; Protein; 461 AA.			
XX	AAU07745;				
XX	04-DEC-2001	(first entry)			
XX	Humanised monoclonal antibody Hu266, heavy chain.				
XX	Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;				
KW	Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;				
KW	gene therapy.				
XX					
OS	Mus sp.				
OS	Homo sapiens.				
OS	Synthetic.				
XX					
FH	Key	Location/Qualifiers			
FT	Peptide	1..19			
FT		/label= Signal_peptide			
FT	Protein	20..461			
FT		/label= Mature_Hu266_heavy_chain			
FT		/note= "This sequence is specifically claimed in			
FT		claim 17"			
XX					
PN	WO200162801-A2.				
XX					
PD	30-AUG-2001.				
XX					
PF	26-FEB-2001; 2001WO-US06191.				
XX					
PR	24-FEB-2000; 2000US-0184601.				
PR	08-DEC-2000; 2000US-0254465.				
PR	08-DEC-2000; 2000US-0254498.				
XX					
PA	(UNIW) UNIV WASHINGTON.				
PA	(ELIL) LILLY & CO ELI.				
XX					
PI	Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;				
PI	Vasquez M;				
XX					
XX	WPI; 2001-550087/61.				
XX					
PT	New humanised antibody for the treatment of Alzheimer's comprises the				
PT	inhibition and reduction of the formation of amyloid plaques -				
XX					
PS	Example 13; Fig 5; 63pp; English.				
XX					
CC	The invention relates a humanised antibody that specifically binds				
CC	an epitope contained within positions 13-28 of amyloid beta peptide,				
CC	Abeta. The antibody is useful to inhibit and reduce the formation of				
CC	amyloid plaques or the effects of toxic soluble Abeta species in humans				
CC	their fragments are used for the manufacture of a medicament This includes				

the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.

Seq	Sequence	461 AA;
Query	Match	92.8%; Score 2236.5; DB 22; Length 461;
Best Local Similarity	93.8%;	pred. No. 1.6e-125;
Matches	423; Conservative	7; Mismatches 12; Indels 9; Gaps 1;
Qy	1	QVLVQSGGGLVPGGSGURLSCAASGFTFRSNAMGVQAPKGLGWVSGTISGGSGSTYY 60
Db	20	EVQLVESGGGLVPGGSGURLSCAASGFTFRSYSMVSRVQAPKGLGLVAQINSVGNSTYY 79
Qy	61	ADSVKGRRTISRDNSKNTLYIQMNSLRADETAVYYCAKHTGGVWDPTDYNGOGTLFTVTS 120
Db	80	PDTVKGRETIISRDNAKNTLYIQMNSLRADETAVYYCASG-----DYNGOGTLFTVTS 130
Qy	121	SASTKGPVFFPLAPSSKSTSGTAAIGLCVLKDYFPPEPTVSWNSGALTSGVHTFPVAVLQS 180
Db	131	SASTKGPVFFPLAPSSKSTSGTAAIGLCVLKDYFPPEPTVSWNSGALTSGVHTFPVAVLQS 190
Qy	181	SGLSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCCPAPPELLG 240
Db	191	SGLSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCCPAPPELLG 250
Qy	241	GPSVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVFENYVDGVEVHNNAKTKPREEQY 300
Db	251	GPSVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVFENYVDGVEVHNNAKTKPREEQY 310
Qy	301	NSTYRVSVTLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYITLPSSRD 360
Db	311	NSTYRVSVTLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYITLPSSRD 370
Qy	361	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLVVDKSR 420
Db	371	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLVVDKSR 430
Qy	421	WQGVNFCGSVMHEALHNHYTQKSLSLSPGK 451
Db	431	WQGVNFCGSVMHEALHNHYTQKSLSLSPGK 461

RESULT 5	
AAU14288	
ID	AAU14288 standard; Protein; 477 AA.
XX	
XX	
AC	AAU14288;
XX	
XX	
DT	24-OCT-2001 (first entry)
DE	Human novel protein #159.
XX	
XX	Human; novel protein; Antianaemic; osteopathic; antinflammatory;
KW	immunomodulatory; cytosolic; neuroprotective; vulnerary; nootropic;
KW	anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW	antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW	tissue regeneration; immune disorder.

XX	25-JAN-2000; 2000US-0491404.
PR	(HYSE-) HYSEQ INC.
XX	Tang VT, Liu C, Drmanac RT;
XX	WPI; 2001-451939/48.
XX	N-PSDB; AAS22593.
XX	Isolated polypeptides useful for treating anti-inflammatory diseases,
XX	nervous system disorders, and for regenerating bone and cartilage -
XX	Example 4; Page 611-612; 894pp; English.
XX	The invention relates to polynucleotides encoding novel human
CC	proteins or their active domains. The polypeptides, polynucleotides and
CC	antibodies raised against the polypeptides are used in a method of
CC	treatment of a mammal and prevention of disorders caused by the aberrant
CC	protein expression or activity. The polypeptides can be used as
CC	molecular weight markers, food supplements, and in antibody production.
CC	The polypeptides are used to identify compounds which bind to the
CC	polypeptides. Polynucleotides of the invention are used as probes and
CC	primers, for sequencing, for chromosome or gene mapping, in the
CC	production of recombinant proteins, and in generating anti-sense DNA or
CC	RNA and in gene therapy. Polypeptides of the invention can be used to
CC	target drugs to a tumour, in assays to determine biological activity, to
CC	raise antibodies/elicit an immune response, to determine quantitative
CC	protein levels, as tissue markers, and to isolate receptors or ligands.
CC	Polypeptides of the invention may also be useful in treating platelet
CC	disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC	ligament and/or nerve tissue, wound healing, treating burns, promoting
CC	the proliferation, differentiation and survival of stem cells, as a
CC	contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC	Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC	sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC	fungal infection or from autoimmunity, cancer, allergy, asthma,
CC	graft-versus-host disease, eczema, haemophilia, thrombosis,
CC	anti-inflammatory diseases, nervous system disorders, and infection.
CC	The present sequence represents a protein of the invention.

```

Query Match          92.5%; Score 2229.5; DB 22; Length 477;
Best Local Similarity 91.5%; Pred. No. 4.3e-125;
Matches 422; Conservative 10; Mismatches 16; Indels 13; Gaps
2;

QY      1 QVQLVQSGGGLVQPQGSIRLSCAASGFTFRSNGMWVRQAPGKGLEWVSGISGSGSTYY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20 QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAPGKLEWVAALWDSGNKY 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 ADSVKGRTISRDNSKNTLYLQMSLRAEDTAVFYCAKHTGGGVWDP-----IDY 110
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 ADSVKGRTISRDNSKNTLYLQMSLRAEDTAVFYCARE---GRWRYRTVTITGYFFDY 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      111 WGOGTLVTIVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSMNSGALTSG 170
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      137 WGOGTLVTIVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSG 196
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      197 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVRPEPKSCDKTHTC 256
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 290
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      257 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 316
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      291 AKTKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTTISKAKGQPREP 350
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      317 AKTKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTTISKAKGQPREP 376
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSFFL 410
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention.

XX
SQ Sequence 582 AA;
Query Match 91.9%; Score 2216; DB 22; Length 582;
Best Local Similarity 92.7%; Pred. No. 3.4e-124;
Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVOLVSGGGLVOPGGSLRLSCAASGFTFRSNAMGMVROAPKGLEWVSGISGGSGTYY 60
DB 1 EVQLVSGGDFVOPGGSLRVSAASGAFSHVAMSVROAPKGLEWVAYISSGGSGTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPTIDYWGQGLTVTS 120
DB 61 SDSVKGRFTISRDNKNTLYLQMNLSRAEDSAVYFCTRVKLGTY--FDVWGQGLTVTS 118
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQS 180
DB 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQS 178
QY 181 SGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYVDKVEPKSCDKTHTCPPCPAPPELLG 240
DB 179 SGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYVDKVEPKSCDKTHTCPPCPAPPELLG 238
QY 241 GPSVFELPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 300
DB 239 GPSVFELPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 298
QY 301 NSTYRVVSVLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
DB 299 NSTYRVVSVLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 420
DB 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 418
QY 421 WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 419 WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

RESULT 8
AAV29458
ID AAY29458 standard; Protein; 452 AA.
AC AAY29458;
XX 05-OCT-1999 (first entry)
XX Recombinant immunoglobulin SEQ ID NO:71.
XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX fusion protein.
XX Synthetic.
XX WQ9937779-A1.
XX 29-JUL-1999.
XX 19-JAN-1999; 99WO-US01081.
XX 24-JUL-1998; 98US-0122513.
XX 22-JAN-1998; 98US-0012116.
XX 20-FEB-1998; 98WO-US03337.
XX 24-JUL-1998; 98US-0121952.
XX (GETH) GENENTECH INC.

PI Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
PI Zapata GA;
XX WPI; 1999-469134/39.
DR
XX
XX New conjugates of nonproteinaceous polymers with antibody fragments,
XX used for treating inflammatory disorders
PS Disclosure; Page 354-355; 360pp; English.

XX The present invention describes a novel conjugate having one or more
XX antibody fragments covalently attached to one or more nonproteinaceous
XX polymer molecules, where the apparent size of the conjugate is at least
XX about 500 kDa. Conjugates of antibody fragments which bind the human
XX interleukin (IL) 8 with a nonproteinaceous polymer can be used for
XX treating inflammatory disorders e.g. acute lung injury, ischaemic
XX reperfusion disorder, and autoimmune diseases. They can also be used
XX for treating e.g. inflammatory skin diseases including psoriasis and
XX atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
XX diseases. The conjugates can also be used as reagents in an animal
XX model system for in vivo study of the biological functions of the
XX antigen recognised by the conjugate. The present sequence represents
XX a recombinant immunoglobulin protein from the present invention.

XX Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 20; Length 452;
Best Local Similarity 92.5%; Pred. No. 4.8e-124;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVSGGGLVOPGGSLRLSCAASGFTFRSNAMGMVROAPKGLEWVSGISGGSGTYY 60
DB 1 EVQLVSGGGLVOPGGSLRLSCAASGYSFSSHYMHWVROAPKGLEWVGYIDPSNGETTY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK--HTGGVWDPTIDYWGQGLTVT 118
DB 61 NQKFGRTLSRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDW-FDVGQGLTVT 119
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 179
QY 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYVDKVEPKSCDKTHTCPPCPAPEL 238
DB 180 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYVDKVEPKSCDKTHTCPPCPAPEL 239
QY 239 LGGPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
DB 240 LGGPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 299
QY 299 QYNSTYRVVSVLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
DB 300 QYNSTYRVVSVLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418
DB 360 REMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 419
QY 419 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 420 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 9
AAB30322
ID AAB30322 standard; Protein; 452 AA.
XX
XX AAB30322;
XX
XX 12-FEB-2001 (first entry)
XX
XX Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.

KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.

OS Unidentified.

PN US6133426-A.

PD 17-OCT-2000.

PF 20-FEB-1998; 98US-0026985.

PR 21-FEB-1997; 97US-0038664.

PR 22-JAN-1998; 98US-0074330.

XX (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

XX WPI; 2000-686027/67.

XX Humanized anti-interleukin 8 monoclonal antibody variant useful for

PT treating inflammatory disorders, such as adult respiratory distress

PT syndrome, hypovolemic shock and ulcerative colitis -

XX Disclosure; Column 199-202; 240pp; English.

XX The present invention provides a number of humanised monoclonal anti-IL-8

CC antibodies which can be used in the diagnosis and treatment of

CC inflammatory disorders, including adult respiratory distress syndrome,

CC septic shock, multiple organ failure, bacterial pneumonia and

CC inflammatory bowel disease. The present sequence comprises one of the

XX antibodies of the invention.

SQ Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;
Best Local Similarity 92.5%; Pred. No. 4.8e-124;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSIGSGGSTYY 60

DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVVRQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAK--HTGGGVMDPIDYWGQGLT 118

DB 61 NQKFKGRFTLSRDNSKNTAVLQMNSLRAEDTAVYYCARGDYRYNGDWF-FDVWGQGLT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 179 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPPCPAPEL 239

QY 239 LGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 298

DB 240 LGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 299

QY 299 QYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

DB 300 QYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 359

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

DB 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 419

QY 419 SRWQQGNVFCSCVNHAEALHNHYTQKSLSLSPGK 451

DB 420 SRWQQGNVFCSCVNHAEALHNHYTQKSLSLSPGK 452

RESULT 10

AAAY77766

XX AAY77766 standard; Protein; 452 AA.

XX AC AAY77766;

XX DT 06-JUN-2000 (first entry)

XX DE Humanised anti-IL-8 antibody related protein seq ID No:71.

XX KW Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6GAV1IN35A;

XX KW inflammatory disorder; adult respiratory distress syndrome;

XX KW affinity purification.

XX OS Homo sapiens.

XX PN US6025158-A.

XX PD 15-FEB-2000.

XX PF 20-FEB-1998; 98US-0027449.

XX PR 21-FEB-1997; 97US-0038664.

XX PR 22-JAN-1998; 98US-0074330.

XX PA (GETH) GENENTECH INC.

XX PI Presta LG, Leong SR, Gonzalez TN;

XX DR WPI; 2000-181809/16.

XX PT New nucleic acid molecule encodes a polypeptide which is an

PT anti-interleukin-8 monoclonal antibody or antibody fragment useful for

PT the production of anti-interleukin-8 monoclonal antibodies or fragments

XX Examples; Columns 199-202; 188pp; English.

XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody

CC (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs

CC (complementarity determining regions) of the humanized anti-IL-8

CC 6G4.2.5V1IN35A light chain; and amino acids 24-253 of the humanized

CC anti-IL-8 6G4.2.5V1IN35A heavy chain. The anti-IL-8 MAb and fragments

CC can be used in diagnosis, for affinity purification of IL-8 from

CC recombinant cell culture or natural sources and for the treatment of

CC inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic

CC acids encoding the anti-IL-8 MAb can be associated in a vector with

CC another gene encoding another protein or protein fragment to produce a

CC fusion protein which can make isolation and/or purification of the

XX protein an easier process.

SQ Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;
Best Local Similarity 92.5%; Pred. No. 4.8e-124;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSIGSGGSTYY 60

DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVVRQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAK--HTGGGVMDPIDYWGQGLT 118

DB 61 NQKFKGRFTLSRDNSKNTAVLQMNSLRAEDTAVYYCARGDYRYNGDWF-FDVWGQGLT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 179 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPPCPAPEL 239

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QY 239 LGGPSVFLPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||
Db 240 LGGPSVFLPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
|||||
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
|||||
Db 300 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 359
|||||
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
|||||
Db 360 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 419
|||||
QY 419 SRWQGNVFSCSVMHREALNHHYTKQSLSPGK 451
|||||
Db 420 SRWQGNVFSCSVMHREALNHHYTKQSLSPGK 452
|||||

RESULT 11
AAR42066
ID AAR42066 standard; Protein; 459 AA.
XX
AC AAR42066;
XX
DT 29-APR-1994 (first entry)
XX
DE Human anti-HBs heavy chain.
XX
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..9
FT Protein /label= sig_peptide
FT /10..459
FT /label= mat_protein

W09320205-A.
XX
XX
XX
PD 14-OCT-1993.
XX
XX 30-MAR-1993; 93WO-JP00396.
XX
XX 30-MAR-1992; 92JP-0074678.
XX
XX (SUNR ) SUNTORY LTD.
XX
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
XX
XX WPI; 1993-336913/42.
XX
XX N-PSDB; AAQ49944.
XX
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
XX
XX Disclosure; Fig 6-8; 46pp; Japanese.
XX
XX Polynucleotides encoding the L and H chains of human anti-HBs
CC
CC Ab are given in AAQ49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
XX
XX
SQ Sequence 459 AA;
Query Match 91.6%; Score 2207.5; DB 14; Length 459;
Best Local Similarity 92.7%; Pred. No. 8.4e-124;
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGRSLRLSCAASGFTFRSNAMGWVRAQPGKGLWVGISGSGSTYY 60
|||||
Db 10 QVQLVESGGGVQPGRLSLRLSCAASGFTFSNSMHWVRAQPGKGLWVAIVLYDGNHKFY 69
|||||
QY 61 ADSVKGRFTISRDNKNTLYLEKSLQTEDTGVYICRDQTYGV-HRFDSWGOGTLTVTS 120
|||||
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Db 70 ADSVKGRFTISRDNKNTLYLEKSLQTEDTGVYICRDQTYGV-HRFDSWGOGTLTVTS 128
|||||
QY 121 SASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180
|||||
Db 129 SASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 188
|||||
QY 181 SGLYSLSVTVTPSSISLTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELLG 240
|||||
Db 189 SGLYSLSVTVTPSSISLTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELLG 248
|||||
QY 241 GPSVFLPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
|||||
Db 249 GPSVFLPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 308
|||||
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
|||||
Db 309 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 368
|||||
QY 361 ELTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 420
|||||
Db 369 ELTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 428
|||||
QY 421 WQGNVFSCSVMHREALNHHYTKQSLSPGK 451
|||||
Db 429 WQGNVFSCSVMHREALNHHYTKQSLSPGK 459
|||||

RESULT 12
AAW69316
ID AAW69316 standard; Protein; 452 AA.
XX
AC AAW69316;
XX
DT 15-FEB-1999 (first entry)
XX
DE Anti-IL-8 humanised antibody 6G4V1N35A.choSD.9.
XX
XX Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW ischaemic reperfusion; adult respiratory distress syndrome;
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
KW therapy; 6G4V1N35A.choSD.9.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
XX W09837200-A2.
XX
XX 27-AUG-1998.
XX
XX 20-FEB-1998; 98WO-US03337.
XX
XX 22-JAN-1998; 98US-0012116.
PR 21-FEB-1997; 97US-080444.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z;
PI Zapata GA;
XX
XX WPI; 1998-467563/40.
DR N-PSDB; AAW4956.
XX
XX New conjugates of antibody fragments - having covalently attached
PT non-proteinaceous polymer molecules, particularly polyethylene
PT glycol, for improving the residence time in the circulation.
XX
```


Db 444 KSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 477
|||||

RESULT 14
AAR24812
ID AAR24812 standard; Protein; 466 AA.

AC AAR24812;

DT 28-DEC-1992 (first entry)

DE Sequence encoded by the chimeric H chain cDNA contained in pTb1373.

DE Chimeric monoclonal antibody; anti-fibrin antibody; primer;

KW antithrombotic agent; myocardial infarction therapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 13..19

FT /label= Leader

FT Region 20..134

FT /label= VH

FT Region 135..232

FT /label= CH1

FT Region 233..247

FT /label= hinge

FT Region 248..357

FT /label= CH2

FT Region 358..464

FT /label= CH3

FT Misc-difference 465

FT /note= "translated stop codon"

XX

XX EP491351-A.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-0121591.

XX 18-DEC-1990; 90JP-0413829.

XX 11-NOV-1991; 91JP-0294464.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX N-PSDB; AAQ25692.

XX Chimeric monoclonal antibodies - contain anti-human fibrin

PT antibody light and heavy chain variable and constant for treating

PT thrombotic conditions e.g. myocardial infarction

XX Example; Figure 11; 87pp; English.

XX Plasmid pTb1373 contains the whole length of a mouse-human

CC chimeric anti-human fibrin heavy chain cDNA open reading

CC frame. It was pred. using Poly(A)+ RNA from the anti-fibrin

CC chimeric AB-producing transformant FIB1-H01/X63 as a template

CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as

CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH

CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding

CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain

CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader

CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'C1H

CC respectively as a primer for first strand cDNA synthesis and the

CC primer combination of 5'C1H and 3'C2H, of 5'1H and 3'C1H and of

CC 5'SH and 3'1H respectively as primers for PCR. The amplified gene

CC products were isolated and used to produce plasmids. After

CC confirmation of the cDNA sequence of each plasmid, the cDNA

CC encoding LH, VH, CH1 and CH2CH3 were joined together to give

CC plasmid pTb1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,

SQ Sequence 466 AA;

Query Match 90.7%; Score 2186; DB 13; Length 466;

Best Local Similarity 90.9%; Pred. NO. 1.6e-122;

Matches 410; Conservative 19; Mismatches 16; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60

DB 20 EVQLVESGGGLVPGGSLKLSRAASGFTFSNYDMNVQRQTPERRLEWVASIS-VGGTTY 78

QY 61 ADSYKGRFTISRDNKNTLYQMNSLRADTAIVYYCAKHTGGGVGDPIDYWGOGTLTVTS 120

DB 79 PDSMKGRFTISRDNARNILYLQSLSLRSEDTAMYYC-----GNFADAMDYWGOGTLTVTS 133

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180

DB 134 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 193

QY 181 SGLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTCPAPPELLG 240

DB 194 SGLYSLSVVTVPSSSLGTQYICTVNHKPSNTKVDKRVKPSKDKTHTCTCPAPPELLG 253

QY 241 GPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 300

DB 254 GPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 313

QY 301 NSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

DB 314 NSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIEKTISKAKGQPREPQVYTLPPSRD 373

QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYYLSSLTVDKSR 420

DB 374 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYYLSSLTVDKSR 433

QY 421 WQGNVFCSCVMHEALHNHYTKQSLSLSPGK 451

DB 434 WQGNVFCSCVMHEALHNHYTKQSLSLSPGK 464

RESULT 15

AAR33311

ID AAR33311 standard; Protein; 453 AA.

XX AAR33311;

XX AAR33311;

DT 05-JUL-1993 (first entry)

DE Humanised MaE11 Version 1 (Intact IgG) heavy chain.

XX Antibody; high affinity; FCEH; low affinity; FCEL;

KW IgE receptor; histamine; mast cell; basophil; Kabat;

KW CDR; murine; MAE11; Fab; humael1v1.

XX Synthetic.

OS WO9304173-A.

PN WO9304173-A.

XX 04-MAR-1993.

XX 14-AUG-1992; 92WO-US06860.

XX 14-AUG-1991; 91US-0744768.

XX 07-MAY-1992; 92US-0879495.

XX (GETH) GENENTECH INC.

PA Jardieu PM, Presta LG;

PI WPI; 1993-094004/11.

XX

PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and VI
CC region kappa subgroup I). A first version, humaeli1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
XX
SQ Sequence 453 AA;
Query Match 90.3%; Score 2177; DB 14; Length 453;
Best Local Similarity 91.6%; Pred. No. 5.4e-122;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLEWVSGISGGSTY 59
Db :||||:||||:||||:||||:| : : |||||:|: |||
1 EVQLVESGGGLVPGGSLRLSCAVSYITSGYSWNIRQAPGKLEWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTFLQNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGT 118
Db :||||:||||:||||:||||:||||:| : | |||||
60 YADSVKGRFTISRDNKNTFLQNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGT 118
QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 176
Db :||||:||||:||||:||||:||||:||||:| : |||||
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QY 177 VLQSSGLYSLSVWTVPSSSLGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPPCPAP 236
Db :||||:||||:||||:||||:||||:||||:||||:| : |||||
179 VLQSSGLYSLSVWTVPSSSLGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPPCPAP 238
QY 237 ELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
Db :||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
239 ELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 EQYINSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
299 EQYINSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
QY 357 PSRDELTKNOVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 416
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
359 PSREEMTKNOVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 418
QY 417 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
419 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

Search completed: March 14, 2003, 11:47:40
Job time : 43.1559 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run On: March 14, 2003, 11:45:34 ; Search time 14.1473 Seconds
(without alignments)
937.967 Million cell updates/sec

Title: US-09-822-698A-26
Perfect score: 2411
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHHVTKLSLSLSPCK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2214.5	91.8	449	US-09-679-397-2	Sequence 2, Appli
2	2214.5	91.8	449	US-09-680-148-2	Sequence 2, Appli
3	2211.5	91.7	452	US-09-027-449-71	Sequence 71, Appl
4	2211.5	91.7	452	US-09-026-985-71	Sequence 71, Appl
5	2211.5	91.7	452	US-09-121-952A-71	Sequence 71, Appl
6	2211.5	91.7	452	US-09-234-340A-71	Sequence 7, Appli
7	2207.5	91.6	459	US-08-157-101A-7	Sequence 8, Appli
8	2177	90.3	453	US-08-466-151-8	Sequence 8, Appli
9	2177	90.3	453	US-08-466-163B-8	Sequence 8, Appli
10	2169	90.0	451	US-08-887-352B-14	Sequence 14, Appl
11	2169	90.0	451	US-08-887-352B-16	Sequence 16, Appl
12	2169	90.0	451	US-08-466-151-65	Sequence 65, Appl
13	2169	90.0	451	US-09-109-207C-14	Sequence 14, Appl
14	2169	90.0	451	US-09-109-207C-16	Sequence 16, Appl
15	2169	90.0	451	US-09-296-005-14	Sequence 14, Appl
16	2169	90.0	451	US-09-296-005-16	Sequence 16, Appl
17	2168	89.9	451	US-08-887-352B-18	Sequence 18, Appl
18	2168	89.9	451	US-09-109-207C-18	Sequence 18, Appl
19	2168	89.9	451	US-09-282-505-2	Sequence 2, Appli
20	2168	89.9	451	US-09-054-255-2	Sequence 2, Appli
21	2168	89.9	451	US-09-296-005-18	Sequence 18, Appl
22	2160	89.6	478	US-08-487-550-8	Sequence 8, Appli
23	2116	87.8	449	US-08-458-516-13	Sequence 13, Appl
24	2102.5	87.2	446	US-08-397-411-7	Sequence 7, Appli
25	2090	86.7	443	PCT-US96-13152-4	Sequence 4, Appli
26	2089	86.6	468	US-09-485-737B-67	Sequence 67, Appl
27	2089	86.6	711	US-09-485-737B-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1

US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: PL241RLD2
; CURRENT APPLICATION NUMBER: US/09/679,397
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match	91.8%	Score 2214.5;	DB 4;	Length 449;
Best Local Similarity	92.7%	Pred. No. 4.5e-167;		
Matches 417;	Conservative 12;	Mismatches 20;	Indels 1;	Gaps 1;

QY	1	QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSGTYY	60
Db	1	EVQLVESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSGTYY	60
QY	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAKHTGGVWDPDYDYGQGTFTVTS	120
Db	61	ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYCSRWGGDGFY-AMDYWGQGTFTVTS	119
QY	121	SASTKGPSVFPLAPSSKTSKGTAAALGCLVKDYDPEPEPTVTSWNSGALTSGVHTFPAVLQ	180
Db	120	SASTKGPSVFPLAPSSKTSKGTAAALGCLVKDYDPEPEPTVTSWNSGALTSGVHTFPAVLQ	179
QY	181	SGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKDKKVEPKSCDKTHTCTCPCPAPELLG	240
Db	180	SGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKDKKVEPKSCDKTHTCTCPCPAPELLG	239
QY	241	GPSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY	300
Db	240	GPSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY	299
QY	301	NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD	360

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Db      300  NSTYRVVSVLTVLHQDWLNGCKVKVSNKALPAPIEKTISTAKGQPREPQVYITLPPSRE 359
Qy      361  ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 420
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      360  EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 419
Qy      421  WQOGNVFSCVMHEALHNHYTQKSLSLSPG 450
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      420  WQOGNVFSCVMHEALHNHYTQKSLSLSPG 449

RESULT 2
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRP
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
; US-09-680-148-2

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RESULT 3
 US-09-027-449-71
 ; Sequence 71, Application US/09027449
 ; Patent NO. 6025158
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/027,449
 ; FILING DATE: 20-Feb-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/074,330
 ; FILING DATE: 22-Jan-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/038,664
 ; FILING DATE: 21-Feb-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1085R3-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 452 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 US-09-027-449-71

三

Db 300 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPVLDSDGSFSLYSLKLTVDK 418
Db 360 REMTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPVLDSDGSFSLYSLKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 4
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVSGGGLVQPGGSLRSLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 1 EVQLVSGGGLVQPGGSLRSLCAASGSPSSHYMHWRQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRTLSRDNKNTLYLQNSLRADTAVYYCAK--HTGGGVWDPIDYWGOGTLVT 118
Db 61 NQFKGRFTLSRDNKNTLYLQNSLRADTAVYYCARGDYRYNGDF--FDVWGOGTLVT 119

QY 119 VSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 179

QY 179 QSGLGLSLSVVTPVPSLSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPEL 238
Db 180 QSGLGLSLSVVTPVPSLSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPEL 239

QY 239 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Db 240 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
QY 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 300 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPVLDSDGSFSLYSLKLTVDK 418
Db 360 REEMTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPVLDSDGSFSLYSLKLTVDK 419

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVSGGGLVQPGGSLRSLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 1 EVQLVSGGGLVQPGGSLRSLCAASGSPSSHYMHWRQAPGKLEWGYIDPSNGETTY 60

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;
; 61 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAVYYCAK--HTGGGVWDPIDYWGQGTLLVT 118
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; 61 NQKFKGRFTLSRDNKNTLYLQMNLSLRADTAVYYCARGDYRYNGDWF-FDWGQGTLLVT 119
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 179
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 180 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 239
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 239 LGGPSVFLFPPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 240 LGGPSVFLFPPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 299 QYNSTYRVVSVLTVQLHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 300 QYNSTYRVVSVLTVQLHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 648532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-234-340A-71

Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Qy 1 QQLVQSGGGLVQPGSLRLSCAASGFTFRSNAGWVWRQAPGKLEWVSGISGGSTYY 60
;      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFSHYMHVWRQAPGKLEWVGYIDPSNGETTY 60
;      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAVYYCAK--HTGGGVWDPIDYWGQGTLLVT 118
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGRFTLSRDNKNTLYLQMNLSLRADTAVYYCARGDYRYNGDWF-FDWGQGTLLVT 119
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 179
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 239
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 239 LGGPSVFLFPPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 LGGPSVFLFPPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 299 QYNSTYRVVSVLTVQLHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 QYNSTYRVVSVLTVQLHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452
;      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
```


; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 91.6%; Score 2207.5; DB 1; Length 459;
Best Local Similarity 92.7%; Pred. No. 1.6e-166;
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRAQPGKGLVWVGISGGSTYY 60
DB 10 QVQLVESGGGVQPGSLRLSCAASGFTFSNMMHWVRAQPGKGLWVAVILYDGNHKFY 69
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTS 120
DB 70 ADSVKGRFTISRDNKNTLYLQVSLQEDTGVYICRDQTYGV-HRFDWGGQGLTVTS 128
QY 121 SASTKGSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVLIQS 180
DB 129 SASTKGSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALASGVHTFPVLIQS 188
QY 181 SGLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHHTCPPAPPELLG 240
DB 189 SGLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHHTCPPAPPELLG 248
QY 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
DB 249 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 308
QY 301 NSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
DB 309 NSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 368
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
DB 369 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 428
QY 421 WQGNVFSCSVMHREALNHYTKQSLSLSPGK 451
DB 429 WQGNVFSCSVMHREALNHYTKQSLSLSPGK 459

RESULT 8
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-8

Query Match 90.3%; Score 2177; DB 3; Length 453;
Best Local Similarity 91.6%; Pred. No. 4.1e-164;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRAQPGKGLWVVGISGGSTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNWNIRQAPGKGLWVAVIT-YDGSFN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLTVT 118
DB 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHH-FAVWGQGLTVT 118
QY 119 VSSAST--KGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPA 176
DB 119 VSSASTKKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPA 178
QY 177 VLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHHTCPPAP 236
DB 179 VLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHHTCPPAP 238
QY 237 ELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
DB 239 ELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
DB 299 EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 416
DB 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 418
QY 417 DKSRWQGNVFSCSVMHREALNHYTKQSLSLSPGK 451
DB 419 DKSRWQGNVFSCSVMHREALNHYTKQSLSLSPGK 453

RESULT 9

US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-08-466-163B-8

Query Match 90.3%; Score 2177; DB 4; Length 453;

Best Local Similarity 91.6%; Pred. No. 4,1e-164;

Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSN-AMGWVROAPGKGLVWVSGISGGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSNWIROAPGKGLWVASIT-YDGSN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGVWDPIDVWGQGLT 118
Db 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARGSHYFGHW-FAVWGQGLT 118
Qy 119 VSSAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 176
Db 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Qy 177 VQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 236
Db 179 VQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 238
Qy 237 ELGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPR 296
Db 239 ELGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPR 298
Qy 297 EEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPTEKTSISKAGOPREPQVYTL 356
Db 299 EEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPTEKTSISKAGOPREPQVYTL 358
Qy 357 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 416
Db 359 PSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 418
Qy 417 DKSRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 451
Db 419 DKSRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 453

RESULT 10

US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-14

Query Match 90.0%; Score 2169; DB 2; Length 451;

Best Local Similarity 91.4%; Pred. No. 1.8e-163;

Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSN-AMGWVROAPGKGLVWVSGISGGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSNWIROAPGKGLWVASIT-YDGSN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGVWDPIDVWGQGLT 118
Db 60 YNPSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARGSHYFGHW-FAVWGQGLT 118
Qy 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Db 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Qy 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 238
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 238
Qy 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 298
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 298
Qy 299 QNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPTEKTSISKAGOPREPQVYTL 358
Db 299 QNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPTEKTSISKAGOPREPQVYTL 358
Qy 359 RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 418
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 418
Qy 419 SRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 451

RESULT 11

US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-16

Query Match 90.0%; Score 2169; DB 2; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSN-AMGWVRQAPGKGLWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGTLLV 118
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYTCARGSHYFGHHW-FAVWGQGTLLV 118
QY 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298
Db 239 LGGPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPS 358
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-08-466-151-65

Sequence 65, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-65

Query Match 90.0%; Score 2169; DB 3; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSN-AMGWVRQAPGKGLWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGTLLV 118
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYTCARGSHYFGHHW-FAVWGQGTLLV 118
QY 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298
Db 239 LGGPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298

Db 239 LGGPSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLIEWSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPQGGSLRLSCAVSYISITSGYSWNWIRQAPGKGLIEWASIT-YDGSN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTLLV 118
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGTLLV 118
QY 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDVKVPEKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDVKVPEKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
Db 239 LGGPSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLIEWSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPQGGSLRLSCAVSYISITSGYSWNWIRQAPGKGLIEWASIT-YDGSN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTLLV 118
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGTLLV 118
QY 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDVKVPEKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDVKVPEKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
Db 239 LGGPSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352

; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLEWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASIT-YDGS 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDDPIDYWGQGLVT 118
Db 60 YNPVKGRITISRDSKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDDPIDYWGQGLVT 118
QY 119 VSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREE 298
Db 239 LGGPSVLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREE 298
QY 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDK 418
QY 419 SRWQOGNVFSCSVMHAEALHNHYTKSLSPGK 451
Db 419 SRWQOGNVFSCSVMHAEALHNHYTKSLSPGK 451

Search completed: March 14, 2003, 11:50:19
Job time : 16.1473 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 ; Search time 13.7186 Seconds
(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALNHYTKQSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/us08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/us06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/us06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/us07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/us07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/us08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/us09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/us09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/us10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/us10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/us60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	100.0	451	10	US-09-822-698A-26
2	2270	94.2	449	10	US-09-736-371B-21
3	2211.5	91.7	452	9	US-09-726-258-71
4	2177	90.3	453	9	US-09-925-179-8
5	2177	90.3	453	10	US-09-802-077-8
6	2177	90.3	453	10	US-09-802-096-8
7	2169	90.0	451	9	US-09-925-179-65
8	2169	90.0	451	10	US-09-920-171-14
9	2169	90.0	451	10	US-09-920-171-16
10	2168	89.9	451	10	US-09-920-171-18
11	2166	89.8	451	9	US-09-925-179-66
12	2160	89.6	451	9	US-09-925-179-68
13	2160	89.6	478	9	US-10-124-905-8
14	2160	89.6	478	9	US-09-948-429B-8
15	2113.5	87.7	731	10	US-09-825-012-46
16	2113.5	87.7	741	10	US-09-825-012-55
17	2108.5	87.5	729	10	US-09-825-012-52
18	2108.5	87.5	739	10	US-09-825-012-61
19	2102.5	87.2	730	10	US-09-825-012-49

20	2102.5	87.2	740	10	US-09-825-012-58
21	2092	86.8	476	10	US-09-747-669-3
22	2090	86.7	443	10	US-09-917-410-4
23	2066	85.7	476	9	US-10-124-905-12
24	2066	85.7	476	9	US-09-948-429B-12
25	2044	84.8	476	9	US-10-124-905-4
26	2044	84.8	476	9	US-09-948-429B-4
27	2038	84.5	470	10	US-09-859-053-32
28	2038	84.5	470	10	US-09-859-053-36
29	2026.5	84.1	475	10	US-09-740-002-27
30	2021.5	83.8	475	10	US-09-740-002-25
31	2019.5	83.8	450	9	US-09-996-288-216
32	2019.5	83.8	450	9	US-09-996-288-218
33	2019.5	83.8	450	9	US-09-996-288-250
34	2019.5	83.8	450	10	US-09-796-848A-43
35	2019.5	83.8	450	10	US-09-796-848A-49
36	2017.5	83.7	450	9	US-09-996-288-222
37	2017.5	83.7	450	9	US-09-996-288-224
38	2017.5	83.7	450	10	US-09-796-848A-39
39	2017.5	83.6	450	10	US-09-796-848A-41
40	2015.5	83.6	450	9	US-09-996-288-220
41	2015.5	83.6	450	10	US-09-796-848A-37
42	2012.5	83.5	450	9	US-09-996-288-212
43	2012.5	83.5	450	9	US-09-996-288-214
44	2012.5	83.5	450	9	US-09-996-288-226
45	2012.5	83.5	450	9	US-09-996-288-252

ALIGNMENTS

RESULT 1

US-09-822-698A-26

; Sequence 26, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hooqenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DIX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 26

; LENGTH: 451

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1

Query Match	100.0%;	Score 2411;	DB 10;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 6.1e-116;		
Matches 451;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRS	NAMGWVQAPGKLEWVSGISGGSTYY	60
Db	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRS	NAMGWVQAPGKLEWVSGISGGSTYY	60
Qy	61	ADSVKGFRTISRDNSKNTLYLQMSLRAEDTAVY	CAKHTGGGVWDPIDYWGOGTLVTWS	120
Db	61	ADSVKGFRTISRDNSKNTLYLQMSLRAEDTAVY	CAKHTGGGVWDPIDYWGOGTLVTWS	120
Qy	121	SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY	FPPEPTVSWNSGALTSGVHFFPAVLQS	180
Db	121	SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY	FPPEPTVSWNSGALTSGVHFFPAVLQS	180
Qy	181	SGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTK	VKKVEPKSCDKTHTCTPCPAPPELLG	240
Db	181	SGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTK	VKKVEPKSCDKTHTCTPCPAPPELLG	240

Qy 241 GPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 241 GPSVFLPPKPKADTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Qy 301 NSTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Db 301 NSTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 420
Db 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 420
Qy 421 WOOGNVFSCVMHEALHNNHYTKLSLSPGK 451
Db 421 WOOGNVFSCVMHEALHNNHYTKLSLSPGK 451
RESULT 2
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US2002013198A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736.371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21
Query Match 94.2%; Score 2270; DB 10; Length 449;
Best Local Similarity 94.9%; Pred. No. 8.9e-109;
Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 EVQLLEGGGLVQPGGSLRLSCAASGFTFSFPMWVROAPGKGLWVSTISTSGRTYY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAK---HTGGGVWDPIDYWGQGLTV 117
Db 61 RDSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAKFRQYSGG----FDYWGQGLTV 115
Qy 118 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177
Db 116 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
Qy 178 LQSSGLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPE 237
Db 176 LQSSGLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPE 235
Qy 238 LLGGPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297
Db 236 LLGGPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
Qy 298 EQYNSYRVVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 357
Db 296 EQYASTYRVVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
Qy 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD 417
Db 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD 415

Qy 418 KSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 451
Db 416 KSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 449
RESULT 3
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/234,182
; APPLICATION NUMBER:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-726-258-71
Query Match 91.7%; Score 2211.5; DB 9; Length 452;
Best Local Similarity 92.5%; Pred. No. 8.4e-106;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVROAPGKGLWVGYIDPSNGETTY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCAK--HTGGGVWDPIDYWGQGLTV 118
Db 61 NQKFKGRFTISRDNKNTAYLQMNSLRADTAIVYCAGRDYRNGDWF--FDVWGQGLTV 119
Qy 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179
Qy 179 QSSGLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238

Db 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPPAP 239
QY 239 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 240 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 299
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISRAKAGQPREPQVYTL 358
Db 300 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISRAKAGQPREPQVYTL 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
QY 419 SRWQOGNFCSCVMHEALHNYTKQSLSPGK 451
Db 420 SRWQOGNFCSCVMHEALHNYTKQSLSPGK 452

RESULT 4

US-09-925-179-8
; Sequence 8, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-925-179-8

Query Match 90.3%; Score 2177; DB 9; Length 453;
Best Local Similarity 91.6%; Pred. No. 4.8e-104;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNIQAPGKGLWVASIT-YDGS 59
QY 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
Db 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
QY 119 VSSAST--KGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
Db 119 VSSASTKGGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPPAP 236
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPPAP 238
QY 237 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
Db 299 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298

Db 239 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 299 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
Db 359 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 417 DKSRWQOGNFCSCVMHEALHNYTKQSLSPGK 451
Db 419 DKSRWQOGNFCSCVMHEALHNYTKQSLSPGK 453

RESULT 5

US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-802-077-8

Query Match 90.3%; Score 2177; DB 10; Length 453;
Best Local Similarity 91.6%; Pred. No. 4.8e-104;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNIQAPGKGLWVASIT-YDGS 59
QY 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
Db 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
QY 119 VSSAST--KGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
Db 119 VSSASTKGGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPPAP 236
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPPAP 238
QY 237 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
Db 239 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 299 ELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298

QY 357 PSRDELTKNOVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTV 416
Db 359 PSREMTKNOVSLTCLVKGYFSDTAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 418
QY 417 DKSRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 451
Db 419 DKSRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 453

RESULT 6
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain

US-09-802-096-8

Query Match 90.3%; Score 2177; DB 10; Length 453;
Best Local Similarity 91.6%; Pred. No. 4,8e-104;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIQAPGKGLEWVASIT-YDGSIN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGYNDPIDYWGQGLTV 118
Db 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGLTV 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPA 176
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPA 178

QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 236
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 238

QY 237 ELGGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPR 296
Db 239 ELGGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPR 298

QY 297 EEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
Db 299 EEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358

QY 357 PSRDELTKNOVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTV 416
Db 359 PSREMTKNOVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTV 418

QY 417 DKSRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 451
Db 419 DKSRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 453

Db 419 DKSRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 453

RESULT 7
US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2CIDICIUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of T

US-09-925-179-65

Query Match 90.0%; Score 2169; DB 9; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.2e-103;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIQAPGKGLEWVASIT-YDGSIN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGYNDPIDYWGQGLTV 118
Db 60 YNPSYKGRITISRDNKNTLYLQMSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGLTV 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPA 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPA 178

QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 238

QY 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPRE 298
Db 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPRE 298

QY 299 QYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
Db 299 QYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358

QY 359 RDELTKNOVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTV 418
Db 359 REEMTKNOVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTV 418

QY 419 SRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 451
Db 419 SRWQOQGNFVSCVMHEALHNNHYTKQSLSPGK 451

RESULT 8

US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 90.0%; Score 2169; DB 10; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.2e-103;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVQLVQSGGGLVQPGGSLRLSAAAGFTFSN-AMGWVROAPGKGLWVGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNIHQAPGKGLWVASIT-YDGSN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGLT 118
Db 60 YNPVKGRITISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGLT 118
QY 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
Db 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNOVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDK 418
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US

US-09-920-171-17
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16
Query Match 90.0%; Score 2169; DB 10; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.2e-103;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVQLVQSGGGLVQPGGSLRLSAAAGFTFSN-AMGWVROAPGKGLWVGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNIHQAPGKGLWVASIT-YDGSN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGLT 118
Db 60 YNPVKGRITISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGLT 118
QY 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
Db 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNOVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDK 418
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Query Match 89.9%; Score 2168; DB 10; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.4e-103;
Matches 414; Conservative 12; Mismatches 23; Indels 4; Gaps 4;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLEWVSGISGGSTY 59
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIROAPGKGLEWVASIKYS-GETK 59
QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGVMDPDIYWGQGTTLV 118
Db 60 YNPSLKGRITISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGTTLV 118
QY 119 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDK 418
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of Tabl

US-09-925-179-66
Query Match 89.9%; Score 2168; DB 9; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.4e-103;
Matches 414; Conservative 12; Mismatches 23; Indels 4; Gaps 4;

Query Match 89.8%; Score 2166; DB 9; Length 451;
Best Local Similarity 91.2%; Pred. No. 1.7e-103;
Matches 413; Conservative 14; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLEWVSGISGGSTY 59
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIROAPGKGLEWVASIT-YDGSTN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGVMDPDIYWGQGTTLV 118
Db 60 YNPSLKGRITISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHHW-FAVWGQGTTLV 118
QY 119 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDK 418
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Ta

US-09-925-179-68
Query Match 89.6%; Score 2160; DB 9; Length 451;
Best Local Similarity 90.5%; Pred. No. 3.5e-103;
Matches 410; Conservative 16; Mismatches 23; Indels 4; Gaps 4;

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8

Query Match      89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3.6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 8; Gaps 3;

QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGISGGSTY 59
Db 1 EVOLVESGGGLVQPGSLRLSCAVSGYSITGSYNNWIRQAPGKLEWMSGIT-YDGSIN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG-GGVNDPIDYWGQGLVT 118
Db 60 YNDSLKGRITVSRDSDSKNTFYQLNSARAEDTAVYICARGSHYFGHH-FAVWQGGFLVT 118

QY 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVHTFPAVL 178
Db 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVHTFPAVL 178

QY 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPEL 238

QY 239 LGGPSVFLPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWVDGVGEVHNAKTKPREE 298
Db 239 LGGPSVFLPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWVDGVGEVHNAKTKPREE 298

QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358

QY 359 RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-10-124-905-8
; Sequence 8, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
```

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8

Query Match      89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3.6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 8; Gaps 3;

QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISG--SGST 58
Db 20 EVOLVESGGGLVQPGSLRLSCAVSGFTFSDHYWYFRQAPGKPEWVGFRNKPNGTT 79

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCA----KHTGGV--WDPIDYWG 112
Db 80 EVAASVKDRFTISRDDSLSIAVLQWSSLKIEDTAVYCTTSYISHCRGGVCYGYFEFWG 139

QY 113 QGTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVH 172
Db 140 QGALVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVH 199

QY 173 TPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPP 232
Db 200 TPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKAEPKSCDKTHTCPP 259

QY 233 CPAPELLGGPSVFLPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVINAK 292
Db 260 CPAPELLGGPSVFLPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVINAK 319

QY 293 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV 352
Db 320 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV 379

QY 353 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYS 412
Db 380 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYS 439

QY 413 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478

RESULT 14
US-09-948-429B-8
; Sequence 8, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-4298-8

Query Match 89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3 6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 8; Gaps 3;
Qy 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVROAPGKLEWVSGISG--SGGST 58
Db 20 EVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPWEVGFIRKPNGGTT 79
Qy 59 YYADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYCA---KHTGGGV--WDPIIDYWG 112
Db 80 EYAAASVKDRFTISRDNKNTLYIQMNSLRADDTAVYCTTSYISHCRGGVCGYGFEPFWG 139
Qy 113 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYDVFPEPVTVSNWNSGALTSGVH 172
Db 140 QGALVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYDVFPEPVTVSNWNSGALTSGVH 199
Qy 173 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPP 232
Db 200 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKAEPKSCDKHTHTCPP 259
Qy 233 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 292
Db 260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319
Qy 293 TKPREEQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQV 352
Db 320 TKPREEQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQV 379
Qy 353 YLPSPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYS 412
Db 380 YLPSPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYS 439
Qy 413 KLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451
Db 440 KLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 478

RESULT 15
US-09-825-012-46
Sequence 46, Application US/09825012
Patent No. US20020122798A1
GENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46

LENGTH: 731
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-46
Query Match 87.7%; Score 2113.5; DB 10; Length 731;
Best Local Similarity 88.2%; Pred. No. 1.2e-100;
Matches 398; Conservative 20; Mismatches 30; Indels 3; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVROAPGKLEWVSGISGSGSTFY 60
Db 20 QVQLVQSGAENVKPKASVKSCASGYTFSAYIEWRQAPGKLEWGEILPGSNRSRY 79
Qy 61 ADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYCAKHTGGVWDPIIDYWGQGLTVTVS 120
Db 80 NEKFKGRVTVTRDTSTNTAYMELSLRSEDVAVYCAR-SYDFAW--FAYWGQGLTVTVS 136
Qy 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYDVFPEPVTVSNWNSGALTSGVHTFPVAVLQS 180
Db 137 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYDVFPEPVTVSNWNSGALTSGVHTFPVAVLQS 196
Qy 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPPAPPELLG 240
Db 197 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPPAPPELLG 256
Qy 241 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 257 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 316
Qy 301 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
Db 317 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 376
Qy 361 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSR 420
Db 377 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSR 436
Qy 421 WQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451
Db 437 WQGNVFCSCVMHEALHNHYTOKSLSLSPGK 467

Search completed: March 14, 2003, 11:51:51
Job time : 14.7186 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:54 ; Search time 18.4344 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-26
Perfect score: 2411
Sequence: 1 QVOLVQSGGLVQPGSLRL.....MHEALHNHYTKLSLSLSPGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	73.3	330	1 GHU	Ig gamma-1 chain C
2	1630.5	67.6	377	2 A23511	Ig gamma-3 chain C
3	1628.5	67.5	377	2 A60764	Ig gamma-3 chain C
4	1604	66.5	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	66.0	327	1 G4HU	Ig gamma-4 chain C
6	1513	62.8	470	2 S22080	Ig heavy chain pre
7	1499.5	62.2	444	2 PC4436	monoclonal antibod
8	1451.5	60.2	469	2 S37483	Ig gamma-2a chain
9	1435	59.5	446	2 S40295	Ig gamma-2a chain
10	1433	59.4	374	2 S69339	Ig gamma-2a chain
11	1430	59.3	472	2 S31459	Ig heavy chain V r
12	1382	57.3	474	1 G2MSL1	Ig gamma-1 chain -
13	1376.5	57.1	475	2 S01321	Ig gamma-2b chain
14	1263	52.4	328	2 I47159	Ig gamma-2a chain
15	1260	52.3	255	4 S31866	Ig gamma-1 chain C
16	1257	52.1	328	2 I47160	Ig gamma 2b chain
17	1254	52.0	234	2 P70207	Ig gamma 2b chain
18	1231	51.1	328	2 I47158	Ig gamma chain C r
19	1230.5	51.0	323	1 GHRB	Ig gamma 1 chain c
20	1227	50.9	328	2 I47161	Ig gamma chain C r
21	1216.5	50.5	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	48.2	308	2 C30554	Ig gamma-2 chain C
23	1152	47.8	326	2 PS0017	Ig heavy chain C r
24	1151	47.7	289	1 G3HUI	Ig gamma-1 chain C
25	1146.5	47.6	333	2 PS0018	Ig gamma-3 heavy c
26	1142	47.4	324	1 GLMS	Ig gamma-2b chain
27	1141	47.3	329	1 G3MSC	Ig gamma-1 chain C
28	1137	47.2	393	1 GLMSC	Ig gamma-3 chain C
29	1130	46.9	398	1 G3MSM	Ig gamma-3 chain C

30 1126 46.7 330 1 G2MSA
31 1123.5 46.6 335 1 G2MSAB
32 1121 46.5 399 1 G2MSAM
33 1118.5 46.4 329 2 S00847
34 1112 46.1 322 2 PS0019
35 1093 45.3 548 2 S38864
36 1092.5 45.3 327 2 S06611
37 1082 44.9 405 1 G2MSBM
38 1066 44.2 277 2 I47162
39 891.5 37.0 249 2 S69340
40 881.5 36.6 572 2 B46529
41 866.5 35.9 549 2 S04845
42 842 34.9 218 2 A36040
43 814 33.8 220 2 A49444
44 792.5 32.9 241 2 S69131
45 779 32.3 627 2 S14683

ALIGNMENTS

RESULT 1

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S38861; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J
Submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, R',98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-ArG
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q',156-165, 'Q',178-194, 'N',196-197, 'D',199-238, 'E',2
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', '36-96, 'K', '98-115, 'Q', '117-197, 'D', '199-238, 'D', '240, 'L', '242-268, 'E', '271-330
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', '268-271, 'D', '273-330 <SCH
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enamide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMTM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:243-310/Domain: immunoglobulin homology <IM2>
F:27-63,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 73.3%; Score 1767; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.6e-94;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 ASTKGSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 ASTKGSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVTVPPSSSLGTQYICNVNKPNTKVDKVPKSCDTHTCPCPAPPELLGG 241
Db 61 GLYSLSVTVPPSSSLGTQYICNVNKPNTKVDKVPKSCDTHTCPCPAPPELLGG 120

QY 242 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAAKTPKREEQYN 301
Db 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAAKTPKREEQYN 180

QY 302 STYRVSVLTVLHQQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 361
Db 181 STYRVSVLTVLHQQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 421
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300

QY 422 QQGNVFSCSYMHALNHHYTKQSLSPGK 451
Db 301 QQGNVFSCSYMHALNHHYTKQSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 1630.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 1.3e-86;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 122 ASTKGSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 ASTKGSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVTVPPSSSLGTQYICNVNKPNTKVDKVPKSCDTHTCPCPAPPELLGG 254
Db 61 GLYSLSVTVPPSSSLGTQYICNVNKPNTKVDKVPKSCDTHTCPCPAPPELLGG 120

QY 220 -----EPKSCDTHTCPCPAPPELLGGPSVFLPPKPKDT 254
Db 121 DTPPPCPPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKPKDT 180

QY 255 LMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAAKTPKREEQYNSTYRVVSVLTVHL 314
Db 181 LMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAAKTPKREEQYNSTYRVVSVLTVHL 240

QY 315 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 374
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 300

QY 375 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFSCSYMHE 434
Db 301 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFSCSYMHE 360

QY 435 ALNHHYTKQSLSPGK 451
Db 361 ALNHHYTKQSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 67.5%; Score 1628.5; DB 2; Length 377;
 Best Local Similarity 82.0%; Pred. No. 1.6e-86;
 Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 122 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSS 181
 Db 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSS 60

QY 182 GLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKV----- 219
 Db 61 GLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKV----- 120

QY 220 -----EPKSCDKTHTPCPCAPPELLGGPSVFLFPPPKPDT 254
 Db 121 DTPPPCPRCPEPKSCDTPPCPCPEPKSCDTPPCPCAPPELLGGPSVFLFPPPKPDT 180

QY 255 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLVTLVH 314
 Db 181 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLVTLVH 240

QY 315 QDWLNGKEYCKVSNKALPAPIETKISKAKQPREPOVYITLPPSRDELTKNQVSLTCLVK 374
 Db 241 QDWLNGKEYCKVSNKALPAPIETKISKAKQPREPOVYITLPPSRDELTKNQVSLTCLVK 300

QY 375 GFYPDSIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRWQOGNVFSCSVNHE 434
 Db 301 GFYPDSIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRWQOGNVFSCSVNHE 360

QY 435 ALHNHYTQKSLSLSPGK 451
 Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 4
 G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
 C:Accession: A93906; A92809; A90752; A93132; A02148
 R:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 A:Reference number: A93906; MUID:82197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: GB:V00554; GB:J00230; NID:q32759; PIDN:CAB58438.1; PID:96066056
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein T11
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132

A:Molecule type: protein
 A:Residues: 238-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.5%; Score 1604; DB 1; Length 326;
 Best Local Similarity 91.2%; Pred. No. 3.5e-85;
 Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 122 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSS 181
 Db 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSS 60

QY 182 GLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKVFPKSCDKTHTPCPCAPPELLGG 241
 Db 61 GLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKVFPKSCDKTHTPCPCAPPELLGG 241

QY 242 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 301
 Db 117 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 176

QY 302 STYRVVSVLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRW 421
 Db 177 STYRVVSVLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRW 236

QY 362 LTKNQVSLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRW 421
 Db 237 MTKNQVSLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSFFLYSLTKVDSKRW 296

QY 422 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 451
 Db 297 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 326

RESULT 5
 G4HU
 Ig gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
 R:Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: The sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.0%; Score 1590.5; DB 1; Length 327;
Best Local Similarity 90.9%; Pred. No. 2.1e-84;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

Qy 122 ASYKGPSVFLPSSKSTSGTAAALCLVKDYPPEVTVSNWNGALTSVHFPVAVLQSS 181
Db 1 ASYKGPSVFLPSPKSTSESTAAALCLVKDYPPEVTVSNWNGALTSVHFPVAVLQSS 60
Qy 182 GLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCTPCPAPELLGG 241
Db 61 GLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCTPCPAPELLGG 117
Qy 242 PSVFLFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDVEVHNKAKYPREQYN 301
Db 118 PSVFLFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDVEVHNKAKYPREQYN 177
Qy 302 STYRWVSVLTVLHQLDNLNGEYKCKYSNKPALPAIEKTIKSKAGQPREQVYTLPSRDE 361
Db 178 STYRWVSVLTVLHQLDNLNGEYKCKYSNKPALPAIEKTIKSKAGQPREQVYTLPSQEE 237
Qy 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGGFFLYSKLTVDKSRW 421
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGGFFLYSKLTVDKSRW 297
Qy 422 QQGNVFCVSNHEALHNHYTQKSLSLSPGK 451
Db 298 QEGNVFCVSNHEALHNHYTQKSLSLSPGK 327

RESULT 6
S22080
Ig heavy chain precursor (B/Mt.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A:Reference number: S06610; MUID:90097956; PMID:2513487
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 1513; DB 2; Length 470;
Best Local Similarity 64.2%; Pred. No. 8.9e-80;
Matches 292; Conservative 55; Mismatches 100; Indels 8; Gaps 6;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNASMGVWRQAPGKLEWVSGISGGSGTYY 60
Db 20 QVQLRESGFLVLPKPSQTLISLCTVSGFSLSYALTWRQAPGKALEWVGIT--SGGTYY 78
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYIYCAKHTGGVWDP--IDYWGQGTILVT 118
Db 79 NPALKSRLSITKENSQVLSVSVTPEDTATYICARSTYGEVGDGAIADAMGQGLLVT 138
Qy 119 VSSASTKGPSVFLPAPSSKSTSGTAAALCLVKDYFPEPTVSNWNGALTSVHFPVAVL 178
Db 139 VSSATTTAPKVPYLPSSCCGDKSSSTVTLGCLVSYMPEPVTVWNSGALKSGVHTFPVAVL 198
Qy 179 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCTPCPAPEL 238
Db 199 QSSGLYSLSVWTVPGTSG--QTFTCNVAHPASSTKVDKAVDP--TC-KPSPCDCCPPEL 255
Qy 239 LGGPSVFLFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDVEVHNKAKYPREE 298
Db 256 PGGPSVFLFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDVEVHNKAKYPREE 315
Qy 299 QYNSYRVVSVLTVLHQLDNLNGEYKCKYSNKPALPAIEKTIKSKAGQPREQVYTLPPS 358
Db 316 QYNSYRVVSVLTVLHQLDNLNGEYKCKYSNKPALPAIEKTIKSKAGQPREQVYTLAPP 375
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSGGFFLYSKLTV 416
Db 376 QEELSKSTVSLTCMVTSTFVPDYIAVEWQNGQPESEDKYGTTPQLDADSSYFLYSLRV 435
Qy 417 DKSRNQGNVFCVSNHEALHNHYTQKSLSLSPGK 451
Db 436 DRNSWQEGDTYTCVYVWHEALHNHYTQKSTKSAGK 470

RESULT 7
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kanachi, M.; Harada,
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
A:Reference number: J05810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 62.2%; Score 1499.5; DB 2; Length 444;
Best Local Similarity 61.0%; Pred. No. 5e-79;
Matches 278; Conservative 73; Mismatches 88; Indels 17; Gaps 7;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGIS--GSGGST 58
DB 1 EQVAVETGGGLVLRGNSLKSLTSLTFTSNYRHHMLRQPPGKRLEWIAVITVKSNDYGA 60
QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVW-DFPIDYWGQGLTV 117
DB 61 KYAESVGRGFTISRDKSSVYLQMLNRLREEDTATYYCCRT- ---WVYAWDCWGQGTSV 116
QY 118 TVSNASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAP 177
DB 117 IVSSAKTTPPSVFLPAPGSAATNSMTVTLGCLVKGYFPEPTVTWNSGLSGVHTFPAP 176
QY 178 LQSSGLYSLSSVWTPSSSLGTQYICNVNHPKSNKVDKKVPKSCDKTHTCPP--CPA 235
DB 177 LQSD-LYTLSSSVTPSSWPEITVTCNVAHPASSTKVDKKIVPRDGG---CKPCICTV 231
QY 236 PELGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 295
DB 232 PEV---SSVTFPPKPKDVLITITPKVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTP 288
QY 296 REEQNSTYRVVSVTLVHODWLNKGEYCKVSNKALPAPIETKISKAGQPREPOVYTL 355
DB 289 REEQNSTFRSVSELPIMHQDWLNKGEYCKRVNSAAPPAPIETKISKGRKAPQVYTI 348
QY 356 PPSRDELTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSKIT 415
DB 349 PPKPEQAKDKVSLTCDITDFPEPDITVQWQNGQPAENYKNTQIMTDTGVSFVYSKLN 408
QY 416 YDKSPWQGNVFCSCVMHEALHNHYTKSLSPGK 451
DB 409 VOKSNWEAGNTFTCSVLHLEGLHNHTTKSHSPGK 444

RESULT 8
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 1451.5; DB 2; Length 469;
Best Local Similarity 59.8%; Pred. No. 3e-76;
Matches 271; Conservative 71; Mismatches 106; Indels 5; Gaps 4;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTY 60
DB 20 QIQLOQSGPELVKPCASVKISKASGYFTDYIINWVKQPGQGLKWIWYFASGNTKY 79
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 80 NENFKGKATLVDTSSSTAYMQLSSTSEDVAVYFCARMGATA-TLLDYWGQGLTVTS 138
QY 121 SASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAPVLOS 180
DB 139 SAKTTPAPSVFLPAPCGDTTSGSVTLGCLVKGYFPEPTVLTWNSGSLSSGHTFPAPVLOS 198
QY 181 SGLYSLSSVWTPSSSLGTQYICNVNHPKSNKVDKKVPKSCDKTHTCPP--CPAPEL 238
DB 181 SGLYSLSSVWTPSSSLGTQYICNVNHPKSNKVDKKVPKSCDKTHTCPP--CPAPEL 238

Query Match 59.5%; Score 1435; DB 2; Length 446;
Best Local Similarity 60.0%; Pred. No. 2.5e-75;
Matches 271; Conservative 69; Mismatches 104; Indels 8; Gaps 5;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTY 60
DB 1 QIQLOQSGPELVKPCASVKISKASGYFTDYIINWVKQPGGGLWIGWYFPGSNTKY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 61 NEKFKGKATLVDTSSSTAYMQLSSTSEDVAVYFCAR---GGKF-AMDYWGQGLTVTS 116
QY 121 SASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAPVLOS 180
DB 117 SAKTTPAPSVFLPAPCGDTTSGSVTLGCLVKGYFPEPTVLTWNSGSLSSGHTFPAPVLOS 176
QY 181 SGLYSLSSVWTPSSSLGTQYICNVNHPKSNKVDKKVPKSCDKTHTCPP--CPAPEL 238
DB 177 D-LYTLSSSVTPSSWPEITVTCNVAHPASSTKVDKKIEPRG-PTIKPCPCCKCAPNL 234
QY 239 LGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
DB 235 LGGPSVFLPAPKPKDKVLMISLPMVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTPQTHRE 294

DB 199 D-LYTLSSSVTPSSWPEITVTCNVAHPASSTKVDKKIEPRG-PTIKPCPCCKCAPNL 256
QY 239 LGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
DB 257 LGGPSVFLPAPKPKDKVLMISLPLVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTPQTHRE 316
QY 299 QYNSTYRVVSVFLVHODWLNKGEYCKVSNKALPAPIETKISKAGQPREQVYTLPPS 358
DB 317 DYNSTLRVVSALPIQHODWNSGKFEKCVNNKDLPAPIETKISKPGSVRAFPQVYVLP 376
QY 359 RDELTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSKITVDK 418
DB 377 EEMTKKQVLTICMTDFPEPDITVQWQNGQPAENYKNTQIMTDTGVSFVYSKLRVEK 436
QY 419 SRWQGNVFCSCVMHEALHNHYTKSLSPGK 451
DB 437 KMWERNYSYSCVVHLEGLHNHTTKSFRTPGK 469

RESULT 9

S40295
Ig gamma-2a chain (mab735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mab735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:227/Binding site: carbonylate (Asn) {covalent} #status experimental

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obara, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: The sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
R:Oillo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A:Cross-references: GB:J00461
R:Kim, H.; Yanaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A:Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:157-222/Domain: immunoglobulin homology <IMI>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 57.3%; Score 1382; DB 1; Length 474;
Best Local Similarity 56.8%; Pred. No. 3e-72;
Matches 260; Conservative 73; Mismatches 115; Indels 10; Gaps 3;
QY 1 QVOLQSGGGLVOPGGSRLRSCAASGFTFRSNAMGWVRQAPGKLEWYSGISGGSTYY 60
Db 20 EVOLQSGGPELVNPGASVSKSCASGYTFITYVHWVWKPGQGLEWIGYINPNKDGTF 79
QY 61 ADSVKGRTISRDNSKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 80 NEKFKGATLTVDKSSNTAYLHLSLSTSEDSAVYFCAGPRQVGLL-PFGYWGQGLTVTVS 136
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180
Db 198 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
Query Match 57.1%; Score 1376.5; DB 2; Length 475;
Best Local Similarity 57.2%; Pred. No. 6.1e-72;
Matches 262; Conservative 71; Mismatches 116; Indels 9; Gaps 4;
QY 1 QVOLVOSGGGLVOPGGSRLRSCAASGFTFRSNAMGWVRQAPGKLEWYSGISGGSTYY 60
Db 20 QVOLQSGAELARPGASVKLSCKASGYTLTSVGIWVKQRTQGLEWIGEIVPGSGNSYF 79
QY 61 ADSVKGRTISRDNSKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 80 NEKFKGATLTVDKSSNTAYLHLSLSTSEDSAVYFCAGPRQVGLL-PFGYWGQGLTVTVS 138
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180
Db 139 AAKTTPPSVYPLAPCGGDTTGSSTVLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
QY 181 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
Db 198 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
QY 234 PAPELGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
Db 258 PAPNLEGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
QY 294 KPREEQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVY 353
Db 318 QTHREDYNSTIRVVSALPQHQDWMSGKEFKCKVNNKDLPAPIETISKIKGLVRAQVY 377
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

Db 137 AAKTTPPSVYPLAPCGGDTTGSSTVLCGLVKGYFPESTVTVNSGSLSSSVHTLSQALLQ 196
QY 181 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTLSQALLQ 196
Db 197 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTLSQALLQ 196
QY 234 PAPELGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
Db 257 PAPNLEGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
QY 294 KPREEQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVY 353
Db 317 QTHREDYNSTIRVVSALPQHQDWMSGKEFKCKVNNKDLPAPIETISKIKGLVRAQVY 376
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
Db 377 ILPPPAEQLSRKDVSLTCLVGVFNPDISVEWTSGHTTEENYKDTAPVLDSDGSFYIYSK 436
QY 414 LTVDKSRMOQGNVFCSCVMHEALHNYTKLSLSPGK 451
Db 437 LNMKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPGK 474
RESULT 13
S01321
.. Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DEI>
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>
Query Match 57.1%; Score 1376.5; DB 2; Length 475;
Best Local Similarity 57.2%; Pred. No. 6.1e-72;
Matches 262; Conservative 71; Mismatches 116; Indels 9; Gaps 4;
QY 1 QVOLVOSGGGLVOPGGSRLRSCAASGFTFRSNAMGWVRQAPGKLEWYSGISGGSTYY 60
Db 20 QVOLQSGAELARPGASVKLSCKASGYTLTSVGIWVKQRTQGLEWIGEIVPGSGNSYF 79
QY 61 ADSVKGRTISRDNSKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 80 NEKFKGATLTVDKSSNTAYLHLSLSTSEDSAVYFCAGPRQVGLL-PFGYWGQGLTVTVS 138
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180
Db 139 AAKTTPPSVYPLAPCGGDTTGSSTVLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
QY 181 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
Db 198 SGLYSLSSSVTVPPSSSQTGSSVTLCGLVKGYFPESTVTVNSGSLSSSVHTFPALLQ- 197
QY 234 PAPELGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
Db 258 PAPNLEGGPSVFLPAPSKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKT 293
QY 294 KPREEQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVY 353
Db 318 QTHREDYNSTIRVVSALPQHQDWMSGKEFKCKVNNKDLPAPIETISKIKGLVRAQVY 377
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match	52.3%	Score 1260;	DB 4;	Length 255;
Best Local Similarity	97.5%	Pred. No. 1.5e-65;		
Matches 233;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

Qy 213 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 272
Db 17 TVAQADVESKCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy 273 EDPEVKENWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKAL 332
Db 77 EDPEVKENWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKAL 136

Qy 333 PAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 392
Db 137 PAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy 393 NNYKTTTPVLDSGSGFFLYSKLTVDKSRWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 451
Db 197 NNYKTTTPVLDSGSGFFLYSKLTVDKSRWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 255

Search completed: March 14, 2003, 11:51:09
Job time : 19.4344 secs

Db 378 ILSPPEQLSRKDVSLTCLAVGSPEDISVETNSNGHTSEENYKDTAPVLDSGSGYFIYSK 437

Qy 414 LVVDKSRWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 451

Db 438 LNMKTSKWEKTSFSCNVNHEGLKNYILKKTIISRSPGK 475

RESULT 14

I47159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47159

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153: 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124

C:Genetics:

A:Gene: IgG2a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match	52.4%	Score 1263;	DB 2;	Length 328;
Best Local Similarity	69.6%	Pred. No. 1.3e-65;		
Matches 231;	Conservative 43;	Mismatches 52;	Indels 6;	Gaps 2;

Qy 122 ASFKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 181

Db 1 APTAFSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVMNSGALSSGVHTFSPVLQPS 60

Qy 182 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPCPAPELLGG 241

Db 61 GLYSLSVTVTPASSLSKSYTCNVNHPATTTKVDKRVGKTKPPCPCIPACESP----G 116

Qy 242 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 301

Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 176

Qy 302 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 361

Db 177 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPHAE 236

Qy 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 419

Db 237 LSRKSVISITCLVTGFPDIDVEMQRNGQPEPEGNVRTTPQDDVDGTYFLYSKFSVDKA 296

Qy 420 RWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 451

Db 297 SWGGGIFQCAVMHEALHNHYTQKSLSKTPGK 328

RESULT 15

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C>Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C:Keywords: immunoglobulin

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 10.289 Seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALHNHYTKSLSLSPCK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1767	73.3	330	1 GCL_HUMAN	P01857 homo sapien
2	1604	66.5	326	1 GCL_HUMAN	P01859 homo sapien
3	1590.5	66.0	327	1 GCL_HUMAN	P01861 homo sapien
4	1230.5	51.0	323	1 GC_RABIT	P01870 oryctolagus
5	1216.5	50.5	329	1 GC2_CAVPO	P01862 cavia porce
6	1156	47.9	290	1 GC3_HUMAN	P01860 homo sapien
7	1152	47.8	326	1 GCL_RAT	P20759 rattus norv
8	1146.5	47.6	333	1 GCB_RAT	P20761 rattus norv
9	1142	47.4	324	1 GCL_MOUSE	P01868 mus musculu
10	1141	47.3	329	1 GC3_MOUSE	P22436 mus musculu
11	1137	47.2	393	1 GC1M_MOUSE	P01869 mus musculu
12	1130	46.9	398	1 GC3M_MOUSE	P03987 mus musculu
13	1126	46.7	330	1 GC2A_MOUSE	P01863 mus musculu
14	1123.5	46.6	335	1 GCB_MOUSE	P01864 mus musculu
15	1121	46.5	339	1 GCAM_MOUSE	P01865 mus musculu
16	1118.5	46.4	329	1 GCC_RAT	P20762 rattus norv
17	1112	46.1	322	1 GCA_RAT	P20760 rattus norv
18	1087	45.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1082	44.9	405	1 GCBM_MOUSE	P01867 mus musculu
20	492	20.4	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	20.1	429	1 EPC_RAT	P01855 rattus norv
22	471	19.5	117	1 HV3C_HUMAN	P01764 homo sapien
23	468	19.4	421	1 EPC_MOUSE	P06336 mus musculu
24	466.5	19.3	114	1 HV3B_HUMAN	P01763 homo sapien
25	456.5	18.9	122	1 HV3G_HUMAN	P01768 homo sapien
26	450.5	18.7	122	1 HV3A_HUMAN	P01762 homo sapien
27	449.5	18.6	116	1 HV3T_HUMAN	P01781 homo sapien
28	447	18.5	121	1 HV3J_HUMAN	P01771 homo sapien
29	444	18.4	454	1 MUC_HUMAN	P01871 homo sapien
30	440	18.2	455	1 MUC_MOUSE	P01872 mus musculu
31	439	18.2	458	1 MUC_RABIT	P03988 oryctolagus
32	438.5	18.2	116	1 HV05_CARAU	P19181 carassius a
33	437.5	18.1	122	1 HV3H_HUMAN	P01769 homo sapien

34	437.5	18.1	126	1 HV3K_HUMAN	P01772 homo sapien
35	435.5	18.1	136	1 HV16_MOUSE	P01783 mus musculu
36	435	18.0	115	1 HV3D_HUMAN	P01765 homo sapien
37	432	17.9	117	1 HV02_CANFA	P01785 canis famil
38	430	17.8	476	1 MUCM_MOUSE	P01873 mus musculu
39	429	17.8	479	1 MUCM_RABIT	P04221 oryctolagus
40	428	17.8	119	1 HV3I_HUMAN	P01770 homo sapien
41	427	17.7	115	1 HV3F_HUMAN	P01767 homo sapien
42	422.5	17.5	120	1 HV3U_HUMAN	P01782 homo sapien
43	422	17.5	457	1 MUC_SUNMU	P20768 suncus muri
44	419.5	17.4	119	1 HV3M_HUMAN	P01774 homo sapien
45	419	17.4	120	1 HV3E_HUMAN	P01766 homo sapien

ALIGNMENTS

RESULT 1
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments HI-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -I- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPE MARKER, 97-K, & THE
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
CC MARKER & THE GLM (NON-1) MARKERS.
CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR Genew; HGNC:5525; IGHL1.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 98
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223
FT DOMAIN 224 330 CH2.
FT DISULFID 27 83 CH3.
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT VARIANT 241 241
FT STRAND 123 126
N- LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY.
K -> R (IN GLM(3) MARKER).
/FTId=VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FTId=VAR_003887.
L -> M (IN GLM(NON-1) MARKER).
/FTId=VAR_003888.

FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT TURN 287 296
FT HELIX 297 301
FT STRAND 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
Query Match 73.3%; Score 1767; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.4e-114;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 122 ASTKGPSVFPLAPSKSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 181
DB 1 ASTKGPSVFPLAPSKSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
QY 182 GLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 241
DB 61 GLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
QY 242 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 301
DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 302 STYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYITLPPSRDE 361
DB 181 STYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYITLPPSRDE 240
QY 362 LFNKQVSLTCLVKGPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 421
DB 241 LFNKQVSLTCLVKGPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300
QY 422 QQGNVFSCVMHEALHNHYTOKLSLSLSPGK 451
DB 301 QQGNVFSCVMHEALHNHYTOKLSLSLSPGK 330
RESULT 2
GC2_HUMAN STANDARD; PRT; 326 AA.
ID GC2_HUMAN
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGUG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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Db 176 QYNTTFRVSVLPFIOHQDLRGKFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
QY 359 RDELTKNOVSLTCLVKGFPYSDIAVWESNGOP--ENNKTTPPVLDSDGSFFLYSKLTV 416
Db 236 RDELSKSKSVTCLLIINFFADHIVWASNRVPVSEKEYKNTPTPIEDADGSYFLYSKLTV 295
QY 417 DKSRWQGVNFCVSMVMEALHNHYTKSLSLSPG 450
Db 296 DKSANDQGVTVTCVMHEALHNHVTKAISRSPG 329

RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
ID GC3_HUMAN
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelen T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
Structure of the FC fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
REF.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CH1 REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).
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```

RESULT 7	GCL1_RAT	STANDARD;	PRT;	326 AA.
AC	GCL1_RAT	STANDARD;	PRT;	326 AA.
AC	P20759;			
DT	01-FEB-1991	(Rel. 17, Created)		
DT	01-FEB-1991	(Rel. 17, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ig gamma-1 chain C region.			
DE	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RI	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89232738; PubMed=3149946;			
RA	Brueggemann M.;			
RL	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";			
RL	Gene 74:473-482(1988).			
DR	PIR: PS0017; PS0017.			
DR	HSSP: P01842; 7FAB.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003597; Ig_CL.			
DR	Pfam: PF00047; Ig; 3.			
DR	SMART: SM00407; IGcl; 2.			
DR	PROSITE: PS00290; IG_MHC; 1.			
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.			
FT	NON_TER	1		
FT	DOMAIN	1	97	CH1.
FT	DOMAIN	98	112	HINGE.
FT	DOMAIN	113	219	CH2.
FT	DOMAIN	220	326	CH3.
FT	DISULFID	27	82	
FT	DISULFID	102	102	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	111	111	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	140	200	
FT	DISULFID	246	304	
FT	CARBOHYD	176	176	
FT	SEQUENCE	326 AA;	35946 MW;	013BAB45EF49B9DA CRC64;
FT	SEQUENCE	326 AA;	35946 MW;	013BAB45EF49B9DA CRC64;
QY	Query Match	47.8%;	Score 1152;	DB 1; Length 326;
Db	Best Local Similarity	63.1%;	Pred. No. 2.6e-72;	
Db	Matches 210;	Conservative 53;	Mismatches 60;	Indels 10; Gaps
QY	122	ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVLQSS	181	
Db	1	ATTETASVPLAPGALKNSMTGLGCLVGYPEPTVTWNSGALSSGVHTFPAVLQ-S 59	1	
QY	182	GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSCDKTHCTCPCPAPELGG	24H	
Db	60	GLYTLSSVTVTPSSWTPSQVTVCNVAHPASSTKVDKIVPRNCG--GDCKPC---ICTG	113	
QY	242	---PSVFLPPPKDGLMISTPEVTCVVVDVSDHEPEVKFNWYVDGVEVNAKTKPREE	298	
Db	114	SEVSSVFIIPPKPKDVLITLPKVTICVVDISQDDPEVHFQSFVDDVVEVHTAQRPEE	173	
QY	299	QYNSTYRVSVLTILHQLDWLNGKEYCKCKSNKALPAPIETKISKAKGQRPQVYTLPPS	358	
Db	174	QFNSTERSVSELPILHQLDWLNGRTFRCKVTSAAFPSPGIETKISKPEGRTPVHYTKSPT	233	
QY	359	RDELTKNOVSLCLVKGYFPPSDIAVENESNGQPENYKTPPVVLDSDGSFFLYSKLTVDK	418	
Db	234	KEWTONQSVITCMWKGYPDPDIVEWQMGQEQENYKNTPTPTMDTDSFYLYSKLVKK	293	
QY	419	SRMOQGNFVSCSMHEALRNHYTKQSLSLSPGK	451	
Db	294	EKWOQGNFTTCSVLHGLNHNHTKSLSHSGPGK	326	

AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=80045036; PubMed=6769752;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seldman J.G., Peterlin B.M., Leder P., Honjo T.; sequences
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salsler W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gamma chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC -----
 CC EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR EMBL; V00793; CAA24175.1; -;
 DR EMBL; V00795; CAA24176.1; -;
 DR EMBL; A02159; GIMS.
 DR HSP; P01842; 7FAB.
 DR GlycoSuiteDB; P01868; -;
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq-cl.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT

FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT /FTID=CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3DF2C93 CRC64;
 Query Match 47.4%; Score 1142; DB 1; Length 324;
 Best Local Similarity 62.0%; Pred. No. 1.3e-71;
 Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;
 Qy 122 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 181
 Db 1 AKTTPPSVYPLAPSGAAQTNSMVTGLGLVKGYRPEPTVTWNSGSLSSGVHTFPAVLQSD 60
 Qy 182 GLYSLSSVTVPSLSGLTQTYICNVNKPSTKVDKVKPEKSCDKTHTCPP--CPAPELL 239
 Db 61 -LYTLSSSVTVPSPPRPSETVTCNVAHPASSTKVDKXIVPRDCG-----CKPCICTVPEV- 114
 Qy 240 GGPSVFELPPPKDGLMTSRTPETVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
 Db 115 --SSVFIFPPPKDVLITITPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172
 Qy 300 YNSTYRVVSVLTIVLHQLNGKEYCKKYSNKKALPAPIETKISKAKGQPREPQVYTLPPSR 359
 Db 173 FNSITFRSVSELPIMHQLDNLCKEFCRVSAAFPAPIETKISKGRPKAPQVYTIPIPK 232
 Qy 360 DELTKNQVSLTCLVKGYFIPPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
 Db 233 EQMAKDKVSLTCDITDFEFDITVEQWNGQPAENYKNTQPIMTNGSYFVYSKLVQKS 292
 Qy 420 RWOOGNFECSVMHEALNHYTKQSLSLSPGK 451
 Db 293 NWEAGNTFTCSVLHGLEHNLHTEKSLSHSPGK 324
 RESULT 10
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
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 CC -----
 CC

Db 61 -LYTLSSSVTPSSPRPSETVTCNVAHPASSTKVDDKIVPRDCG----CKPCICTVPEV- 114

Qy 240 GGPVSFLFPKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREEQ 299

Db 115 --SSVFIKPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREEQ 172

Qy 300 YNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359

Db 173 FNSTFRSVELPIMHODWLNGKEFKCRVNSAFAPIEKTISKYGRKAPQVYTIIPPK 232

Qy 360 DDLTKNOVSLTCLVGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS 419

Db 233 EQWADKVSILCMITDFPEDITVWQNGQPAENYKNTQIPMTNGSYFYYSKLNQKS 292

Qy 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPG 450

Db 293 NNEAGNTFTCSVLHEGLHHHTKSLSHSPG 323

RESULT 12

GC3M_MOUSE STANDARD; PRT; 398 AA.

AC P03987;

DT 23-OCT-1986 (Rel. 02, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-3 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE=85027161; PubMed=6092053;

RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;

RT "Structural analysis of the murine IgG3 constant region gene.";

RL EMBO J. 3:2041-2046(1984).

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=84041483; PubMed=6314258;

RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,

RA Wall R.;

RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene segment.";

RL Nucleic Acids Res. 11:6775-6785(1983).

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CC -----

DR EMBL; J00451; AAB59655.1; -

DR EMBL; V01526; CAA24767.1; ALT_SEQ.

DR PIR; A02155; G3MSM.

DR HSSP; P01857; 1FCA.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003600; Ig-like.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00410; Ig-like; 1.

DR SMART; SM00407; IG1; 2.

DR PROSITE; PS00290; IG_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Transmembrane; Alternative splicing.

FT NON_TER 1 1

FT DOMAIN 97 CH1.

FT DOMAIN 98 113 HNGE.

FT DOMAIN 114 223 CH2.

FT DOMAIN 224 327 CH3.

FT TRANSMEM 346 362 POTENTIAL.

FT DOMAIN 333 338 CYTOPLASMIC (POTENTIAL).

FT CONFLICT 333 333 E -> G (IN REF. 2).

FT CONFLICT 342 342 E -> Q (IN REF. 2).

FT CONFLICT 388 388 P -> F (IN REF. 2).

SQ SEQUENCE 398 AA; 43929 MW; CF7E264B50A41B95 CRC64;

Query Match 46.9%; Score 1130; DB 1; Length 398;

Best Local Similarity 63.8%; Pred. No. 1.1e-70;

Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

Qy 123 STKGPSVFPPLAPSKSTSGTAALGLVXDYPPEPVTVSWNSGALTSQVHTTTPAVLQSSG 182

Db 1 TTTAPSVYPLVPGSDTSSTGSSVTLGLVKGYPPEPVTVKWNKGALSSGVRTVSSVLQ-SG 59

Qy 183 LYSLSVVTVTPSSSLGTQTQYICNVNHPKSNKVDKVEPKSCDKHTCP--PCPAPELLG 240

Db 60 FYSLSLVTVTPSSVTPQVTCVNAHPASKTELIIKKRIEPR-IPKSTPPGSSGCPGNIIG 118

Qy 241 GPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREQY 300

Db 119 GPSVFIKPKPKDMLSLTPKVTCCVVVDVSEDDPDVHVSWEVDNKEVHTAQTQPREAQY 178

Qy 301 NSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360

Db 179 NSTFRVVSALPIQHDMMRGKEFKCKVNNKALPAPIERTISKPKRAQTQPVYTIIPPRE 238

Qy 361 ELTKNOVSLTCLVKGYPVSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420

Db 239 QMSKKVSLVLTCLVTFNFFSEALSVEWERNGELODYKNTFPILDSDGTGYFLYSLKLTVD 298

Qy 421 WQGNVFCSCVMHEALHNHYTQKSLSLSP 449

Db 299 WLQGEITFCVWHEALHNHHTQKNLSRSP 327

RESULT 13

GCAA_MOUSE STANDARD; PRT; 330 AA.

AC P01863;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ig gamma-2A chain C region, A allele.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=81076554; PubMed=6777755;

RA Sikorav J.-L., Auffray C., Rougeon F.;

RT "Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";

RL Nucleic Acids Res. 8:3143-3155(1980).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=81198976; PubMed=6262729;

RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;

RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";

RL Nucleic Acids Res. 9:1365-1381(1981).

RN [3]

RN SEQUENCE FROM N.A.

RX MEDLINE=81223894; PubMed=6787604;

RA Ollio R., Auffray C., Mochamps C., Rougeon F.;

RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";

RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).

RN [4]

RP MYELOMA PROTEIN MOPC 173.


```

RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -----
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CC -----
DR EMBL; V00798; CAA24178.1; -
DR PTR; A02152; G2MSA.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.7%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. No. 1.6e-70;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 122 ASTGPGSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTAPSVPLAPVCGDGTGSSVTGLGCLVKGYFPEPTVLTWNSGSLSGVHTFPAVLQSD 60

QY 182 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPK-----CPAPELL 239
Db 61 -LVTLSSTVTSSTWPSQITCNVAHPASSTKVDKIEPRG-PITKPCPCCKCAPNLL 118

QY 240 GGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNNAKTPRESQ 299
Db 119 GGSVFIFPKIKDVLMLISLPIVTCVVDVSDPDVQISWFNVNVVHTAQTHRED 178

QY 300 YNSTYRWVSVLTLHODWLNKGVCKVSKNKPAPIEKTSKAKGQPREPOVYILPPSR 359
Db 179 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPGSVRAPOVYILPPE 238

QY 360 DELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419
Db 239 EEMTKQVLTLCMTVDPEMDIVVETWNTNGKTELKNTPEVLDSDGSFYFMYSKLRVEK 298

QY 420 RWOQGNVSCSVNHEALHNYTKQSLSPGK 451
Db 299 NWVERNSYSCSVVHEGLNHHHTTKFSRTPGK 330

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RESULT 14
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2a chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IGG2aa and IGG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 46.6%; Score 1123.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. No. 2.5e-70;
Matches 206; Conservative 53; Mismatches 70; Indels 7; Gaps 2;

QY 122 ASTGPGSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTAPSVPLAPVCGDGTGSSVTGLGCLVKGYFPEPTVLTWNSGSLSGVHTFPAVLQ-S 59

QY 182 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPK-----SCDKTHCPCPA 235
Db 60 GLYTLSSSTVTSNTWPSQTITCNVAHPASSTKVDKIEPRVPIQNCPPHQVRPCAA 119

QY 236 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNNAKTP 295
Db 120 PDLGGGSVFLFPKPKIKDVLMLISLSPVTCVVDVSDPDVQISWFNVNVVHTAQQT 179

QY 296 REEQYNSTYRWVSVLTLHODWLNKGVCKVSKNKPAPIEKTSKAKGQPREPOVYTL 355
Db 180 HREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNRNLPSLEKTSIKRPGVRAPQVYL 239

QY 356 PPSRDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 415

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:09 ; Search time 33.4392 Seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALNHVTKQSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2233.5	92.6	471	Q8TC77	Q8tc77 homo sapien
2	1864	77.3	473	Q8TC63	Q8tc63 homo sapien
3	1561.5	64.8	469	Q8R3V9	Q8r3v9 mus musculus
4	1543.5	64.0	437	Q9RIA4	Q9ria4 mus musculus
5	1522.5	63.1	473	Q91Z05	Q91z05 mus musculus
6	1483.5	61.5	463	Q99LC4	Q99lc4 mus musculus
7	1481.5	61.4	473	Q9D8L4	Q9d8l4 mus musculus
8	1453	60.3	468	Q99L31	Q99l31 mus musculus
9	1429.5	59.3	473	Q99L25	Q99l25 mus musculus
10	1397	57.9	474	Q8R3H6	Q8r3h6 mus musculus
11	1266.5	52.5	337	Q95M34	Q95m34 equus caball
12	1264.5	52.4	701	Q96P08	Q96p08 homo sapien
13	968.5	40.2	597	Q96BB9	Q96bb9 homo sapien
14	921	38.2	613	Q8WUK1	Q8wuk1 homo sapien
15	834	34.6	494	Q96K68	Q96k68 homo sapien
16	820.5	34.0	487	Q99KA4	Q99ka4 mus musculus

17	778.5	32.3	479	11	Q91WP5	Q91wp5 mus musculus
18	768.5	31.9	614	4	Q96GA6	Q96ga6 homo sapien
19	766	31.8	486	11	Q91Z07	Q91z07 mus musculus
20	755.5	31.3	480	11	Q91XE1	Q91xe1 mus musculus
21	747	31.0	278	11	Q921K1	Q921k1 mus musculus
22	738	30.6	613	11	Q8VCX7	Q8vcx7 mus musculus
23	728.5	30.2	597	4	Q9BU10	Q9bu10 homo sapien
24	725	30.1	613	4	Q96EY0	Q96ey0 homo sapien
25	722.5	30.0	597	4	Q9BQ88	Q9bqb8 homo sapien
26	721	29.8	484	11	Q8VEA0	Q8vea0 mus musculus
27	718.5	29.8	588	4	Q8WUX4	Q8wux4 homo sapien
28	718.5	29.8	618	4	Q96AA6	Q96aa6 homo sapien
29	711	29.5	573	4	Q8WU38	Q8wu38 homo sapien
30	702	29.1	496	4	Q96DK0	Q96dk0 homo sapien
31	696	28.9	496	4	Q96KX8	Q96kx8 homo sapien
32	692	28.7	500	4	Q9BRV0	Q9brv0 homo sapien
33	686.5	28.5	497	4	Q8WY24	Q8wy24 homo sapien
34	680	28.2	484	11	Q99LA6	Q99la6 mus musculus
35	678	28.1	482	11	Q91X92	Q91x92 mus musculus
36	675.5	28.0	481	11	Q91WT1	Q91wt1 mus musculus
37	661	27.4	488	11	Q91WR1	Q91wr1 mus musculus
38	655.5	27.2	416	4	Q9NPP6	Q9npp6 homo sapien
39	654.5	27.1	489	11	Q8VCX4	Q8vcx4 mus musculus
40	632.5	26.2	481	11	Q8VCV5	Q8vcv5 mus musculus
41	631.5	26.2	481	11	Q91WT3	Q91wt3 mus musculus
42	629	26.1	479	11	Q99W22	Q99w22 mus musculus
43	563.5	23.4	147	4	Q9Y509	Q9y509 homo sapien
44	536.5	22.3	426	11	Q9DCD9	Q9dcd9 mus musculus
45	507	21.0	121	4	Q9UL71	Q9ul71 homo sapien

ALIGNMENTS

RESULT 1

Q8TC77 ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAR24289.1; -
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match		92.6%	Score 2233.5;	DB 4;	Length 471;
Best Local Similarity		93.4%	Pred. No. 2.5e-174;		
Matches 423;		Conservative 9;	Mismatches 18;	Indels 3;	Gaps 2;
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLEWVSGISGGSTYY	60		
Db	20	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYNNWVQAPGKGLEWVSSMSSSSIYY	79		
Qy	61	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG--GGVWDPTIDYWGQGTFLVT	118		
Db	80	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG--GGVWDPTIDYWGQGTFLVT	138		
Qy	119	VSSASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPTVSWNSGALTSGVHTFPAVL	178		
Db	139	VSSASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPTVSWNSGALTSGVHTFPAVL	198		
Qy	179	QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDRKVEPKSCDKHTCTPCPAPEL	238		

Db 199 QSSGLYSLSSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPAPEL 258
QY 239 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db 259 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 318
QY 299 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 319 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 378
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 418
Db 379 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 438
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 439 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 77.3%; Score 1864; DB 4; Length 473;
Best Local Similarity 79.2%; Pred. No. 4.2e-144; Indels 8; Gaps 4;
Matches 359; Conservative 37; Mismatches 49;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTPRSN--MGWVRQAPGKGLWVSGISGGST 58
Db 27 RLQLESGLLKPSTLSLTCTVSGDSVASSSYWGVRQPPGKGLWIGTINFS-GNM 85
QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDIDYWGCGTLVT 118
Db 86 YSPSLRSRVTSADMSNSFYKLDSVTAADTAVYYCA--AGHLVMGFGAHWGQGLVS 143
QY 119 VSSASTKGPSVFLPAPSSKTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFPVAVL 178
Db 144 VSPASTKGPSVFLPAPSSKTSSESTAAALGLVKDYFPEPTVTSWNSGALTSVHTFPVAVL 203
QY 179 QSSGLYSLSSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPAPEL 238
Db 204 QSSGLYSLSSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPAPEL 260
QY 239 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db 261 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 320
QY 299 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 321 QFNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 380
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 418
Db 381 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 440
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

Db 441 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 3
Q8R3V9 PRELIMINARY; PRT; 469 AA.
ID Q8R3V9;
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 64.8%; Score 1561.5; DB 11; Length 469;
Best Local Similarity 63.5%; Pred. No. 2.3e-119; Indels 15; Gaps 6;
Matches 291; Conservative 66; Mismatches 86;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGI--SGSGGST 58
Db 20 EVNLVESGGGLVQPGGSLRLSCAASGFTFTDYMSVVRQPPGKALEWLGFIKANKGYTT 79
QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVW--DPIDYWGQGT 115
Db 80 EYSASVKGRTISRDNQSILYLMNALRAEDSATYCARDRSSYYSGTSFAYWGQGT 139
QY 116 LVTYSSASTKGPSVFLPAPSSKTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFP 175
Db 140 LVTYSAARTTPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTSWNSGSLSGVHTFP 199
QY 176 AVLQSSGLYSLSSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCP--C 233
Db 200 AVLQSD-LYTLSSSVTPSSSTWPSQTTCNVNHPASSTKVDKKIVPRDCG---CKPCIC 254
QY 234 PAPELLGGPSVFLPAPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
Db 255 TVPEV--SSVFIPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQ 311
QY 294 KPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
Db 312 KPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 371
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 413
Db 372 TIPPKEQMAKDKVSLTCMTIDFPEDITVWQWNGQPAENYKNTQPMIDTDSGYFYYSK 431
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 432 LNVQKSNWEAGNTFTCSVLHLEGLHNHHTKSLSHSPGK 469

RESULT 4
Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID Q9RIA4;
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AA040243.1; -
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT 437
FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
Query Match 64.0%; Score 1543.5; DB 11; Length 437;
Best Local Similarity 63.5%; Pred. No. 6.2e-118;
Matches 287; Conservative 67; Mismatches 81; Indels 17; Gaps 6;
QY 2 VQLVQSGGLVQPGGSLRLSQAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYYA 61
DB 1 VQLVQSGGLVQPGGSLRLSQAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYYA 61
QY 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVMDIDYWGQGLTVTVS 121
DB 60 DSVKGRFTISKDRNLTSLQMSLSRSEDYAMYYCAR-----GDYSAYWGPGTLTVSA 113
QY 122 ASTKGPVFPPLAPSSKSTSGTAAALGLVQKDYEPPEVTVSNWNGALTSVHTFPVQLQS 181
DB 114 AKTTPSVVPLAPGSAQAQNSWTLGLVKGYPPEVTVSNWNGALTSVHTFPVQLQSD 173
QY 182 GLYSLSSVTVPSSSLGTQTYICNVNKPNTKVDKVPKSCDKTHTCPP--CPAPELL 239
DB 174 -LVTSSSVTVPSSTPSEVTVTCNVNKPNTKVDKVPKSCDKTHTCPP--CPAPELL 227
QY 240 GGSVFLFPKPKDGLMISRTPEVTVVVDVSHEDPEYKFNWYVDGVEVHNAAKTPRE 299
DB 228 --SSVFLFPKPKDGLMISRTPEVTVVVDVSHEDPEYKFNWYVDGVEVHNAAKTPRE 285
QY 300 YNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPAEKTSKAKGQPREPVYTLPPSR 359
DB 286 FNSTERSVSLPIMHODWLNKKEYKCKVSNKALPAPAEKTSKAKGQPREPVYTLPPSR 345
QY 360 DELTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD 419
DB 346 EQAKDKVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD 405
QY 420 RWQGGNVFSCVMEALHNNHYTKQSLSLSPGK 451
DB 406 NWEAGNTFTCSVLHEGLHHHTKLNLSHPGK 437
RESULT 5
Q91205 ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
Query Match 63.1%; Score 1522.5; DB 11; Length 473;
Best Local Similarity 63.0%; Pred. No. 3.6e-116;
Matches 289; Conservative 64; Mismatches 93; Indels 13; Gaps 5;
QY 1 QVQLVQSGGGLVQPGGSLRLSQAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
DB 20 EVQLVESGGGLVQPGGSRKLSQAASGFTFSYDGMHWRQAPGKGLVWVAYINSGSTIYY 79
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVW-DPIDYWGQGLTVTV 119
DB 80 ADTVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVW----LWLRIDYWGQGLTVTV 135
QY 120 SSASTKGPVFPPLAPSSKSTSGTAAALGLVQKDYEPPEVTVSNWNGALTSVHTFPVQLQ 179
DB 136 SSASTKGPVFPPLAPSSKSTSGTAAALGLVQKDYEPPEVTVSNWNGALTSVHTFPVQLQ 195
QY 180 SGLYSLSSVTVPSSSLGTQTYICNVNKPNTKVDKVPKSCDKT-HTCPP----- 232
DB 196 -SGLYSLSSVTVPSSTPSEVTVTCNVNKPNTKVDKVPKSCDKTHTCPP----- 254
QY 233 CPAPPELLGSPVFLPFPKPKDGLMISRTPEVTVVVDVSHEDPEYKFNWYVDGVEVHNAAK 292
DB 255 CPAPNELGSPVFLPFPKPKDGLMISRTPEVTVVVDVSHEDPEYKFNWYVDGVEVHNAAK 314
QY 293 TKPREQVNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPAEKTSKAKGQPREPV 352
DB 315 TQTHREDNSTIRVVSALPIQHDWMSCKEYKCKVSNKALPAPAEKTSKAKGQPREPV 374
QY 353 YLPPEPDELTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYS 412
DB 375 YLPPEPDELTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYS 434
QY 413 KLTVDKSRWQGGNVFSCVMEALHNNHYTKQSLSLSPGK 451
DB 435 KLDIKTSKWEKTSFSCNVRHEGLKNNYKTKTISRSPGK 473
RESULT 6
Q991C4 ID Q991C4 PRELIMINARY; PRT; 463 AA.
AC Q991C4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 61.5%; Score 1483.5; DB 11; Length 463;
Best Local Similarity 59.6%; Pred. No. 5.5e-113;
Matches 270; Conservative 78; Mismatches 94; Indels 11; Gaps 5;

QY 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
DB 20 QVQLQSGAELARPGASVRLSKASGYTFTGYGVSWVKQRTGQGLEWGEIYPGSGNTYY 79
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
DB 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSDSAVYFCARSSYYYS-YDLFAYWGQGLTVTVS 138
QY 121 SASTKGPSVFPPLAPSKSTSGGTAALGLVQDYFFPEPTVTVSNAGLTSGVHTFPVAVLOS 180
DB 139 AAKTTPPSVYPLAPGSAAGTNSMVTLGCLVKGYPPEPTVTVWNSGSLSGSVHTFPVAVLOS 198
QY 181 SGLYSLSSVYVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKCDKTHTCPP--CPAPEL 238
DB 199 D-LYTSSSVYVTPSSVTPWSPSETVCNVAHPASSTKVDKKVLRDCCG----CKPCICTVPEV 253
QY 239 LGGPSVFLFPKPKDLMISRTPEVTCVYVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
DB 254 ---SSVFIPPKPKDVLITLTPKVKTVVVDISKDPEQVSWFVDVDEVHTAQTPREE 310
QY 299 QYNSTVRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
DB 311 QFNSTFRSVSELPIMHQDWLNGKEFKRVSNAAPPAIEKTIKTKGRPKAPQVYTIPTPP 370
QY 359 RDELTKNOVSLTCLVKGFPDIAVWESNGOPENNYKTPPVLDSDSGFFLYSKLTVDK 418
DB 371 KEQMAKDVKSLTICWITDFPEDITVQWQNGQPAENYKNTQIMDTDGSFYIYSKLNQVK 430
QY 419 SRMQQGVSCSYVMHEALHNHYTKSLSLSPGK 451
DB 431 SNWEAGNTFTCSVLHEGLHNHHTPEKSLSLSPGK 463

RESULT 7
Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 181006009RIK protein.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohcsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 61.4%; Score 1481.5; DB 11; Length 473;
Best Local Similarity 59.5%; Pred. No. 8.2e-113;
Matches 272; Conservative 76; Mismatches 100; Indels 9; Gaps 3;

QY 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
DB 20 QVQLKQSGAELVKGASVVKISKASGYTFTDYINWQKRPQGQGLEWIGIGPGSGSTYY 79
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
DB 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR--SGDYDFWFAWQGLTVTVS 137
QY 121 SASTKGPSVFPPLAPSKSTSGGTAALGLVQDYFFPEPTVTVSNAGLTSGVHTFPVAVLOS 180
DB 138 AAKTAPSVYPLAPVCGGTGSSVTLGCLVKGYPPEPTVTVWNSGSLSGSVHTFPALLQ- 196
QY 181 SGLYSLSSVYVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPK-----SCDKTHTCPPCP 234
DB 197 SGLYTLSSSVTVTNTWPSQTITCNVAHPASSTKVDKKIEPRVPIQNCPPLKECPPCA 256
QY 235 APELLGSPSVFLFPKPKDLMISRTPEVTCVYVVDVSHEDPEVKFNWYDGVGVHNAKTK 294
DB 257 APDLGGSPSVFIFFPKIKDVLMLSLSPWTCVYVVDVSEDDPDVQISWFNWVEVHTAQTK 316
QY 295 PREEQYNSTVRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYT 354
DB 317 THREDYNSTLRVVSALPIQHDWMSGKFEKCKVNNRALSPIEKTISKPRGPVRAPOVYV 376
QY 355 LPPSRDELTKNQVSLTCLVKGYFSDIAVWESNGQPENNYKTPPVLDSDSGSFYSLSKL 414
DB 377 LPPPAEEMTKFEFSLTCTMITGLFPAEIAVDWTSNQTQNTATVLDSDSGSFYSLSKL 436
QY 415 TVDKSRWQGVNFGVSCVMHEALHNHYTKSLSLSPGK 451
DB 437 RVQKSTWERSGLFACSVVHEGLHNHLLTKTISRSLGK 473

RESULT 8
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 181006009 gene.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGcl; 3.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 60.3%; Score 1453; DB 11; Length 468;
Best Local Similarity 60.6%; Pred. No. 1.7e-110;
Matches 275; Conservative 64; Mismatches 107; Indels 8; Gaps 5;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSIGSGGSTYY 60
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 EVQLQSGAEALVRPGASVKLSCTASGFTFRSNAMGWVRQAPGKGLVWSIGSGGSTYY 79
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKH-TGGGVWDPIDYWGQGLTVT 119
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 APKFDKATITADSSNTAYLQSLTSEDTAIYCARNLGYGYY---DYWGQGLTIV 136

QY 120 SSASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 179
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 SSATKTPSVPLAPVCGDITGSSVTLGCLVKGYFPEPVTVSNMGSALTSGVHTFPAVLQ 196

QY 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCPP--CPAPE 237
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 SD-LYTLSSVTVTSSTWPSQITCNVAHPASSTKVDKKEPKSCDKTHTCPP--CPAPE 254

QY 238 LIGGPSVFLPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 297
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 LLGPSVFIFPPKIKDVLMIKSLSPWTCVVDVSEDDPDVQISFWFNNVEVLTAQTQTHR 314

QY 298 EQYNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPREPVTLPP 357
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 EDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIETKISKPKGSVRAPQVTLPP 374

QY 358 SRDELTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 417
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 PEEETMKQVTLTCMVTDMPEDIIYVEWTNNGKTELNYKNTPEVLDSDGSFFLYSKLTVD 434

QY 418 KSRVQGNVFCVSMHEALHNYTKOKSLSLSPGK 451
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 KKNWVERNSISCVVHEGLHNNHHTTKSFSRTPGK 468

RESULT 9
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGcl; 3.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 59.3%; Score 1429.5; DB 11; Length 473;
Best Local Similarity 59.0%; Pred. No. 1.5e-108;
Matches 270; Conservative 69; Mismatches 108; Indels 11; Gaps 5;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSIGSGGSTYY 60
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLQSDAELVKPGASVKISCKVSGYTFDTHIHWVKQRPQGLEWIGYIYPRDGSYKY 79
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKH-TGGGVWDPIDYWGQGLTVT 115
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSR--GGSIYGYGLYFYDWGQGT 137

QY 116 LVTVSASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSNMGSALTSGVHTFP 175
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 TITVSSAKTAPSVPLAPVCGDITGSSVTLGCLVKGYFPEPVTVSNMGSALTSGVHTFP 197

QY 176 AVLQSGSLYSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCPP--C 233
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 AVLQSD-LYTLSSVTVTSSTWPSQITCNVAHPASSTKVDKKEPKSCDKTHTCPP--C 255

QY 234 PAPELLGGPSVFLPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTK 293
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 PAPNLGGPSVFLPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTK 315

QY 294 KPREEQYNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVY 353
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 QTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIETKISKPKGSVRAPQVY 375

QY 354 TLPPSRDELTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 VLPPPEEEMTKQVTLTCMVTDMPEDIIYVEWTNNGKTELNYKNTPEVLDSDGSFFLYSK 435

QY 414 LTVDKSRVQGNVFCVSMHEALHNYTKOKSLSLSPGK 451
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 LRVEKKNWVERNSISCVVHEGLHNNHHTTKSFSRTPGK 473

RESULT 10
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AA025447.1; -.
DR Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

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Query Match          57.9%; Score 1397; DB 11; Length 474;
Best Local Similarity 57.6%; Pred. No. 6.7e-106;
Matches 264; Conservative 72; Mismatches 112; Indels 10; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLCAASGFTFRSNAMGWVROAPKGLGWVSGISGSGGTY 60
Db 20 QVQLVQSGGGLVQPGGSLRLCAASGFTFRSNAMGWVROAPKGLGWVSGISGSGGTY 79
QY 61 ADSVKGRTISRDNSKNTLYLQMSNRAEDTAYVYCAKHTGGVNDPDIYWGQGLTVTS 120
Db 80 SGKFGQKAKLTADKSSVTAFQLTSLTSDSAVYFCARDSDYG--DYDFDQGGQATVTS 137
QY 121 SASTKGPSVFPLAPSSKSTSGGTAAALGLVLDYFPEPTVTVSNAGALTSVGHVTFPAVLQS 180
Db 138 SAKTTPSPVYPLAPGCGDTGSSVTLGLVLDYFPEPTVTVSNAGALTSVGHVTFPAVLQS 196
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKT--HTCPP-----C 233
Db 197 SGLYTWSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKT--HTCPP-----C 256
QY 234 PAPELLGGSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNATK 293
Db 257 PAPNLEGGSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNATK 316
QY 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 353
Db 317 QTHREDYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 376
QY 354 TLPPSRDELTKNOVSLTCLVKGYPSDIAVEVESNQPNKYTKTISKAKGQPREPQVY 413
Db 377 ILPPPAEQLSRKDVSLTCLVKGYPSDIAVEVESNQPNKYTKTISKAKGQPREPQVY 436
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 437 LDIKTSKWEKTSFSCNVRHGLKNLYLKTIISRSPEK 474

RESULT 11
Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region
DE (Fragment).
GN IGHCI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
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Query Match 52.5%; Score 1266.5; DB 6; Length 337;
Best Local Similarity 69.2%; Pred. No. 2e-95;

```
Matches 234; Conservative 43; Mismatches 52; Indels 9; Gaps 3;

QY 122 ASTKGPSVFPLAPSSKSTSGGTAAALGLVLDYFPEPTVTVSNAGALTSVGHVTFPAVLQS 181
Db 1 ASTAPKVFALAPCGGTSDSTVALGCLVSGYFPEPVKVSWSNGLTSGVHTFPSVLQSS 60
QY 182 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEP-----KSCDKTHTCPPCPA 235
Db 61 GFYSLSNMVTPASWTSETYICNVVHAASFVKDKRIEIPDNHOKVCDMS-KCPKCPA 119
QY 236 PELGGSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNATK 295
Db 120 PELGGSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNATK 179
QY 296 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 355
Db 180 KEEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 239
QY 356 PPSRDELTKNOVSLTCLVKGYPSDIAVEVESNQPNKYTKTISKAKGQPREPQVY 413
Db 240 APHDELKSKSVSLTCLVKGYPSDIAVEVESNQPNKYTKTISKAKGQPREPQVY 299
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 300 LSVDRNRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 337

RESULT 12
Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98;12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 9AC6CEB42CC92F CRC64;
```

Query Match 52.4%; Score 1264.5; DB 4; Length 701;
Best Local Similarity 70.1%; Pred. No. 8.1e-95;

QY	178	LOSSGLSSLVVTPSSSL--GTQTY-ICNVNHKPSN-----TKVDKKVE	220
Db	199	LR-GGKYAATSQVLLPSKDVNMQGTDEHVCKVQHPNGKKNVPLPVIAELPKVSVFVP	257
QY	221	PKS-----CDKTHTCP-----PCPAPELLGSPS----	243
Db	258	PRDGGFNGPRKSLICQATGFSRQIQVSWLREGKQVSGVTTDQVQAERAKESGPTTKV	317
QY	244	-----VFLEPPKPKDTLMIS	258
Db	318	TSTLTIKESDMSMFTCRVDHRLGLTFQNASCMKVPDQDTAIRFAIPPS-FASIFLT	376
QY	259	RTPEVTCVVVDVSHEDPEVKENWTVGDVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL	318
Db	377	KSTKLTLVTLTIYD-SVTISWTRQNGEAVKTHTNISESHPNATESAVGEASICEDDWN	435
QY	319	NGEYKCKVSNKALPAPIEKTISKAKGQ-REPOQVYTLPPSRDELTKNQVSLTCLVKGF	376
Db	436	SGERTCTVTHDLPSPLKQTIISRPKGVALHRPDPVYLLPPAREQLNRESATITCLVTGF	495
QY	377	YPSDIAVWESNGQP--ENNYKTTTPVLD--SDGSFFLYSKLTVDKSRWQQGNVFCGVM	432
Db	496	SPADVFOVMQMGQPLSPEKVTSAHPPEQAPGRYFAHSILTVSEBEWNTGETYTCVA	555
QY	433	HEALHNHYTKQSLSL 448	
Db	556	HEALPNRVTERTVDKS 571	
RESULT 15			
ID	Q96K68	PRELIMINARY; PRT; 494 AA.	
AC	Q96K68;		
DT	01-DEC-2001 (TremBLrel. 19, Created)		
DT	01-DEC-2001 (TremBLrel. 19, Last sequence update)		
DE	CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=MAMMARY GLAND;		
RA	Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagehara K., Masuho Y., Ninomiya K., Iwayanagi T.;		
RT	"NEDO human cDNA sequencing project.";		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK027379; BAB55072.1; -.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	Pfam; PF00047; Ig_4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		
SQ	SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEB4C0E CRC64;		
Query Match 34.6%; Score 834; DB 4; Length 494;			
Best Local Similarity 41.8%; Pred. No. 8.1e-60;			
Matches 199; Conservative 62; Mismatches 171; Indels 44; Gaps 16;			
QY	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVRAQPKGLEWYSGISGGSTYY	60
Db	20	EVLQVESGGGLVQPKGSLRLSCAASGLSFSTYAMNVRQAPKGLEWVSSISRSDIYY	79
QY	61	ADSVKGRFTISRDNKNTLYLQMNSLRAREDATVYYCAKHT--GGGVWDPIDVWGQGLTVV	119
Db	80	RDSVKGRFTISRDNKNTLYLQMNSLRVDVDTAVYYCARDSCNGAICYGFSFWGQGLTVV	139
QY	120	SSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP-EPVTVSNWNSGALTSGVHTFPAVL	178

Db	140	SSASPTSPRVFFPLSLCS-TQPDGNVVIACLVQGFPPQLSVTWSESGQGVTAARFPSPQ	198
QY	179	QSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPSNNTKVDKVEPKSCDKTHTCCPPCAP	236
Db	199	DASGDLTYTSSQLTLPATOCLAGKSVTCHVKHY-TNPSQDVT-----PCPVP	245
QY	237	ELIGGFSVFLFPKPK-----DTLMISRTPEVTCVVVDVSHEDPEVKPNW	281
Db	246	STPPTPSPST-PPTPSPSCCHPRLSLHRLPALEDLLLGSEANLTCLTGL-RDASGVTFW	303
QY	282	YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS	341
Db	304	TPSSGK--SAVOGPPPRDLCCGYSSVSLPGCAEPWNHKGTFCTAAIPESKTPLTATLS	361
QY	342	KAGQPREPOVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVWESNGQ--PENNYKTT	398
Db	362	KS-GNTFRFEVHLLPPSEELALNELVTLTCLARGSPKDLVLRWLQSGQELPREKYLTV	420
QY	399	PPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFCGVMHEALHNHYTKQSLSLSPGK	451
Db	421	ASRQEPSQGTTFPAVTSILRVAEDWKGDTFSCMVGHEALPLAETQKTIDRLACK	476

Search completed: March 14, 2003, 11:49:38
Job time : 35.4392 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 34.7681 Seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1990	100.0	381	AAE12707	Human bivPH1-IL-2
2	1289	64.8	409	AAU04945	Humanised anti-p18
3	1217	61.2	524	AAAY4995	HD70scFv-Ck-interl
4	1072.5	53.9	582	AAAB1987	Ganglioside GD3 sp
5	1052	52.9	281	AAW27560	Consensus single c
6	1027.5	51.6	582	AAAB1991	Ganglioside GD3 sp
7	1002.5	50.4	262	ABP46070	Human BlyS binding
8	987.5	49.6	248	AAAG6590	Anti-hdFv antibody
9	982	49.3	456	AAAY4992	M79scFv-interleuki
10	980	49.2	450	AAAY4991	M79scFv-interleuki

11	969	48.7	581	22	AAAB81972	Ganglioside GD2 sp
12	943	47.4	583	22	AAAB83156	Ganglioside GM2 an
13	914.5	46.0	244	23	ABP45980	Human BlyS binding
14	909	45.7	249	22	AAAB20434	Anti-FIX/FIXa anti
15	883.5	44.4	384	22	AAAM24101	Human EST encoded
16	881	44.3	384	22	AAU14461	Human novel protei
17	881	44.3	384	22	AAU14462	Human novel protei
18	881	44.3	384	22	AAU14463	Human novel protei
19	881	44.3	384	22	AAU14464	Human novel protei
20	879	44.2	307	22	AAU14425	Human novel protei
21	874.5	43.9	247	23	AAU90900	Insulin/insulin-li
22	874.5	43.9	312	22	AAU14227	Human novel protei
23	870	43.7	238	21	AAV53775	An antibody with i
24	862	43.3	247	14	AAAB32091	H and L chain Fv r
25	862	43.3	249	14	AAAB32090	H and L chain Fv r
26	862	43.3	249	17	AAAB5213	Heavy and light ch
27	860.5	43.2	240	20	AAAY02472	A single chain ant
28	858	43.1	249	13	AAAB21262	psCFvNq11 encodin
29	849.5	42.7	240	22	AAAB46040	Human TF anti-idio
30	846.5	42.5	222	22	AAU04972	Synthetic antibody
31	846.5	42.5	233	17	AAAB93013	Lewis-Y antibody B
32	844	42.4	233	16	AAAB72599	Anti-dansyl single
33	843.5	42.4	222	22	AAU04976	Synthetic antibody
34	842	42.3	293	22	AAAG65715	Amino acid sequenc
35	840.5	42.2	240	22	AAAB46046	Human TF anti-idio
36	838.5	42.1	222	22	AAU04974	Synthetic antibody
37	838	42.1	239	23	ABP45911	Human BlyS binding
38	833.5	41.9	240	22	AAAB46038	Human TF anti-idio
39	832.5	41.8	240	22	AAAB46018	Human MUC-1 scFv c
40	831.5	41.8	240	22	AAAB46044	Human TF anti-idio
41	831.5	41.8	240	22	AAAB46045	Human TF anti-idio
42	828.5	41.6	240	22	AAAB45999	Human MUC-1 scFv c
43	828.5	41.6	240	22	AAAB46006	Human MUC-1 scFv c
44	828.5	41.6	240	22	AAAB46042	Human TF anti-idio
45	827.5	41.6	240	22	AAAB46005	Human MUC-1 scFv c

ALIGNMENTS

RESULT 1
AAE12707
ID AAE12707 standard; Protein; 381 AA.
AC AAE12707;
XX
XX
XX
DT 04-JAN-2002 (first entry)
DE Human bivPH1-IL-2 immunocytokine protein.

XX
XX
OS Homo sapiens.
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.

XX
XX
PI Hoogenboom HRJM, Henderikx MPG;
XX
DR WPI; 2001-626437/72.
XX
DR N-PSDB; AAD20732.

XX
XX
PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Claim 9; Page 95-97; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human bivPHI-IL-2
 CC immunocytokine protein. bivPH1 is mucin specific binding portion.
 XX Sequence 381 AA;
 SQ

Query Match 100.0%; Score 1990; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 9.9e-132;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVQAQPGKLEWVSGISGGSTYY 60
 DB 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVQAQPGKLEWVSGISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
 QY 121 SGGGALEIVLTQSPSLPTPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIY 180
 DB 121 SGGGALEIVLTQSPSLPTPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIY 180
 QY 181 SGSHRASGVDPDRFSGSVSGTDTLRLSRVEADGVYVCMQGLQSPFTFGPGTKVDIKRG 240
 DB 181 SGSHRASGVDPDRFSGSVSGTDTLRLSRVEADGVYVCMQGLQSPFTFGPGTKVDIKRG 240
 QY 241 GSGGGALAPTSSTSKTKTQLEHLLDQLMILNGINNYKNPKLTRLTFKPYMPKKATE 300
 DB 241 GSGGGALAPTSSTSKTKTQLEHLLDQLMILNGINNYKNPKLTRLTFKPYMPKKATE 300
 QY 301 LKHLCLEELKPLEVLNLAQSKNPHLRPRDLISNINIVILELKGSETFMCEYADETA 360
 DB 301 LKHLCLEELKPLEVLNLAQSKNPHLRPRDLISNINIVILELKGSETFMCEYADETA 360
 QY 361 TIVEFLNRWITTCQSIISTLT 381
 DB 361 TIVEFLNRWITTCQSIISTLT 381

RESULT 2
 AAU04945
 ID AAU04945 standard; Protein; 409 AA.
 XX
 AC AAU04945;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Humanised anti-pl85 antibody/IL-2 fusion protein.
 XX
 KW Humanised; antibody; pl85; 520C9H; interleukin-2; IL-2; immunoconjugate;
 XX cancer; tumour; adenocarcinoma; fusion protein.
 OS Chimeric - Home sapiens.
 OS Chimeric - Mus sp.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Peptide 1..22 /label= Signal_peptide
 FT Protein 23..409 /label= Mature_fusion_protein
 FT Protein 23..259 /label= Humanised_antibody_520C9H
 FT Region 53..57 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 72..88 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 121..126 /label= CDR
 FT /note= "Complementarity determining region"
 FT Misc-difference 123 /note= "Encoded by GGG"
 FT Peptide 138..152 /label= Synthetic_peptide_linker
 FT /note= "Links the heavy chain to the light chain"
 FT Region 176..186 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 202..208 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 241..249 /label= CDR
 FT /note= "Complementarity determining region"
 FT Peptide 261..276 /label= Synthetic_peptide
 FT /note= "Links the antibody to the IL-2 molecule"
 FT Protein 277..409 /label= IL_2
 FT Misc-difference 406 /note= "Encode by ACA"
 XX WO200153354-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001WO-US01919.
 XX 20-JAN-2000; 2000US-0177258.
 XX (CHIR) CHIRON CORP.
 XX (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
 XX (HAMI-) HAMILTON REGIONAL CANCER CENT.
 FI Austin R, Kwok CS, Ring DB;
 XX WPI; 2001-451904/48.
 XX N-PSDB; AAS09508.
 XX Novel immunoconjugate useful for inhibiting tumour cell growth in vivo
 FT comprises a humanized anti-pl85 antibody linked to an Interleukin-2
 FT polypeptide -
 XX Claim 13; Fig 11; 74pp; English.
 XX The sequence represents a humanised anti-pl85 (520C9) single chain
 CC antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein
 CC (or immunoconjugate) is used to inhibit the growth of tumours or cancers
 CC particularly those characterised by overexpression of pl85 e.g. human
 CC adenocarcinomas and malignant and/or benign tumours of the breast, renal
 CC system, salivary gland, gastrointestinal tract or gastric tumours.
 XX Sequence 409 AA;
 SQ

Query Match 64.8%; Score 1289; DB 22; Length 409;
 Best Local Similarity 65.1%; Pred. No. 1.6e-82;
 Matches 259; Conservative 44; Mismatches 67; Indels 28; Gaps 4;


```
PF 29-SEP-2000; 2000WO-JP06774..
XX
PR 30-SEP-1999; 99JP-0278291.
PR 06-APR-2000; 2000JP-0105086.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3. The antibody and its derivatives are
PT therapy of e.g. tumours, with low antigenicity, little side effects but
PT potent activity in cancer
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention.
XX
SQ Sequence 582 AA;
Query Match 53.9%; Score 1072.5; DB 22; Length 582;
Best Local Similarity 43.5%; Pred. No. 3.8e-67;
Matches 257; Conservative 32; Mismatches 83; Indels 219; Gaps 11;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSGTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSACAAGFAFASHYAMSWVRQAPGKLEWVAISSGGSGTY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPIDYWGQGLTVTVS 120
DB 61 SDSVKGRFTISRDNKNTLYLQMNLSRAEDSAVYFCTRVKLGTY--FDSWGQGLTVTVS 118
QY 121 SGGGALEIVLTQSLPLVPTPG-----EPASISCRSS----- 152
DB 119 SAS-----TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 171
QY 153 -QSLHNSGYTYLDWLQKPGQS--PQLLYSGSHRAS----- 187
DB 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPC 231
QY 188 -----GVPD-----RPSGSVSGTD----- 201
DB 232 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 291
QY 202 -----F 202
DB 292 KPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGPREPQVY 351
QY 203 TLRISRV-----AEDGVGYCMQG-----IQSPFTFGGPK 234
DB 352 TLPPSRDELTKNOVSLTCLVKGFYPDIAVEWESNGQPENNYKTTTPVLDSDSGSEFLYSK 411
QY 235 VDIKRGSGSGGAL-----APTSSSTKTKTQLLEHLLLDLQ 270
DB 412 LTVDKSRWQGNVFCSCWHEALHNHYTQKSLSLSPCKAPTSSSTKTKTQLLEHLLLDLQ 471
QY 271 MILGINNKNPKLTRMLTFKPYMPKATKELKHLQCLEELKPLEEVNLQAQSKNFHLRP 330
DB 472 MILGINNKNPKLTRMLTFKPYMPKATKELKHLQCLEELKPLEEVNLQAQSKNFHLRP 531
QY 331 RDLISNINVLKSGSETTFMCEYADETATVFEFLNRWITFCQSIISLT 381
DB 532 RDLISNINVLKSGSETTFMCEYADETATVFEFLNRWITFCQSIISLT 582
RESULT 5
AAW27560
```

```
ID AAW27560 standard; Protein; 281 AA.
XX
AC AAW27560;
XX
DT 23-JAN-1998 (first entry)
XX
DE Consensus single chain fragment VH3-V-kappa-2.
XX
KW Human; antibody; preparation; library; VH3; variable region;
KW light chain; heavy chain; V-kappa-2; single chain; consensus.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..281
FT Peptide /label= mat_peptide
XX
XX WO9708320-A1.
XX
PD 06-MAR-1997.
XX
XX 19-AUG-1996; 96WO-EP03647.
XX
XX 18-AUG-1995; 95EP-0113021.
XX
XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX
XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
XX
XX WPI; 1997-179277/16.
XX
XX N-PSDB; AAT87958.
XX
XX Preparation of human derived antibody gene library - using synthetic
XX consensus sequences, and signal consensus antibody gene as universal
XX framework for highly diverse antibody libraries
XX
XX Example 2; Fig 8; 436pp; English.
XX
XX The present sequence is the consensus single chain fragment
XX VH3-V-kappa-2. VH3-V-kappa-2, which comprises the human antibody
XX heavy and light chain variable region consensus sequences VH3 and
XX V-kappa-2, was used in the preparation of a human derived antibody
XX gene library.
XX
XX Sequence 281 AA;
Query Match 52.9%; Score 1052; DB 18; Length 281;
Best Local Similarity 81.5%; Pred. No. 4.4e-66;
Matches 207; Conservative 11; Mismatches 20; Indels 16; Gaps 2;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGTY 60
DB 26 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVAISSGGSGTY 85
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPIDYWGQGLTVTVS 120
DB 86 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 144
QY 121 -----SGGGALEIVLTQSLPLVPTPGEPASISCRSSQSLHNSGYTVLD 165
DB 145 SAGGSGGGGSGGGGGSDIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTVLD 204
QY 166 WYLOKPGSQPLLIIYSGSHRASGVDPDRFSGVSGDFTFLRISRVEAEDGVGYCMQGLQS 225
DB 205 WYLOKPGSQPLLIIYLSGNRASGVDPDRFSGSGSGDFTFLKISRVEAEDGVGYCQOHTT 264
QY 226 PFTFGPGTKVDIKR 239
DB 265 PPTFGGQTKVEIKR 278
```



```
FT Domain 316..450
FT /label= Interleukin-2_domain
FT Region 451..456
FT /label= His_tag
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP05416.
XX
PR 28-JUL-1998; 98EP-0114082.
XX
PA (MICR-) MICROMET GES BIOMEDIINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR N-PSDB; AAZ50585.
XX
XX New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis
XX
PS Example 9; Fig 48; 166pp; English.
CC
CC The patent discloses heteroninobodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CHI-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteroninobodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas.
CC
CC The present sequence is a fusion protein comprising murine
CC 17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the
CC N-terminus, human interleukin-2 at the C-terminus and a tetramerisation
CC domain between them. This construct was prepared to find out whether
CC an oligomerisation domain characterised in bacterial expression system
CC is applicable for expression of fully functional and secretable
CC recombinant protein in mammalian host cells. This tetrameric construct
CC was found to be expressed as secretable and fully functional protein
CC in mammalian cells.
XX
SQ Sequence 456 AA;
Query Match 49.3%; Score 982; DB 21; Length 456;
Best Local Similarity 55.18; Pred. No. 6.4e-61;
Matches 217; Conservative 27; Mismatches 50; Indels 100; Gaps 10;
QY 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
DB 142 QVKLQESGPGVLVQPSQSISITCTVSGFLTSYGVHVRQSPGKGLEWL-QVIWSGGSTDY 200
QY 61 ADSVKGRTTISRDNKNTLYLQMSLRADETAVYCAKHTGGVWDPIYWGQGLTVTS 120
DB 201 NNAFTSRISIDNSKQSVFFKMSLQANDTAIYICARMEN---WS-FATWGQGLTVTS 256
QY 121 SGGGALEIVLTQSPILSPVTPFCEPASISCRSSQLHSNGYTYLDWYLQKPGQSPQLLY 180
DB 257 E-----FTPLG-----DTTHTSG-----KP----- 271
QY 181 SGSHRASGVDPFSGSVSGTDFTLRI-----SRVEADGVYVCMQGLQSPF 227
DB 272 -----LDGEFTLQIGRGRFEMFRELNELKDA-----QAGKEP- 308
QY 228 TFGPGTKVDIKRGGSGGALAPTSSSTKTKQLQLEHLLLDLQMLNGINNKNPKLTRM 287
Db 309 -----GGSGGAPAPTSSSTKTKQLQLEHLLLDLQMLNGINNKNPKLTRM 354
QY 288 LTFKFFMPKKATELKHLCLEELKPLEEVNLNLAQSKNPHLRPRDLISINIVILELKS 347
Db 355 LTFKFFMPKKATELKHLCLEELKPLEEVNLNLAQSKNPHLRPRDLISINIVILELKS 414
QY 348 ETTFMCEYADETATIVFELNLRWITFCQSIITLT 381
Db 415 ETTFMCEYADETATIVFELNLRWITFCQSIITLT 448
RESULT 10
AAY44991
ID AAY44991 standard; Protein; 450 AA.
XX
XX AAY44991;
AC
XX
XX 23-MAY-2000 (first entry)
DT
XX
DE M79scFv-interleukin 2-fusion protein containing dimerisation domain.
XX
XX Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv;
XX fusion construct; human; interleukin 2; IL-2; dimerisation domain;
XX heteroninobody; multifunctional compound; constant domain;
XX immunoglobulin; cytosstatic; immunostimulatory; antileukaemia; diagnosis;
XX antiproliferative; prevention; treatment; malignant; haematopoietic cell;
XX lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Leader_peptide
FT Region 20..126 /label= M79scFv_light_chain_variable_region
FT Region 127..141 /label= Gly-Ser_linker
FT Region 142..256 /label= M79scFv_heavy_chain_variable_region
FT Region 259..268 /note= "murine IgG3 upper hinge region with
FT additional residues"
FT Domain 269..303
FT Peptide 304..309 /label= dHLX-dimerisation_domain
FT Peptide /label= Short_peptide_linker
FT Domain 310..444 /label= Interleukin-2_domain
FT Region 445..450 /label= His_tag
XX
XX WO200006605-A2.
XX
XX 10-FEB-2000.
XX
XX 28-JUL-1999; 99WO-EP05416.
XX
XX 28-JUL-1998; 98EP-0114082.
XX
XX (MICR-) MICROMET GES BIOMEDIINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
XX WPI; 2000-195265/17.
XX
XX N-PSDB; AAZ50584.
XX
XX New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis
XX
PS Example 9; Fig 47; 166pp; English.
```

CC The patent discloses heterominoibodies which are multifunctional compounds
 CC produceable in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises, a CHI-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CL-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heterominoibodies have
 CC cytostatic, immunostimulatory, anticellulemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is a fusion protein comprising murine
 CC 17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the
 CC N-terminus, human interleukin-2 at the C-terminus and a dimerisation
 CC domain between them. This construct was prepared to find out whether
 CC an oligomerisation domain characterised in bacterial expression system
 CC is applicable for expression of fully functional and secretable
 CC recombinant protein in mammalian host cells. The dimerisation domain used
 CC in this construct proved to be not applicable in mammalian host cells.

XX Sequence 450 AA;
 SQ Query Match 49.2%; Score 980; DB 21; Length 450;
 Best Local Similarity 56.4%; Pred. No. 8.7e-61;
 Matches 215; Conservative 30; Mismatches 56; Indels 80; Gaps 10;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 60
 DB 142 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 200
 QY 61 ADSVKGRFTISRDNKNTLYLQMSNLAEDTAVYCAKHTGGVWDPIYWGQGLTVTVS 120
 DB 201 NAAFIISRLSKDQNSQVFFKMSLQANDTALYICARMEN---WS-FAYWGQGLTVTVS 256
 QY 121 SGGGALVLTQSPLSLPTVPGPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIY 180
 DB 257 E-----FPKPSFP-----PGSSGEL--- 271
 QY 181 SGSHRASGVDPDRSGVSGTDFTLIRSRVPAEDGVYVCMQGLQSPFTGPGTKVDIKRG 240
 DB 272 --BELLKHLKELKPKRG-----ELEEL---LKHLLK-----BLLKG 303
 QY 241 GSGGGALPTSSSTKTKQLQLEHLLDQLMILNGINNYKNPKLTRMLTFKFMPPKATE 300
 DB 304 G--SGGAPATSSSTKTKQLQLEHLLDQLMILNGINNYKNPKLTRMLTFKFMPPKATE 361
 QY 301 LKHLQCLEELKPLEEVLNLAQSKNHLRPRDLISINIVLELKGSETTFMCEYADETA 360
 DB 362 LKHLQCLEELKPLEEVLNLAQSKNHLRPRDLISINIVLELKGSETTFMCEYADETA 421
 QY 361 TIVEFLNRWITFCOSIISTLT 381
 DB 422 TIVEFLNRWITFCOSIISTLT 442

RESULT 11
 AAB81972
 ID. AAB81972 standard; Protein; 581 AA.
 XX AAB81972;
 AC
 XX
 XX
 DT 03-JUL-2001 (first entry)
 XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
 DE Ganglioside; GD2; complementation determining region; CDR; antibody;
 XX Ganglioside; GD2; complementation determining region; CDR; antibody;
 KW mouse; cancer.
 KW
 XX Synthetic.
 OS

XX WO200123573-A1.
 PN 05-APR-2001.
 XX 29-SEP-2000; 2000WO-JP06773.
 PF 30-SEP-1999; 99JP-0278290.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266163/27.
 DR Human type complementation-determining domain transplanted antibody and
 XX derivatives against ganglioside GD2, useful in diagnosis and therapy of
 PT e.g. tumours, has low antigenicity, little side effects but potent
 PT activity in cancer -
 XX Example 3; Page 111-114; 123pp; Japanese.
 XX The present invention describes an antibody, which can react specifically
 CC with ganglioside GD2, and is transplanted with a human type
 CC complementation-determining domain (CDR), or its fragments. The antibody
 CC and its derivatives are useful in diagnosis and therapy of tumours,
 CC particularly cancer diagnosis. The present sequence is a protein
 CC used in the exemplification of the invention.
 XX Sequence 581 AA;
 SQ Query Match 48.7%; Score 969; DB 22; Length 581;
 Best Local Similarity 40.3%; Pred. No. 6.9e-60;
 Matches 238; Conservative 40; Mismatches 93; Indels 220; Gaps 12;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 60
 DB 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 59
 QY 61 ADSVKGRFTISRDNKNTLYLQMSNLAEDTAVYCAKHTGGVWDPIYWGQGLTVTVS 120
 DB 60 NSALMSRLTISKDQNSQVFFKMSLTAADTAVYCAKRDSDYWS--FAYWGQGLTVTVS 117
 QY 121 SGGGALVLTQSPLSLPTVPGPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIY 152
 DB 118 SAS-----TKGPVFFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 170
 QY 153 -QSLHNSGYTYLDWYLOKPGQS--PQLLYSGSHRAS----- 187
 DB 171 PPAVLQSSGLYSLSWTVVPSSSLGTQYICNVNHPKSNTRKVDKVKPEKCDKTHTCPPC 230
 QY 188 -----GVPD-----RFGSVSGTD----- 201
 DB 231 PAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 290
 QY 202 -----F 202
 DB 291 KPREEQYNSTYRVSVLTVLHQDLNKGKEYCKCKVSNKALPAPIEKTIKAKGQPREPOVY 350
 QY 203 TLRISRV-----AEDGVVYCMQG-----LQSPFTFGPGTK 234
 DB 351 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSK 410
 QY 235 VDIKRGSGSGGAL-----APTSSTKTKQLQLEHLLDQL 270
 DB 411 LTVDSRWQGNVFCVSVWHEALHNHYTQKSLSLSPGKAPTSSTKTKQLQLEHLLDQL 470
 QY 271 MILINGINNYKNPKLTRMLTFKFMPPKATELKHLCLEELKPLEEVLNLAQSKNHLR 330
 DB 471 MILINGINNYKNPKLTRMLTFKFMPPKATELKHLCLEELKPLEEVLNLAQSKNHLR 530
 QY 331 RLISINIVIVLELKGSETTFMCEYADETATIVFELNHWITFCOSIISTLT 381

CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX
SQ Sequence 244 AA;
Query Match 46.0%; Score 914.5; DB 23; Length 244;
Best Local Similarity 72.6%; Pred. No. 1.7e-56;
Matches 183; Conservative 22; Mismatches 26; Indels 21; Gaps 4;
QY 1 QVQLVQSGGGLVOPGSGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWYSGISGGSTYY 60
DB 1 EVQLVQSGGGLVPGGSLRLSCAASGFTFSYMMNWVRQAPCKGLEWYSSISSSSHIYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAK-HTGGGVWMDIDYWGQGLTVTV 119
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCARVHSSGS-----WGQGLTVTV 113
QY 120 SGGG-----ALEIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWY 167
DB 114 SGGGGGGGGGGGSGALDVTMTQSPSLPVTGQPASISCRSSQSLVHSDGNTYLNWF 173
QY 168 LQPGQSPOLLVYSGSHRASGVDPDRFSGVSGTDFTLRISRVEAEDVGYYCMQGLQSPF 227
DB 174 QRPQSPRLLYKVSNRDFGVPDRFSGSGGTFTLKISRVEAEDVGYYCMQGTHR-I 232
QY 228 TFGPGTKVDIKR 239
DB 233 TFGQGRLEIKR 244

RESULT 14
AAB20434
ID AAB20434 standard; Protein; 249 AA.

XX AAB20434;
XX
XX 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/K2 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

XX Chimeric - Mus musculus.
OS Chimeric - Synthetic.

XX Key Location/Qualifiers
FH Protein 1..121
FT /label= VH
FT Region 98..110
FT Peptide 122..135
FT /label= Linker
FT Protein 136..249
FT /label= VL
FT Region 230..238
FT /label= CDR3

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP08936.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT) BAXTER AG.

XX Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;

XX WPI: 2001-290358/30.

XX N-PSDB; AAF30724.

XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Claim 10; Fig 15; 138pp; English.

XX The present sequence is that of a single chain Fv (scFv) derivative
CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain
CC variable regions of 193/K2 joined by an artificial, flexible linker
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 193/K2 VH and VL regions and cloning in vector pDAP2. 193/K2 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
CC including scFv and CDR3 fragments, have factor VIIIa (FVIIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
CC in the absence of FVIII or FVIIIa, and in the case of FVIII
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis.

XX Sequence 249 AA;

Query Match 45.7%; Score 909; DB 22; Length 249;

Best Local Similarity 69.9%; Pred. No. 4.1e-56;

Matches 174; Conservative 28; Mismatches 37; Indels 10; Gaps 1;

QY 1 QVQLVQSGGGLVOPGSGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWYSGISGGSTYY 60

DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTYTHMSVVRQTPKRLKLEWATISSGGSTYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWMDIDYWGQGLTVTVS 120

DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGHHGYSDFYWGQGLTVTVS 120

QY 121 -----SGGGALEIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLOK 170

DB 121 SGGGSGSGRAGSGGSGQIVLTQSPSLPVLSDQASISCRSSQSLHNSGYTLDWYLOK 180

QY 171 PGQSPOLLVYSGSHRASGVDPDRFSGVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTF 230

DB 181 PGQSPKLLIYKVSNRFGVDPKFSGSGSGDFTLKISRVEAEDLGVIYCFQGSHPVPTFG 240

QY 231 PGTKVDIKR 239

DB 241 GGTKLEIKR 249

RESULT 15

AAM24101

ID AAM24101 standard; Protein; 384 AA.

XX AAM24101;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1626.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;

KW biodiversity; gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

```
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR N-PSDB: AAH98760.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 20: Page 1102-1103; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX Sequence 384 AA;
XX
Query Match 44.4%; Score 883.5; DB 22; Length 384;
Best Local Similarity 66.3%; Pred. No. 4.2e-54;
Matches 185; Conservative 22; Mismatches 47; Indels 25; Gaps 5;
QY 1 QVQLVQSGGGLVPGGSLRLCAASGFTFRSNAMGWVRQAPGKLEWWSGISGGSTYY 60
Db :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
20 EVQLVESGGGLVPGGSLRLCAASGFTFSYAMSWVRQAPGKLEWWSGISGGSTYY 79
QY 61 ADSVKGRTISRDNSKNTLYLQMSLRAEDTAVYYCAK-----HTGGGVWDP-----I 108
Db :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 ADSVKGRTISRDNSQNTLYLQMSLRAEDTAVYYCAKSHPAYYSGSYSHYYGYGM 139
QY 109 DWVGQGLTVTVSSG-----GGAL--EIVLTQSLPLPVTGPAPASICRSQSLLHSN 159
Db :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 DWVGQGLTVTVSSGSGSGSGAGSTGEIVLTQSPGTLISLSPGERATLSCRASQSVSS- 198
QY 160 GYTYLDWYLOKPGSQPLLIVSGSHRASGVPDRFSGVSGTDFTLIRSRVEADGVYYC 219
Db :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 ---YLAWYQKPEQAPRLIYGCASSRATGIPDRFSGSGSDFTLTISRLEPEDFAVIYC 255
QY 220 MQGLQSPFTFGPTKVDIKRGSGGGGALAPTSSSTRKT 258
Db :||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 QQYGSPTTFGGQTKRVEIKRTVAAPSVFIFPPSDEQLKS 294
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Search completed: March 14, 2003, 11:47:36
Job time : 37.7681 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:34 ; Search time 11.9515 seconds
(without alignments)
937.967 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1052	52.9	281	4	US-09-025-769B-178
2	862	43.3	247	4	US-09-227-693-34
3	862	43.3	248	1	US-08-331-398A-34
4	862	43.3	248	2	US-08-331-397B-34
5	862	43.3	248	2	US-08-759-804A-34
6	798	40.1	245	4	US-08-918-148-75
7	797	40.1	289	3	US-09-184-658-63
8	790	39.7	366	3	US-08-875-811-55
9	781	39.2	282	2	US-08-860-174A-10
10	778	39.1	245	4	US-08-918-148-78
11	776.5	39.0	301	2	US-08-661-052-14
12	776.5	39.0	301	4	US-09-188-082-14
13	776.5	39.0	301	4	US-09-364-088-14
14	776.5	39.0	301	4	US-09-102-716-14
15	776.5	39.0	553	2	US-08-661-052-16
16	776.5	39.0	553	4	US-09-188-082-16
17	776.5	39.0	553	4	US-09-364-088-16
18	776.5	39.0	553	4	US-09-102-716-16
19	770.5	38.7	365	3	US-08-875-811-53
20	765.5	38.5	244	4	US-08-918-148-77
21	765	38.4	245	4	US-08-918-148-76
22	764	38.4	263	2	US-08-752-844-66
23	763	38.3	284	4	US-08-564-164A-2
24	758	38.1	277	2	US-08-256-790-2
25	750	37.7	228	5	PCT-US92-08257-9
26	731.5	36.8	248	2	US-08-887-352B-22
27	731.5	36.8	248	4	US-09-109-207C-22

28 731.5 36.8 248 4 US-09-236-005-22 Sequence 22, Appl
29 730.5 36.7 248 2 US-08-887-352B-23 Sequence 23, Appl
30 730.5 36.7 248 4 US-09-109-207C-23 Sequence 23, Appl
31 730.5 36.7 248 4 US-09-296-005-23 Sequence 23, Appl
32 730 36.7 252 1 US-08-133-804-4 Sequence 4, Appl
33 730 36.7 252 1 US-08-461-838-4 Sequence 4, Appl
34 730 36.7 252 2 US-08-461-886-4 Sequence 4, Appl
35 728.5 36.5 535 4 US-08-983-035A-38 Sequence 38, Appl
36 726.5 36.5 236 2 US-08-190-199A-65 Sequence 65, Appl
37 717 36.0 240 2 US-08-459-354-4 Sequence 4, Appl
38 717 36.0 240 2 US-08-077-253-4 Sequence 4, Appl
39 717 36.0 240 3 US-08-333-840-4 Sequence 4, Appl
40 713 35.8 223 2 US-08-190-199A-63 Sequence 63, Appl
41 713 35.8 240 1 US-08-488-113B-148 Sequence 148, Appl
42 713 35.8 240 1 US-08-477-484B-148 Sequence 148, App
43 713 35.8 240 2 US-08-646-360-148 Sequence 148, App
44 713 35.8 240 4 US-08-839-765-148 Sequence 148, App
45 713 35.8 240 4 US-09-136-389-148 Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/025,769B
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 52.9%; Score 1052; DB 4; Length 281;
Best Local Similarity 81.5%; Pred. No. 1.le-81;
Matches 207; Conservative 11; Mismatches 20; Indels 16; Gaps 2;

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QY 1 QVLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPKGLWVSGISGGSTYY 60
Db 26 EQLVSGGGLVQPGGSLRLSCAASGFTFSYAMSWVQAPKGLWVSAISGGSTYY 85
QY 61 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS 120
Db 86 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCARWGGDGY-ANDYWGQGLTVTVS 144
QY 121 -----SGGGALEIVLTQSPSLPVTTPGEPASISCRSSQSLHLSNGYTYLD 165
Db 145 SAGGSGGGGSGGGGSDIVMTQSPSLPVTTPGEPASISCRSSQSLHLSNGYNYLD 204
QY 166 WYLQRPQSPQLLIYSGSHRASGVPDRFSGSVSGTDFTLRLSRVEAEDVGYVYCMQGLQS 225
Db 205 WYLQRPQSPQLLIYLSNRASGVPDRFSGSGSGTDFTLKLSRVEAEDVGYVYCOOHYTT 264
QY 226 PTFEGGPTKVDIKR 239
Db 265 PTFEGGPTKVDIKR 278

RESULT 2
US-09-227-693-34
; Sequence 34, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Ital
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/331,396
; FILING DATE:
; APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-227-693-34
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Query Match 43.3%; Score 862; DB 4; Length 247;
Best Local Similarity 67.6%; Pred. No. 1.3e-65;
Matches 167; Conservative 28; Mismatches 40; Indels 12; Gaps 2;

QY 2 VQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPKGLWVSGISGGSTYYA 61
Db 3 VKLVESGGGLVQPGGSLRLSCATSGFTSDYMYWVROTPEKRLWVAYISNDSSAAYS 62
QY 62 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS- 120
Db 63 DTVKGRFTISRDNARNTLYLQMNSLRAEDTAVYYSCARGLAWGAW--FAYWGQGLTVTVSS 120
QY 121 -----SGGGALEIVLTQSPSLPVTTPGEPASISCRSSQSLHLSNGYTYLDWYLQKP 171
Db 121 GGGSGGGGSGGGGSDVMTQSPSLPVSIGDQASISCRSSQIIIVHSNGNTYLEWYLQKP 180
QY 172 GQSPQLLIYSGSHRASGVPDRFSGSVSGTDFTLRLSRVEAEDVGYVYCMQGLQSPETFGP 231
Db 181 GQSPKLLIYKVSNRFRSGVPDRFSGSGSGTDFTLKLSRVEAEDLGVIYCFQGSHPVTFGS 240
QY 232 GTKVDIK 238
Db 241 GTKLEIK 247

RESULT 3
US-08-331-398A-34
; Sequence 34, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1261100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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MOLECULE TYPE: protein

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:	
; LENGTH: 248 amino acids	
; TYPE: amino acid	
; TOPOLOGY: linear	
; MOLECULE TYPE: protein	
US-08-759-804A-34	
Query Match 43.3%; Score 862; DB 2; Length 248;	
Best Local Similarity 67.6%; Pred. No. 1.3e-65;	
Matches 167; Conservative 28; Mismatches 40; Indels 12; Gaps 2;	
QY 2	VQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTIYA 61
Db 3	VKLVESGGGLVQPGSLKSCATSGFTSDYMYWVRQPEKRLWEVAYISNDSSAAYS 62
QY 62	DSYVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGWDPIDYWGQGTLTVTVS- 120
Db 63	DTVKGRFTISRDNARNTLYLQMSRLKSEDTATYSCARGLAWGAW--FAYWGQGTLTVTVS 120
QY 121	-----SGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLLSHNGTYTLDWLQRP 171
Db 121	GGSGGGGGGGSDVIMTQSPSLPVSIGDQASISCRSSQLIIVHSNGTYLEWYLQRP 180
QY 172	GQSPQLIYSGSHRAGVDPDRFSGVSGTDFTLIRISRVEADVGVIYCMQGLQSPPTFGP 231
Db 181	GQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEADVLGVYCFQGSHPVPTFGS 240
QY 232	GTRVDIK 238
Db 241	GTKLEIK 247
RESULT 6	
US-08-918-148-75	
; Sequence 75, Application US/08918148A	
; Patent No. 6342220	
; GENERAL INFORMATION:	
; APPLICANT: Adams, Camellia	
; APPLICANT: W.	
; APPLICANT: Carter, Paul J.	
; APPLICANT: Fendly, Brian M.	
; APPLICANT: Gurney, Austin L.	
; TITLE OF INVENTION: Agonist Antibodies	
; FILE REFERENCE: P0979	
; CURRENT APPLICATION NUMBER: US/08/918,148A	
; CURRENT FILING DATE: 1997-08-25	
; NUMBER OF SEQ ID NOS: 79	
; SEQ ID NO 75	
; LENGTH: 245	
; TYPE: PRT	
; ORGANISM: artificial	
US-08-918-148-75	
Query Match 40.1%; Score 798; DB 4; Length 245;	
Best Local Similarity 63.1%; Pred. No. 3.4e-60;	
Matches 157; Conservative 27; Mismatches 47; Indels 18; Gaps 3;	
QY 1	QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTIY 60
Db 3	EVQLVQSGGGLVKPGSLRLSCAASGFTFSDYMSWIRQAPGKLEWVSISSGSTIY 62
QY 61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGWDPIDYWGQGTLTVTVS 120
Db 63	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWSGE---DAFDIWGQGTMTVTVS 119
QY 121	-----SGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLLSHNGTYTLDWLQK 170
Db 120	SGGGGGGGGGSDVIMTQSPSLIIVHSNGTYTLDWLQK 174
QY 171	PQSPQLIYSGSHRAGVDPDRFSGVSGTDFTLIRISRVEADVGVIYCMQGLQSPPTFG 230
Db 175	PKAPKLLIYKASSLASGAPSRFSGSGGADFTLTLSLQPDPTATYYCQYSNPLTFG 234

; SEQUENCE CHARACTERISTICS:	
; LENGTH: 248 amino acids	
; TYPE: amino acid	
; TOPOLOGY: linear	
; MOLECULE TYPE: protein	
US-09-184-658-63	
Query Match 40.1%; Score 797; DB 3; Length 289;	
Best Local Similarity 62.7%; Pred. No. 5.2e-60;	
Matches 156; Conservative 33; Mismatches 44; Indels 16; Gaps 2;	
QY 1	QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTIY 60
Db 23	EVQLVESGGGVQPGSLKSCAASGFTNTYGMWVRQTPDKRLWEVATINSNGLTFY 82
QY 61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGWDPIDYWGQGTLTVTVS 120
Db 83	ADSVKGRFTISRDNKNTLYLQMNRLKSGDSGMYYCVRG-----YSNVARWQGALVTVS 137
QY 121	S-----GGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLLSHNGTYTLDWLQ 169
Db 138	SGGGGGGGGGSDVIMTQSPSLIIVHSNGTYTLDWLQ 197

Qy	168	LQPPGSPQLIYSGSHRASGVPDRSGSVSGDFTFLIRSRVFAEDVGVIYCMQGLQSPF	227
		: : : : : : :	
Db	200	QKPGQPCKLLIYMASTRESGVDRFTASGSGDFTLLTSSQAEDLAVIYCONDYTFP	259
		: : : : : : :	
Qy	228	TFPGTKVDIKR	239
		:	
Db	260	TFGGGTKLEIKR	271
		:	

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RESULT 10
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

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Query Match	39.1%	Score	778:	DB	4:	Length	245;
Best Local Similarity	62.2%;	Pred.	No.	1.7e-58;			
Matches	155;	Conservative	27;	Mismatches	49;	Indels	18; Gaps
Qy	1	QVQLVQSGLGVLPGQGSURLSCAASGGFTFRSNAMGVWRQAPKGLGWYSGISGGSGSTYY	60				
Db	3	QVQLVESGGGLVLPKGSSURLSCAASGGFTFSHNNMNVWRQAPKGLWYSSISSSSSIYY	62				
Qy	61	ADSVKGRFTISRDNKNTLYIQMNSLRAREDVAIVYCAKHGTGGVWDPTDYWGCGTLFVTVS	120				
Db	63	ADSVKGRFTISRDNAKNSLYIQMNSLRAREDVAIVYCARDGS---	119				
Qy	121	-----SGGGALEITLVQPSLSPDVTPEPASIISCRSSQSLHHNGTYTLDWYLQK	170				
Db	120	SGGGSGGGSGGGGSKIQMTQSPETLSASIGDRVYITCRASEGIYH-----WLAWYQQK	174				
Qy	171	PCOSPOLLIYSGSHRASGVDPFFSGVSGTGDTFLRISVEAEDVVGYCMOGLOSPFFTG	230				
Db	175	PKAPKLIIYIKASSLWASGNPFSGSGGTDFTTXTISSLQDDPFATYICQOYSNYPILFG	234				
Qy	231	PGTKVDIKR	239				
Db	235	GGTKLEIR	243				

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RESULT 11
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezlan Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS
; TITLE OF INVENTION: OF ANTI-FC R
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-14

	Query Match	39.08;	Score	776.5;	DB 2;	Length	301;
	Best Local Similarity	61.5%;	Pred.	No. 3e-58;	51;	Indels	21;
	Matches	160;	Conservative	28;	Mismatches	51;	Gaps
Qy	2	VQLVQSGLLVPQGSLRSLCAASGTFRRSNAMGVWRQAPKGLEWVGISGGSGTYAA	61	:	:	:	:
Db	21	LQLVESGGVVQPGRSLRLCSSSGFESDNYMYVRQAPKGLEWATISDGSYTYP	80	:	:	:	:
Qy	62	DSVKGRFTISRDNKNLTLYLNLSLRADTTAVYCA----	117	:	:	:	:
Db	81	DSVKGRFTISRDNKNLTFLQMDSLURPDTGYFCARYYRFGA-----	135	:	:	:	:
Qy	118	TVS-----SGGGALEIVLTQSPILSPVTGPPEPASISCRSSQSLH-SNGVTYLDW	166	:	:	:	:
Db	136	TVSSGGGSGGGSGGGSDIQTQSPSSLASVDGRVITICKSQSVLYSSNQKNYLAW	195	:	:	:	:
Qy	167	YLQPCQSPOLLIIYSGSHRASCPDRFSGSVSGTDFTLRIRVEAEADVGVYCMOGLOSP	226	:	:	:	:
Db	196	YOQPGKAPKLIIYWASTRESGVPSRFSGSGSDFTFTISSLPEDTATYYCHQYLS-	254	:	:	:	:
Qy	227	FTFGPGTKVIDIKRGGSGGG	246	:	:	:	:
b	255	WTFGGGTKEVIKSSCGSGG	274	:	:	:	:

RESULT 12
US-09-188-082-14
; Sequence 14, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston

```
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-188-082-14

Query Match          39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGSGGTYTA 61
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Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 TVS-----SGGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLH-SNGYTYLDW 166
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 136 TVSSGGGGGGGGGGSDIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNYLAW 195
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 167 YLQPGQSPQLLIYSGHRSAGVDPDRFSGVSGTDFTLRLSRVEAEDVGVIYCMQGLQSP 226
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGGTDFTTISSLQPEDIAITYYCHQYLSS- 254
QY 227 FTFGPGTKVDIKRGGSGG 246
Db :||| ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 255 WTFGGGTKEIKSSCSGGG 274
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RESULT 13
US-09-364-088-14
; Sequence 14, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-364-088-14

Query Match          39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGSGGTYTA 61
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QY 62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCA----KHTGGGVWDPIDYWGQGLV 117
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QY 118 TVS-----SGGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLH-SNGYTYLDW 166
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QY 136 TVSSGGGGGGGGGGSDIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNYLAW 195
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QY 167 YLQPGQSPQLLIYSGHRSAGVDPDRFSGVSGTDFTLRLSRVEAEDVGVIYCMQGLQSP 226
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QY 196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGGTDFTTISSLQPEDIAITYYCHQYLSS- 254
QY 227 FTFGPGTKVDIKRGGSGG 246
Db :||| ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 255 WTFGGGTKEIKSSCSGGG 274

RESULT 14
US-09-102-716-14
; Sequence 14, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
;              Joel Goldstein
;              Robert Graziano
;              Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/102,716
;   FILING DATE: 22-Jun-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/661,052
;     FILING DATE: <unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Arnold, Beth E.
;     REGISTRATION NUMBER: 35,430
;     REFERENCE/DOCKET NUMBER: MXI-043CP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 301 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

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Query Match      39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

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QY  62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 117
Db  81 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 135

QY  118 TVS-----SGGGALEIVLTQSLPLVTPGEPASISCRSSQSLH-SNGYTYLDW 166
Db  136 TVSSGGGGGGGGGGSDIQLTQSPSSLSASVGDRTITCKSSQSVLYSSNQKNYLAW 195

QY  167 YLQKPGQSPOLLISYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEAEDVGVYCMQGLQSP 226
Db  196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGGTDFTTTISLQPEDIAITYYCHQYLSS- 254

QY  227 FTFGPGTKVDIKRGGSGGG 246
Db  255 WTFGGTKVEIKSSCSGGG 274

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RESULT 15
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
;
; GENERAL INFORMATION:
;   APPLICANT: yashwant M. Deo
;   APPLICANT: Joel Goldstein
;   APPLICANT: Robert Graziano
;   APPLICANT: Chezhian Somasundaram
;   TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;   TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: LAHIVE & COCKFIELD
;     STREET: 60 State Street, Suite 510
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/661,052
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/484,172
;     FILING DATE: 07-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Arnold, Beth E.
;     REGISTRATION NUMBER: 35,430
;     REFERENCE/DOCKET NUMBER: MXI-043CP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 553 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   US-08-661-052-16

Query Match      39.0%; Score 776.5; DB 2; Length 553;
Best Local Similarity 61.5%; Pred. No. 7e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY  2 VQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVATISDGGSTYYA 61
Db  21 IQLVESGGGVQPGSLRLSCSSGFIISDNMYMYVRQAPGKLEWVATISDGGSTYYTP 80

QY  62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 117
Db  81 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 135

QY  118 TVS-----SGGGALEIVLTQSLPLVTPGEPASISCRSSQSLH-SNGYTYLDW 166
Db  136 TVSSGGGGGGGGGGSDIQLTQSPSSLSASVGDRTITCKSSQSVLYSSNQKNYLAW 195

QY  167 YLQKPGQSPOLLISYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEAEDVGVYCMQGLQSP 226
Db  196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGGTDFTTTISLQPEDIAITYYCHQYLSS- 254

QY  227 FTFGPGTKVDIKRGGSGGG 246
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Search completed: March 14, 2003, 11:50:16
Job time : 13.9515 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 : Search time 11.5894 Seconds

(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....IVEFLNRWITFCQSIITLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published-Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1990	100.0	381	10	US-09-822-698A-5
2	860.5	43.2	240	9	US-09-968-561A-2
3	860.5	43.2	240	10	US-09-192-854-2
4	842	42.3	288	10	US-09-818-247-22
5	777.5	39.1	241	1	US-08-779-457-50
6	767.5	38.6	268	10	US-09-976-118-1
7	757	38.0	249	12	US-10-039-785-53
8	746.5	37.5	269	12	US-10-027-770-5
9	745.5	37.5	269	12	US-10-027-770-2
10	742	37.3	255	10	US-09-811-737-15
11	731.5	36.8	248	10	US-09-920-171-22
12	730.5	36.7	248	10	US-09-920-171-23
13	730	36.7	252	9	US-09-887-853-4
14	728.5	36.6	535	9	US-09-968-851-38
15	717.5	36.1	262	10	US-09-811-737-19
16	717	36.0	240	9	US-09-782-504-4
17	698	35.1	310	12	US-10-052-798-11
18	680	34.2	133	10	US-09-766-543-8
19	680	34.2	153	10	US-09-149-721-3

20	680	34.2	153	10	US-09-923-246-111
21	678.5	34.1	245	9	US-09-991-470-27
22	676.5	34.0	309	12	US-10-052-798-9
23	674	33.9	133	9	US-10-051-657A-1
24	669	33.6	331	10	US-09-033-525-2
25	667	33.5	451	10	US-08-822-698A-26
26	666	33.5	133	10	US-09-766-543-14
27	663.5	33.3	260	10	US-09-811-737-16
28	663	33.3	312	12	US-10-052-798-10
29	662	33.3	260	9	US-09-782-672-2
30	660	33.2	129	9	US-10-172-399-12
31	644	32.4	121	10	US-09-822-698A-3
32	644	32.4	250	9	US-09-887-853-2
33	637.5	32.0	260	10	US-09-811-737-17
34	635.5	31.9	276	10	US-09-766-543-12
35	628.5	31.6	267	10	US-09-766-543-10
36	618	31.1	240	10	US-09-976-787-28
37	618	31.1	240	10	US-09-865-198-27
38	617.5	31.0	269	9	US-09-749-873-109
39	613	30.8	238	10	US-09-976-787-29
40	613	30.8	238	10	US-09-865-198-28
41	605	30.4	256	9	US-10-247-488-2
42	605	30.4	258	9	US-10-247-488-4
43	604	30.4	249	9	US-10-237-667-18
44	604	30.4	249	9	US-10-237-708-18
45	604	30.4	249	9	US-10-237-866-18

ALIGNMENTS

RESULT 1
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 381
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPHI-IL-2
US-09-822-698A-5

Query Match	100.0%	Score	1990	DB	10	Length	381
Best Local Similarity	100.0%	Pred. No.	6.1e-111				
Matches	381	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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Db	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGISGGSTYY	60				
Qy	61	ADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAKHTGGVMDPIDDYWGQGLTVTS	120				
Db	61	ADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAKHTGGVMDPIDDYWGQGLTVTS	120				
Qy	121	SGGGALEIVLQSPSLPVTPEGPASISCRSSQSLLSHNSGYTLDYWLQKPGSQPLLII	180				
Db	121	SGGGALEIVLQSPSLPVTPEGPASISCRSSQSLLSHNSGYTLDYWLQKPGSQPLLII	180				
Qy	181	SGSHRASCVPRFSGSVSGTDFTLIRISRVEADGVYYCMQGLQSPFTFGPTKVDIKRG	240				
Db	181	SGSHRASCVPRFSGSVSGTDFTLIRISRVEADGVYYCMQGLQSPFTFGPTKVDIKRG	240				

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Db 241 GSGGALAPTSSSTKKTOLQLEHLLDLOMLNGINNYKNPKLTRLTFKFPMPKKATE 300
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QY 301 LKHQCLEELPLEVLNLAQSKNPHLRPRDLISNINVIIVLELKGSETTFMCEYADETA 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 LKHQCLEELPLEVLNLAQSKNPHLRPRDLISNINVIIVLELKGSETTFMCEYADETA 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 TIVEFLNRWITFCQSIISTLT 381
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 2
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US200201642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE OF INVENTION: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2
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Best Local Similarity 68.4%; Pred. No. 2.4e-44;
Matches 171; Conservative 22; Mismatches 36; Indels 21; Gaps 3;

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Db 1 EVQLLESGGGLVQPGGSLRLSCLCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGSTYY 60
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QY 121 S-----GGGALEIVLTQSPSLPVTPEPASISCRSSQSLHNSNGITYLDWYLQ 169
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Db 116 SGGGGSGGGGGGGGSDTDIQTQSPSSLSASVGDRTVITCRASQSI-----SSYLNWYQQ 170
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QY 170 KPGQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVIYCMQGLQSPFTF 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 KPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLPQEDFATYYCQQSYSTPNTF 230
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QY 230 GPGTKVDIKR 239
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Db 231 GQGTKVEIKR 240
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RESULT 3
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
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; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2
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Query Match 43.2%; Score 860.5; DB 10; Length 240;
Best Local Similarity 68.4%; Pred. No. 2.4e-44;
Matches 171; Conservative 22; Mismatches 36; Indels 21; Gaps 3;

QY 1 QVQLVQSGGGLVQPGGSLRLSCLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGLVQPGGSLRLSCLCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGSTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGGVMDPIDYWGQGLTVTVS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKSYGA-----FDYWGQGLTVTVS 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 S-----GGGALEIVLTQSPSLPVTPEPASISCRSSQSLHNSNGITYLDWYLQ 169
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 SGGGGSGGGGGGGGSDTDIQTQSPSSLSASVGDRTVITCRASQSI-----SSYLNWYQQ 170
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 170 KPGQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVIYCMQGLQSPFTF 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 KPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLPQEDFATYYCQQSYSTPNTF 230
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 230 GPGTKVDIKR 239
      |||:|||||:
Db 231 GQGTKVEIKR 240
      |||:|||||:
```

```
RESULT 4
US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostov, Keith E.
; APPLICANT: Chapin, Steven J.
; APPLICANT: Richman-Eisenstat, Janice
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Stalk Region of p19R and Methods of Use T
; FILE REFERENCE: 18062B-0009100S
; CURRENT APPLICATION NUMBER: US/09/818,247
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: WO PCT/US01/09699
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,197
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,198
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match 42.3%; Score 842; DB 10; Length 288;
```


Best Local Similarity 68.5%; Pred. No. 3.6e-43;
Matches 172; Conservative 18; Mismatches 41; Indels 20; Gaps 4;
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
DB 23 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGSGSTYY 82
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKH--TGCGVWDPIDYWGQGTTLV 118
DB 83 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARSTVNSGYF---QHMGQGTTLV 139
QY 119 VS-----SGGCALEIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGYTYLDWYL 168
DB 140 VSSGGGGGGGGGGSEIVLTQSPSLASIGDRVTITCRASEGIYH-----WLAWYQ 194
QY 169 QKPGSPOLLIYSGSHRASGVPDRFSGSVSGTDFTLRLSRVEAEDVGYYCMQGLQSPFT 228
DB 195 QKPGKAPLLIYKASSLASGVPDRFSGSGGTDFTLTSLLOPEDFAFYQCQHYVDSPTPT 254
QY 229 FGPGTKVDIKR 239
DB 255 FGQGTKVDIKR 265

RESULT 5
US-08-779-457-50
; Sequence 50, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-457-50

Query Match 39.1%; Score 777.5; DB 1; Length 241;
Best Local Similarity 63.3%; Pred. No. 2e-39;
Matches 157; Conservative 25; Mismatches 49; Indels 17; Gaps 3;
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
DB 1 QVRLQSGGGLVQPGGSLRLSCAASGFTEDDYAMHWVRQAPGKLEWVSGMTWNSGICY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGTTLVTVS 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAREPHN--TDAFDIWRGRTLTVTS 118
QY 121 -----SGGCALEIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGYTYLDWYLQK 170
DB 119 SGGGGGGGGGGGSDVVTQSPFLSAFVGDITITCRASQGI-----YWLAWYQK 173
QY 171 PGSPOLLIYSGSHRASGVPDRFSGSVSGTDFTLRLSRVEAEDVGYYCMQGLQSPFTFG 230
DB 174 PGKAPKLLIYAASLTQSGVPSRFSRSGSGTFTLTSLSQPEDFGTYTCQQLISYPLTFG 233
QY 231 PGTKVDIK 238
DB 234 GGTKVEIK 241

RESULT 6
US-09-976-118-1
; Sequence 1, Application US/09976118
; Patent No. US20020058033A1
; GENERAL INFORMATION:
; APPLICANT: Raischel, Kevin Paul
; APPLICANT: Curriel, David T.
; APPLICANT: Bonner, James Allen
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFv
; OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1
Query Match 38.6%; Score 767.5; DB 10; Length 268;
Best Local Similarity 63.4%; Pred. No. 8.5e-39;
Matches 161; Conservative 19; Mismatches 51; Indels 23; Gaps 6;
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTSSYAMHWVRQAPGKLEYSALISSNGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVW---DPIDYWGQGTLV 117
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCVKDVGGSSWYADYFDYWGQGTLV 120
QY 118 TVSSGGGA-----LEIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGYTYL 164
DB 121 TVSSGSASAPKLEGEFSEARVQSVLTQPP-SLSVSPQGTASITC-SGDKL----GDKYA 174
QY 165 DWYLOKPGSPOLLIYSGSHRASGVPDRFSGSVSGTDFTLRLSRVEAEDVGYYCMQ-GL 223
DB 175 SNYQKPGSPVLVIYQDKRFRSGIPERFSGSNSGNTATLTISGTQAMDEADYICQAWDS 234
QY 224 QSPFTFGPGTKVDI 237
DB 235 STPYVFGTGTQVTV 248

```

; APPLICANT: KIRCHHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
; OTHER INFORMATION:
US-10-027-770-5

Query Match 37.5%; Score 746.5; DB 12; Length 269;
Best Local Similarity 55.9%; Pred. No. 1.5e-37;
Matches 151; Conservative 40; Mismatches 56; Indels 23; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 6 EVKLVEGGDLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGSTYY 65
Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 114
Db 66 PDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCARRSEFYFYNGTYYISANDYWGQ 125
Qy 115 TLTVSS-----SGGALVLTQSPLSLPTPEGPASISCRSSQSLHNSGYTL 164
Db 126 ASVTVSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 184
Qy 165 DWYLOKPGQSPQLLIYSGSHRASGVPDRFSGSVSGTDTLIRSRVEADGVYYCMQGLQ 224
Db 185 NWFOKPGQPEKLLIYAIISNRGSGVPARFSGSGGTDFSLNIHPVEDDPAMVFCQQTKE 244
Qy 225 SPFTFGPGTKVDIKRGGGGGGGALAPTSSS 254
Db 245 VPTFGGKLEIKRADA-----APIVSA 268

RESULT 9
US-10-027-770-2
; Sequence 2, Application US/10027770
; Patent No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-2
```

```

; APPLICANT: KIRCHHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
; OTHER INFORMATION:
US-10-027-770-5

Query Match 37.5%; Score 746.5; DB 12; Length 269;
Best Local Similarity 55.9%; Pred. No. 1.5e-37;
Matches 151; Conservative 40; Mismatches 56; Indels 23; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 6 EVKLVEGGDLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGSTYY 65
Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 114
Db 66 PDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCARRSEFYFYNGTYYISANDYWGQ 125
Qy 115 TLTVSS-----SGGALVLTQSPLSLPTPEGPASISCRSSQSLHNSGYTL 164
Db 126 ASVTVSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 184
Qy 165 DWYLOKPGQSPQLLIYSGSHRASGVPDRFSGSVSGTDTLIRSRVEADGVYYCMQGLQ 224
Db 185 NWFOKPGQPEKLLIYAIISNRGSGVPARFSGSGGTDFSLNIHPVEDDPAMVFCQQTKE 244
Qy 225 SPFTFGPGTKVDIKRGGGGGGGALAPTSSS 254
Db 245 VPTFGGKLEIKRADA-----APIVSA 268

RESULT 9
US-10-027-770-2
; Sequence 2, Application US/10027770
; Patent No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-2
```

```
Query Match          37.5%; Score 745.5; DB 12; Length 269;
Best Local Similarity 55.9%; Pred. No. 1.7e-37;
Matches 151; Conservative 38; Mismatches 58; Indels 23; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 EVKLVEGGDLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 65
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWDPIDYWGQTLVT 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 PDSVKGRTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWDPIDYWGQTLVT 125
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 115 TLVTVS-----SGGGALEIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYL 164
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 ASVTVSGGGGSGGSDIVLTQSPASLAIVSLGQRATISCRASES-VDNYGFSFM 184
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 165 DWYLOKPGQSPQLLIYSGSHRASGVDPDRFSGVSGTDFTLIRISRVEADGVYVCMQGLQ 224
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 NWFOOKPGQPPKLLIYATSNRSGVGPAPRFGSGSGTDFSLNIHPVERDDSAMVFCQQTKE 244
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 225 SPFTFGPTKVDIKRKGSGGSGALAPTSSS 254
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 VPWTFGGGTLKLEIKRADA-----APTUSA 268
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-811-737-15
; Sequence 15, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Human PAP-alpha-specific antibodies
; FILE REFERENCE: 1-1129
; CURRENT APPLICATION NUMBER: US/09/811,737
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-737-15

Query Match          37.3%; Score 742; DB 10; Length 255;
Best Local Similarity 60.3%; Pred. No. 2.6e-37;
Matches 152; Conservative 27; Mismatches 53; Indels 20; Gaps 3;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGTLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISAGGYIDY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWDPIDYWGQTLVTS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRVTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWQMLDHWGGQTLVTS 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SGG-----GALIVITQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWY 167
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 SASTGPKLEEGEFSEARVDIQMTQSPSSLSASTGDRVTITCRASQDI-----SSYAWY 173
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 168 LOKPGQSPQLLIYSGSHRASGVDPDRFSGVSGTDFTLIRISRVEADGVYVCMQGLQSPF 227
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 QQAPGKAPHLMLMGATTLQTVSPFRSGSGSGTDFTLTITSLQSEDFATYYCQYYIYPP 233
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 228 TFGPTKVDIKR 239
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 TFGGTRVEIKR 245
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-920-171-22
; Sequence 22, Application US/09920171
; Patent No. US20020054878A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/987,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAEL1
US-09-920-171-22

Query Match          36.8%; Score 731.5; DB 10; Length 248;
Best Local Similarity 60.6%; Pred. No. 1.1e-36;
Matches 152; Conservative 30; Mismatches 54; Indels 15; Gaps 6;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLEWVSGISGGSTY 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKLEWVASIT-YDGSSTN 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTG-GGVWDPIDYWGQTLVT 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 YNPVSKGRVTISRDNKNTLYQMNSLRADTAIVYCAKHTG-HYFGHWH-FAVWGQTLVT 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 VSSGGGALE-----IVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYL 168
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 VSSEGGSGEGGSGGSDIQLTQSPSSLSASVGDRTITCRASKP-VDGEGDYLNNYQ 177
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 169 OKPGQSPQLLIYSGSHRASGVDPDRFSGVSGTDFTLIRISRVEADGVYVCMQGLQSPFT 228
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 QRPGKAPKLLIYAASYLESGVPSRFSFGSGGTDFTLTITSLQPEDFATYYCQQSHEDPYT 237
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 229 FGGPTKVDIKR 239
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FGGGTRVEIKR 248
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-920-171-23
; Sequence 23, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/987,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 23
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAEL1
US-09-920-171-23
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Query Match	36.7%;	Score	730.5;	DB	10;	Length	248;
Best Local Similarity	60.6%;	Pred.	No. 1.2e-36;				
Matches	152;	Conservative	29;	Mismatches	55;	Indels	15;
Gaps							
QY	1	QVQLVSGGGLVPGGSLRLSCAASGFTFRSN-AMGWVRQAPKGLEWVSGISGGSGSTY	59	:		:	:
Db	1	EVLVESGGGLVPGGSLRLSCAVSGYSITSGVSWNIHQAPKGLEWVASIKYS-GETK	59	:		:	:
QY	60	YADSVKGRFTIIRDNKSNTLYIQMNSLRRAEDTAYYYCAKHVG-GGVWDIDYWGOGTLVT	118	:		:	:
Db	60	YNPSVKGRIITSRDSSKNFTYIQMNSLRRAEDTAYYYCARGSHYFGHH-FAVWGGTILVT	118	:		:	:
QY	119	VSSGGGALE-----IVLTQSPLSFLPTVPGEPAISCSRSSQLLHSNGITYLDNYL	168	:		:	:
Db	119	VSEGGGSEGEGGGSDIQLTQSPSSLASVSGDRVTITCRASKP-VDEGDSDVNLNMYQ	177	:		:	:
QY	169	QKPGOSPOLLITSGSHRACVPPDRFSGSVSGTGDTFLIRSRVEAADGVGYCMQGQSPT	228	:		:	:
Db	178	QKPGKAPKLIIYAASYLESQVPRFSFGSGSGDTFTLIISLQPEDPATYTCQOSHDPYT	237	:		:	:
QY	229	FPGTKVDIKR	239	:		:	:
Db	238	FGOGTKVEIKR	248	:		:	:

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1  RESULT 13
2  US-09-887-853--4
3  ; Sequence 4, Application US/09887853
4  ; Patent No. US20020168375A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Huston, James S.
7  ; Oppermann, Hermann
8  ; Houston, L. L.
9  ; Ring, David B.
10 ; TITLE OF INVENTION: Biosynthetic Binding Proteins For
11 ; Imaging
12 ; NUMBER OF SEQUENCES: 11
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
15 ; STREET: Exchange Place, 53 State Street
16 ; CITY: Boston
17 ; STATE: Massachusetts
18 ; COUNTRY: USA
19 ; ZIP: 02109
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Floppy disk
22 ; COMPUTER: IBM PC compatible
23 ; OPERATING SYSTEM: PC-DOS/MS-DOS
24 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/09/887,853
27 ; FILING DATE: 21-Jun-2001
28 ; CLASSIFICATION: <Unknown>
29 ; PRIOR APPLICATION DATA:
30 ; APPLICATION NUMBER: US/08/133,804
31 ; FILING DATE: <Unknown>
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: Kelley, Robin D.
34 ; REGISTRATION NUMBER: 34,637
35 ; REFERENCE/DOCKET NUMBER: 2054/22
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: 617-248-7477
38 ; TELEFAX: 617-248-7100
39 ; INFORMATION FOR SEQ ID NO: 4:
40 ; SEQUENCE CHARACTERISTICS:
41 ; LENGTH: 252 amino acids
42 ; TYPE: amino acid
43 ; TOPOLOGY: linear
44 ; MOLECULE TYPE: protein
45 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
46 US-09-887-853--4

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Query Match 36.7%; Score 730; DB 9; Length 252;

[illegible]

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:54 ; Search time 15.5732 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-5
Perfect score: 1990
Sequence: 1 QVOLVQSGGLVQPGGSURL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	36.9	249	2 S41374	single chain Fv an
2	680	34.2	153	1 ICHU2	interleukin-2 prec
3	680	34.2	153	1 ICGI2	interleukin-2 prec
4	583.5	29.3	268	2 A56446	Ig heavy chain v r
5	543	27.3	119	2 S31107	Ig heavy chain - h
6	542	27.2	119	2 C36005	Ig heavy chain v r
7	541	27.2	233	2 JC5322	p53 specific singl
8	537	27.0	136	2 S40357	Ig kappa chain v-J
9	535.5	26.9	120	2 S48798	Ig heavy chain v r
10	534	26.8	140	2 S31686	Ig heavy chain v r
11	533	26.8	135	2 S40342	Ig kappa chain - h
12	531	26.7	119	2 S31108	Ig heavy chain - h
13	530.5	26.7	154	2 JN0698	interleukin 2 prec
14	530	26.6	117	1 K2HUGM	Ig kappa chain pre
15	529	26.6	160	2 S05271	Ig heavy chain pre
16	528	26.5	112	2 S58207	Ig light chain v r
17	528	26.5	119	2 D36005	Ig heavy chain v r
18	528	26.5	121	2 I55673	Ig heavy chain - h
19	528	26.5	132	2 S26882	Ig kappa chain v r
20	527	26.5	127	2 S38489	Ig heavy chain - h
21	527	26.5	140	2 S31588	Ig heavy chain v r
22	526	26.4	125	2 S40356	Ig kappa chain - h
23	526	26.4	134	2 S31699	Ig heavy chain v r
24	522	26.2	112	2 S58206	Ig light chain v r
25	522	26.2	123	2 S31114	Ig heavy chain - h
26	522	26.2	138	2 S31666	Ig heavy chain v r
27	518.5	26.1	124	2 S20782	Ig heavy chain v r
28	518	26.0	120	2 S36278	Ig heavy chain v r
29	511.5	25.7	126	2 S40339	Ig kappa chain - h

30 509.5 25.6 112 2 PH1647 Ig heavy chain v r
31 508.5 25.6 116 2 S31110 Ig heavy chain - h
32 505 25.4 121 2 S40371 Ig kappa chain - h
33 503 25.3 109 2 PH1649 Ig heavy chain v r
34 503 25.3 143 2 S23624 Ig heavy chain v r
35 501 25.2 121 2 S19666 Ig heavy chain v r
36 501 25.2 140 2 A30532 Ig heavy chain pre
37 500 25.1 113 1 K2HUTW Ig kappa chain v-I
38 498 25.0 121 2 G36005 Ig heavy chain v r
39 498 25.0 131 2 S40372 Ig kappa chain v-J
40 496.5 24.9 151 2 A60943 Ig heavy chain pre
41 495.5 24.9 108 2 PH1648 Ig heavy chain v r
42 494.5 24.8 140 2 S70442 Ig heavy chain pre
43 494 24.8 134 2 S31679 Ig heavy chain v r
44 492.5 24.7 122 2 S20772 Ig heavy chain v r
45 492 24.7 121 2 S31113 Ig heavy chain - h

ALIGNMENTS

RESULT 1
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match 36.9%; Score 734; DB 2; Length 249;
Best Local Similarity 58.6%; Pred. No. 1.8e-45;
Matches 146; Conservative 36; Mismatches 55; Indels 12; Gaps 2;

Qy 1 QVOLVQSGGLVQPGGSRLRLSCAASGFTFRSNAMGVWRQAPGKLEWVGSGSGSTYY 60
Db 1 QVOLVQSGGLVQPGGSRLRLSCAASGFTFRSNAMGVWRQAPGKLEWVGSGSGSTYY 60
Qy 61 ADSVKGRFTISRDNSKNTLYLQMSLRADTVAVYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 61 VPRQDKRATITADTSNTAYLLLSLTSEDTAVYCAARR--DTLYTSLGVWGGSGSTVTVS 118
Qy 121 -----SGGALIEIVITQSPSLPVTTPGEPASISCRSSQSLHNSGYTLDWYLOK 170
Db 119 SRGGSGGGSGGGGGSDIELTQSPSPVVIPTGESVSISSCRSSKSLYSDDSYLFWFLQR 178
Qy 171 PQGSPQLLIYSGSHRASGVDPDRFSGSVSGDFTLRISRVEAEADVGVYCMQGLQSPFTFG 230
Db 179 PQGSPQLLIYRMSNLASGVDPDRFSGSGSTFRLISRVEAEADVGVYCMQHREYPLTFG 238
Qy 231 PGTKVDIKR 239
Db 239 AGTKLELKR 247

RESULT 2
ICHU2
interleukin-2 precursor [validated] - human
N:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330695

A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HOL>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2529
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniiguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A:Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <FUJ>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the gene
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:g186302; PIDN:AAA98792.1; PID:g386819
R:Laabli, Y.; Gras, M.P.; Carboneil, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:Z14955
A:Note: This sequence is shown from the beginning of the fragment to the chromosomal break
R:Taniiguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro
Nature 302, 305-310, 1983
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K.;
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.
A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <MAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:Devos, R.; Plaetinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remaut
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <EIZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 5-7, 'F', 9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AAD14264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.

A:Reference number: I52528
A:Accession: I52528
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE2>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508
R:Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes
A:Reference number: I57603; MUID:87064618; PMID:3491296
A:Accession: I57603
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'M', 21-153 <REA>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold with
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimitz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860
A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grabenhorst, E.; Hofer, B.; Nimitz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
C:Genetics:
A:Gene: GDB: IL2
A:Cross-references: GDB:119344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status experimental <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:78-125/Disulfide bonds: #status experimental
Query Match 34.2% Score 680; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 7-2e-42;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 APTSSSTKKTQLQLEHLLDLQMLINGNNYKNPKLTRMLTFKYPMPKATELKHQCLE 308
DB 21 APTSSSTKKTQLQLEHLLDLQMLINGNNYKNPKLTRMLTFKYPMPKATELKHQCLE 80
QY 309 ELKPLEEVNLQAQKNFHLPRDLISNNIVLELKGSETTMCCEYADETATVEFLNR 368
DB 81 EELKPLEEVNLQAQKNFHLPRDLISNNIVLELKGSETTMCCEYADETATVEFLNR 140

Qy 369 WITFCQSIISTLT 381

Db 141 WITFCQSIISTLT 153

RESULT 3

ICG12
Interleukin-2 precursor - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylotates lar (common gibbon); white-banded gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtree,
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that cons
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CHE>
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: The integration of a retrovirus sequence containing a 5' LTR into the 3' noncodi
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status predicted <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:78-125/Disulfide bonds: #status predicted

Query Match 34.2%; Score 680; DB 1; Length 153;

Best Local Similarity 100.0%; Pred. No. 7.2e-42;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 APTSSSTKTKQLQLBHLHLLDQMLINGNNYKNPKLTRLMTFFKPYMPKKATLKHQCLE 308

Db 21 APTSSSTKTKQLQLBHLHLLDQMLINGNNYKNPKLTRLMTFFKPYMPKKATLKHQCLE 80

Qy 309 EEKPLEEVLNLAQSKNFHLPRDLISINIVILELKGSETFMCEYADETATVEFLNR 368

Db 81 EEKPLEEVLNLAQSKNFHLPRDLISINIVILELKGSETFMCEYADETATVEFLNR 140

Qy 369 WITFCQSIISTLT 381

Db 141 WITFCQSIISTLT 153

RESULT 4

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.3%; Score 583.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 1.2e-34;

Matches 119; Conservative 36; Mismatches 75; Indels 19; Gaps 3;

Qy 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Db 3 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 62

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLTVTS 120

Db 63 DPKFGKATIAADSSNTAYLQLSLTSEDTAVYYCASY--LTRYENWGQGLTLTVTS 119

Qy 121 -----SGGALEIVLTQSPSLPVTPGPPASISCRSSQSLHNSNYTYVLDWYLOK 170

Db 120 SGGGSGGGSGGGGSDIELTQSPAIMSALGKVTMSCRASSV-----NFIWYQOK 173

Qy 171 PGQSPQLLYSGSHRASGVDPFRFSGVSGYGTDTFLRISRVEAEADVGVYCMQGLQSPFTFG 230

Db 174 SDASPGLWVYVYTHLPQVGFARFSGSGSNYSLSLTISSEGEADAATYYCQQTSSPFTFG 233

Qy 231 PGTQVDIKR 239

Db 234 SGTLEIKR 242

RESULT 5

S31107

Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62955
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 543; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 3.5e-32;

Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLTVTS 120

Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLTVTS 118

Qy 121 S 121

Db 119 S 119

RESULT 6

C36005

Ig heavy chain V region (30pl) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: C36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 27.2%; Score 542; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 4.2e-32;
Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGGSIYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISATSGSGGSIYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWDPIDYWGQGTLTIVS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKADAGWG--SGFDYWGQGTLTIVS 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 S 121
|
Db 119 S 119

RESULT 7
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Janot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 27.2%; Score 541; DB 2; Length 233;
Best Local Similarity 48.8%; Pred. No. 1.2e-31;
Matches 118; Conservative 33; Mismatches 71; Indels 20; Gaps 5;

QY 6 QSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGGSIYADSVK 65
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ESGAEIVRSGASVKLSCTTSGFINDIYMHVKKRPEQGLEWIGRIDPENGADMTFRSSG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 66 GRTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWDPIDYWGQGTLTIVS----- 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 62 VKATMTADTSSNAYLQLSLTSEDFAVYIC--NAG-----MDYWGQGTIVTSSGGG 113
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 -----SGGGALEIVLTQSPISLPTVTPGEPAISCRSSQSLHNSGYTYLDWYLQKPGQSP 175
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 114 SGRASGGGDIETLTQSPASLAVSLQRTATISCRASKS-VSTSGYSYMHWNQKPGQPP 172
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 176 QLLIYSGSHRASGVPDRFSGSVSGTDFTLISRVEAEDGVYCYCMQGLQSPFTFGPCTKV 235
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 173 RLLIYLVNLESGVPRFSGSGTDFTLNHPVEEADAATYYC-QHIRELTRSEGGTKL 231
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 236 DI 237
:|
Db 232 EI 233
:|

RESULT 8
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 537; DB 2; Length 136;
Best Local Similarity 83.9%; Pred. No. 1.1e-31;
Matches 104; Conservative 9; Mismatches 9; Indels 2; Gaps 1;

QY 116 LVTYSSGGALEIVLTQSPISLPTVTPGEPAISCRSSQSLHNSGYTYLDWYLQKPGQSP 175
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 12 MLWYSSGSG--DIVMTQSPISLPTVTPGEPAISCRSSQSLHNSGYTYLDWYLQKPGQSP 69
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 176 QLLIYSGSHRASGVPDRFSGSVSGTDFTLISRVEAEDGVYCYCMQGLQSPFTFGPCTKV 235
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 70 QLLIYLSNRASGVPDRFSGSGTDFTLISRVEAEDGVYCYCMQALQTPWTFGQGTKV 129
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 236 DIKR 239
:||||
Db 130 EIKR 133
:||||

RESULT 9
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S48798
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48798
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAH>
A:Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 26.9%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.9%; Pred. No. 1.2e-31;
Matches 106; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGGSIYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISATSGSGGSIYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWDPI-DYWGQGTLTIV 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKDR--GEWSGYKDYWGQGTLTIV 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 120 SS 121
||
Db 119 SS 120
||

RESULT 10
S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31686
R:Cuisinier, A.M.; Gauthier, L.; Boubili, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31686
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CU1>
A:Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 26.7%; Score 531; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.6e-31;
Matches 106; Conservative 3; Mismatches 7; Indels 8; Gaps 2;

QY	1	QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY	60
		: :: : : : : : : : : : : :	
Db	1	EVQLVQSGGGLVOPGGSLRLSCAASGFTFSYAMSWVQAPGKLEWVAISGGSTYY	60
QY	61	ADSVKGRFTISRDNSKNTLYQMNSLRAEETAVYYCAKH---TGGGVWDPIDYWGQGTLY	117
		: : : : : : : : : :	
Db	61	ADSVKGRFTISRDNSKNTLYQMNSLRAEETAVYYCAKDRLTG-----TFDIWGQGTLY	115
QY	118	TVSS 121	
Db	116	TVSS 119	

```

RESULT 13
JN0698
interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
C:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761
A:Accession: JN0698
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <CQ>
A:Cross-references: GB:119402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

```

		Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	Length
QY	249	APTSSSTKKTQLEHLHLLDLOMLGNIYNNPKLTRMLTFKFFYMPKKATELKHQCLLE	26.7%; Score 530.5; DB 2;	154;					
Db	21	APASSSTKETQOQLEQLLDRLLLGVNNPENPKLSRMLTFKFYVPKKATELTHLQCLV	78.4%; Pred. No. 3.9e-31;	105;	13;	15;	1;	1;	154;
QY	309	EELKPLEEVLYLAQSNFHLRP-RDLISINIVYVLELKGSETTFMCEYADETATIVFEFLN		367					
Db	81	EELKPLEEVLYLAQSNFHLNHIKELMSINIVTLKLGSETRFTCYNDDETATIVFEFLN		140					
QY	368	RWITFCQSIITSLT	381						
Db	141	KWITFCQSIIFSLT	154						

RESULT 14
K2HUGM

Ig kappa chain precursor V-II region (SM607) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984

A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity

A:Reference number: A01889; MUID:84191506; PMID:6325927

A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene

C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical li

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
 F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>
 F:20-99/Domain: immunoglobulin homology <IMM>
 F:27-97/Disulfide bonds: #status predicted

Query Match 26.6%; Score 530; DB 1; Length 117;
 Best Local Similarity 87.2%; Pred. No. 3e-31;
 Matches 102; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 123 GGALEIVLQSPSLPVPVTPGEPASISCRSSQSLHLSNGYTYLDWYLPQPGSQPQLLIYSG 182

Db 1 GSSGDIVMTQSPSLPVPVTPGEPASISCRSSQSLHLSNGYNYLDWYLPQPGSQPQLLIYLG 60

QY 183 SHRAGVDPDRFSGSVSGTDTLIRISVRAEDGVVYCMQGLQSPETFGGPKVDIKR 239

Db 61 SNRAGVDPDRFSGSGGTDTLIRISVRAEDGVVYCMQGLQTPOTFGGPKVEIKR 117

RESULT 15

S05271
 Ig heavy chain precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
 C:Accession: S05271; S04602
 R:Kishimoto, T.
 submitted to the EMBL Data Library, March 1989
 A:Reference number: S05270
 A:Accession: S05271
 A:Molecule type: mRNA
 A:Residues: 1-160 <KIS1>
 A:Cross-references: EMBL:X14584
 R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
 Nucleic Acids Res. 17, 4385, 1989
 A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
 A:Reference number: S04601; MUID:89296497; PMID:2500644
 A:Accession: S04602
 A:Molecule type: mRNA
 A:Residues: 1-144 <KIS2>
 A:Cross-references: EMBL:X14584
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 529; DB 2; Length 160;
 Best Local Similarity 69.7%; Pred. No. 5.2e-31;
 Matches 108; Conservative 11; Mismatches 18; Indels 18; Gaps 3;

QY 1 QVOLVSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPKGLEWVSGISGSGSTYY 60

Db 20 EVOLLESGLVQPGGSLRLSCAASGFTFTSTAMSWVROAPKGLEWVAISGSGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGV----WDPIDYWGQGT 116

Db 80 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKAVRGRVISYVYGMVWGQGT 139

QY 117 VTVSSGGGALEIVLQSPSLPVPVTPGEPASISCRS 151

Db 140 VTVSSGSAS-----APTLFPL-----VSCEN 160

Search completed: March 14, 2003, 11:51:07
 Job time : 16.5732 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 8.69202 Seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....IVEFLNRWITFCQSIITLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	680	34.2	153	1 IL2_HUMAN	P01585 homo sapien
2	652.5	32.8	154	1 IL2_MACMU	P51498 macaca mula
3	647.5	32.5	154	1 IL2_CERTO	P46649 cercopithecus
4	644.5	32.4	154	1 IL2_MACFA	Q29615 macaca fasc
5	534.5	26.9	154	1 IL2_MIRAN	O62641 mirounga an
6	530.5	26.7	154	1 IL2_FELCA	Q07885 felis silve
7	530	26.6	117	1 KV2E_HUMAN	P06309 homo sapien
8	513.5	25.8	153	1 IL2_RABIT	O77620 oryctolagus
9	502	25.2	155	1 IL2_CANFA	Q29416 canis famil
10	500	25.1	113	1 KV2D_HUMAN	P01617 homo sapien
11	478.5	24.0	112	1 KV2C_HUMAN	P01616 homo sapien
12	478.5	24.0	155	1 IL2_MERUN	Q08081 meriones un
13	472.5	23.7	154	1 IL2_PIG	P26891 sus scrofa
14	471	23.7	117	1 KV3C_HUMAN	P01764 homo sapien
15	467.5	23.5	115	1 KV2A_HUMAN	P01614 homo sapien
16	466.5	23.4	114	1 KV3B_HUMAN	P01763 homo sapien
17	461	23.2	149	1 IL2_HORSE	P37997 equus cabal
18	460.5	23.1	152	1 IL2_ORCOR	O97513 orcinus orc
19	456.5	22.9	122	1 KV3G_HUMAN	P01768 homo sapien
20	455	22.9	113	1 KV2B_HUMAN	P01615 homo sapien
21	450.5	22.6	122	1 KV3A_HUMAN	P01762 homo sapien
22	449.5	22.6	116	1 KV3T_HUMAN	P01781 homo sapien
23	447	22.5	121	1 KV3J_HUMAN	P01771 homo sapien
24	447	22.5	133	1 KV2F_HUMAN	P06310 homo sapien
25	445.5	22.4	155	1 IL2_RAT	P17108 rattus norv
26	438.5	22.0	116	1 HV05_CARAU	P19181 carassius a
27	437.5	22.0	122	1 KV3H_HUMAN	P01769 homo sapien
28	437.5	22.0	126	1 KV3K_HUMAN	P01782 homo sapien
29	435.5	21.9	136	1 HV16_MOUSE	P01783 mus musculu
30	435	21.9	115	1 KV3D_HUMAN	P01765 homo sapien
31	432	21.7	113	1 KV2E_MOUSE	P03976 mus musculu
32	432	21.7	117	1 HV02_CANFA	P01785 canis famil
33	429	21.6	113	1 KV2G_MOUSE	P01631 mus musculu

34	428	21.5	119	1 HV3I_HUMAN	P01770 homo sapien
35	427	21.5	115	1 HV3F_HUMAN	P01767 homo sapien
36	423	21.3	113	1 KV2F_MOUSE	P01630 mus musculu
37	422.5	21.2	120	1 HV3U_HUMAN	P01782 homo sapien
38	419.5	21.1	119	1 HV3M_HUMAN	P01774 homo sapien
39	419	21.1	120	1 HV3E_HUMAN	P01766 homo sapien
40	417.5	21.0	119	1 HV3N_HUMAN	P01775 homo sapien
41	414	20.8	119	1 HV3L_HUMAN	P01773 homo sapien
42	408.5	20.5	169	1 IL2_MOUSE	P04351 mus musculu
43	405	20.4	155	1 IL2_SHEEP	P19114 ovis aries
44	404	20.4	166	1 IL2_MUSSP	Q08867 mus spretus
45	404	20.3	155	1 IL2_BOVIN	P05016 bos taurus

ALIGNMENTS

RESULT 1
IL2_HUMAN
ID IL2_HUMAN STANDARD; PRT; 153 AA.
AC P01585;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
DE (Aldesleukin).
GN IL2.
OS Homo sapiens (Human), and
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9580;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=84247353; PubMed=6330695;
RA Holbrook N.J., Lieber M., Crabtree G.R.;
RT "DNA sequence of the 5' flanking region of the human interleukin 2
gene: homologies with adult T-cell leukemia virus.";
RL Nucleic Acids Res. 12:5005-5013(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=83167472; PubMed=6403867;
RA Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,
RA Yoshimoto T., Hamuro J.;
RT "Structure and expression of a cloned cDNA for human interleukin-2.";
RL Nature 302:305-310(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=84023840; PubMed=6312994;
RA Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,
RA Fujimoto K., Teranishi T., Hirano T., Onoue K.;
RT "Cloning of Interleukin 2 mRNAs from human tonsils.";
RL Biochem. Biophys. Res. Commun. 115:1040-1047(1983).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=63246551; PubMed=6306584;
RA Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,
RA Tavernier J., Remaut E., Fiers W.;
RT "Molecular cloning of human interleukin 2 cDNA and its expression in
E. coli.";
RL Nucleic Acids Res. 11:4307-4323(1983).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=84170356; PubMed=6608729;
RA Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,
RA Wiskocil R.L., Crabtree G.R.;
RT "T-cell growth factor: complete nucleotide sequence and organization
of the gene in normal and malignant cells.";

Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).

[6]
RN
RP
SEQUENCE FROM N.A.
SPECIES=Human;
MEDLINE=84170243; PubMed=6324170;
RX
MEDLINE=84170243; PubMed=6324170;
RA
Fujita T., Takaoka C., Matsui H., Taniguchi T.;
"Structure of the human interleukin 2 gene.";
Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
[7]
RN
RP
SEQUENCE FROM N.A.
SPECIES=Human;
MEDLINE=95239150; PubMed=7722480;
RX
Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
"Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
J. Neurochem. 64:1928-1936(1995).
[8]
RN
RP
SEQUENCE FROM N.A.
SPECIES=Human;
MEDLINE=95239150; PubMed=7722480;
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Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
"Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
J. Neurochem. 64:1928-1936(1995).
[9]
RN
RP
SEQUENCE FROM N.A.
SPECIES=Human;
MEDLINE=95239150; PubMed=7722480;
RX
Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
"Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
J. Neurochem. 64:1928-1936(1995).
[10]
RN
RP
SEQUENCE OF 21-153 FROM N.A.
SPECIES=Human;
MEDLINE=89062420; PubMed=3264184;
RX
Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;
"Structure-activity relationships of recombinant human Interleukin
2.";
Biochemistry 27:6883-6892(1988).
[11]
RN
RP
SEQUENCE OF 1-69 FROM N.A.
SPECIES=Human;
MEDLINE=87064618; PubMed=3491296;
RX
Stebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
Kamoun M., Kant J.A., Crabtree G.R.;
"Promoter region of interleukin-2 gene undergoes chromatin structure
changes and confers inducibility on chloramphenicol acetyltransferase
gene during activation of T cells.";
Mol. Cell. Biol. 6:3042-3049(1986).
[12]
RN
RP
SEQUENCE OF 1-68 FROM N.A.
SPECIES=Human;
MEDLINE=87064618; PubMed=3491296;
RX
Stebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
Kamoun M., Kant J.A., Crabtree G.R.;
"Promoter region of interleukin-2 gene undergoes chromatin structure
changes and confers inducibility on chloramphenicol acetyltransferase
gene during activation of T cells.";
Mol. Cell. Biol. 6:3042-3049(1986).
[13]
RN
RP
SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.
SPECIES=Human;
MEDLINE=85038540; PubMed=6333684;
RX
Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;
"Amino acid sequence and post-translational modification of human
interleukin 2.";
Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).
[14]
RN
RP
CARBOHYDRATE-LINKAGE SITE.
SPECIES=Human;
MEDLINE=90008901; PubMed=2793860;
RX
Conrad H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
Hauser H.;
"Expression of human interleukin-2 in recombinant baby hamster
kidney, Ltk-, and Chinese hamster ovary cells. Structure of O-linked
carbohydrate chains and their location within the polypeptide.";
J. Biol. Chem. 264:17368-17373(1989).

[15]
RN
RP
SEQUENCE FROM N.A.
SPECIES=H.lar;
MEDLINE=86042650; PubMed=3877307;
RX
Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
Greengard J.S., Crabtree G.R., Lin Y.;
"A viral long terminal repeat in the interleukin 2 gene of a cell
line that constitutively produces interleukin 2.";
Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
[16]
RN
RP
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
SPECIES=Human;
MEDLINE=88070646; PubMed=3500515;
RX
Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;
"Three-dimensional structure of interleukin-2.";
Science 238:1707-1709(1987).
[17]
RN
RP
X-RAY CRYSTALLOGRAPHY.
MEDLINE=92335891; PubMed=1631562;
RX
Bazan J.F.;
"Unraveling the structure of IL-2.";
Science 257:410-412(1992).
[18]
RN
RP
RESPONSE TO ABOVE LETTER.
McKay D.B.;
Science 257:412-413(1992).
[19]
RN
RP
STRUCTURE BY NMR.
MEDLINE=92379010; PubMed=1510960;
RX
Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
Campbell I.D.;
"Secondary structure of human interleukin 2 from 3D heteronuclear NMR
experiments.";
Biochemistry 31:7741-7744(1992).
[20]
RN
RP
3D-STRUCTURE MODELING.
MEDLINE=95111955; PubMed=7529123;
RX
Bamorough P., Hedgecock C.J., Richards W.G.;
"The interleukin-2 and interleukin-4 receptors studied by molecular
modelling.";
Structure 2:839-851(1994).
CC
-!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC
-!- SUBCELLULAR LOCATION: Secreted.
CC
-!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
WHICH INVOLVES IL2 AND BCMA.
CC
-!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
in patients with renal cell carcinoma or metastatic melanoma.
CC
-!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
-!- DATABASE: NAME-R&D Systems' cytokine source book: IL2;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=206".
CC

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CC
EMBL: J00264; AAD48509.1; -
DR
EMBL: X01586; CAA25742.1; -
DR
EMBL: X00564; CAA23827.1; -
DR
EMBL: K02056; AAA98792.1; -
DR
EMBL: M13879; AAA59141.1; -
DR
EMBL: K03174; AAA35453.1; -
DR
EMBL: S77834; AAD14263.2; -
DR
EMBL: S82692; ABA46803.1; -
DR

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Query Match          34.2%; Score 680; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2e-47;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 APTSSSTKKTQLEHLLLDLQMLNGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 308
DB 21 APTSSSTKKTQLEHLLLDLQMLNGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 80
QY 309 EELKPLEEVNLAKSKNFHLR-PRDLISNLNVIVLELKGSETTFMCEYADETATIVFEFLNR 368
DB 81 EELKPLEEVNLAKSKNFHLR-PRDLISNLNVIVLELKGSETTFMCEYADETATIVFEFLNR 140
QY 369 WITFCOSIISTLT 381
DB 141 WITFCOSIISTLT 153

RESULT 2
IL2_MACMU
ID IL2_MACMU STANDARD; PRT; 154 AA.
AC P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19847; AAB60400.1; -
DR EMBL; U19852; AAB6714.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
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SQ SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;
Query Match          32.8%; Score 652.5; DB 1; Length 154;
Best Local Similarity 97.0%; Pred. No. 3.2e-45;
Matches 130; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLEHLLLDLQMLNGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 308
DB 21 APTSSSTKKTQLEHLLLDLQMLNGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 80
QY 309 EELKPLEEVNLAKSKNFHLR-PRDLISNLNVIVLELKGSETTFMCEYADETATIVFEFLNR 367
DB 81 EELKPLEEVNLAKSKNFHLR-PRDLISNLNVIVLELKGSETTFMCEYADETATIVFEFLNR 140
QY 368 WITFCOSIISTLT 381
DB 141 WITFCOSIISTLT 154

RESULT 3
IL2_CERTO
ID IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
DR EMBL; U19846; AAB60399.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
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SQ SEQUENCE 154 AA; 17754 MW; 9FEB51814204BA48 CRC64;

Query Match 32.5%; Score 647.5; DB 1; Length 154;
Best Local Similarity 96.3%; Pred. No. 8e-45;
Matches 129; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 249 APTSSSTKTKTQLQLEHLLLDLOMLANGINNYKNPKLTRMLTKFYMPKKATELKHQCLE 308
|||||
Db 21 APTSSSTKTKTQLQLEHLLLDLOMLANGINNYKNPKLTRMLTKFYMPKKATELKHQCLE 80
|||||
QY 309 EELKPLEVLNLAQSKNFHLR-PRDLISININVIVLELKGSETTFMCEYADETATIVFEFLN 367
|||||
Db 81 EELKPLEVLNLAQSKNFHLRDTKDLISININVIVLELKGSETTLMCEYADETATIVFEFLN 140
|||||
QY 368 RWITFCOSIISTLT 381
|||||
Db 141 RWITFCOSIISTLT 154
|||||

RESULT 4
IL2_MACFA STANDARD; PRT; 154 AA.
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Peripheral blood;
RC Yabe M., Matsura Y., Tatsumi M.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
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-----
CC EMBL; D63352; BAA09676.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL.
FT CHAIN 1 20 BY SIMILARITY.
FT CARBOHYD 21 154 INTERLEUKIN-2.
FT DISULFID 23 23 O-LINKED (GALNAC. .) (BY SIMILARITY).
FT SEQUENCE 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17696 MW; 7953FE624A5EA49 CRC64;

Query Match 32.4%; Score 644.5; DB 1; Length 154;
Best Local Similarity 95.5%; Pred No. 1.4e-44;

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Db 21 APTSTKTKTQOOLQLLLDLRLLLNGVNNYEDPKLSRMLTFKFTYPPKKATLTHLQCL 80
QY 309 EELKPLEEVNLQAQSKNFHLRP-RDLISINNVIVLELKGSETTFMCEYADETATIFEFLN 367
Db 81 EELKPLEEVLYLAQSKNFHLTDIKELMSNINVTLLKLGSETRFCEYDDTATITEFLN 140
QY 368 RWITFCQSIISTLT 381
Db 141 KWITFCQSIISTLT 154

RESULT 6
IL2_FELCA STANDARD; PRT; 154 AA.
AC Q07885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) ("TCGF", IL2).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA Leff A.R.;
RT "Sequence and functional characterization of feline interleukin 2.";
RL Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC -----
CC EMBL; L19402; AAA02865.1; -
CC DR EMBL; L25408; AAA51431.1; -
CC DR PIR; JN0698; JN0698.
CC DR HSP; P01585; 3INK.
CC DR InterPro; IPR000779; Interleukin-2.
CC DR Pfam; PF00715; IL2; 1.
CC DR PRINTS; PR00265; INTERLEUKIN2.
CC DR ProDom; PD003649; Interleukin-2; 1.
CC DR SMART; SM00189; IL2; 1.
CC DR PROSITE; PS00424; INTERLEUKIN_2; 1.
CC KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT DISULFID 78 126 BY SIMILARITY.
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 4 KI -> RM (IN REF. 2).
FT CONFLICT 150 150 F -> I (IN REF. 2).
SQ SEQUENCE 154 AA; 17653 MW; 2E71E3BD8B9665EF CRC64;

Query Match 26.7%; Score 530.5; DB 1; Length 154;
Best Local Similarity 78.4%; Pred. No. 1.7e-35;

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Matches 105; Conservative 13; Mismatches 15; Indels 1; Gaps 1;
QY 249 APTSSSTKTKTQOOLQLLLDLRLLLNGVNNYKPKLTRLMTFFKYPKKATLKHLOCLE 308
Db 21 APASSSTKTKTQOOLQLLLDLRLLLNGVNNPENPKUSRLTFFKYPKKATLTHLOCLV 80
QY 309 EELKPLEEVNLQAQSKNFHLRP-RDLISINNVIVLELKGSETTFMCEYADETATIFEFLN 367
Db 81 EELKPLEEVLYLAQSKNFHLNHIKELMSNINVTLLKLGSETRFCTCNYDDTATIFEFLN 140
QY 368 RWITFCQSIISTLT 381
Db 141 KWITFCQSIISTLT 154

RESULT 7
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
CC DR PIR; A01889; K2HUCM.
CC DR HSP; P80362; 1WTL.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003596; Ig_V.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 26.6%; Score 530; DB 1; Length 117;
Best Local Similarity 87.2%; Pred. No. 1.3e-35;
Matches 102; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 123 GGALEIVLTOSPLSLPVTGPEPASISCRSSQSLHNSGYLDWYLOKQPSQLLIYSG 182
Db 1 GSSGDIVMTOSPLSLPVTGPEPASISCRSSQSLHNSGYLDWYLOKQPSQLLIYLG 60

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QY 183 SHRASCVPDRFSGSGTDFTLIRISRVEADVGVIYCMQGLQSPFTFGGKVDIKR 239
 Db 61 SNRASCVPDRFSGSGTDFTLIRISRVEADVGVIYCMQGLQSPFTFGGKVDIKR 117

RESULT 8

IL2_RABIT
 ID IL2_RABIT STANDARD; PRT; 153 AA.
 AC Q77620;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
 European rabbit (Oryctolagus cuniculus).";
 RL Cytokine 12:535-565(2000).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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 CC -----
 DR EMBL; AF068057; AAC23838.1; -;
 DR HSP; P01585; 31NK.
 DR InterPro: IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 153 INTERLEUKIN-2.
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNA. . .) (POTENTIAL).
 FT DISULFID 78 125 BY SIMILARITY.
 SQ SEQUENCE 153 AA; 17256 MW; 8173536B2DD8B86 CRC64;

Query Match 25.8%; Score 513.5; DB 1; Length 153;
 Best Local Similarity 80.9%; Pred. No. 3.9e-34;
 Matches 106; Conservative 9; Mismatches 13; Indels 3; Gaps 3;

QY 249 APTSSSTKTKQLQLEHLLDQLMILGNNYKPKLRLTKFYMPKKATELKHLCIE 308
 Db 21 APTSSSTKTKQLDQLLDQLLVKGVNDYKNSLRLTKFYMPKKVTELKHLCIE 80
 QY 309 EELKPLEEVNLQAQKNFH-LRPDLISNINIVIELKGSFTFMCEYADETATVEFLN 367
 Db 81 EELKPLEEVNLQAQKNGHTRESINIVTLKLGSE-TFMCEY-DETATVEFLN 138
 QY 368 RWITFCQSIIIS 378
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 24 24 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 112 112 N-LINKED (GLCNA. . .) (POTENTIAL).
 FT DISULFID 79 127 BY SIMILARITY.
 FT CONFLICT 4 4 M -> I (IN REF. 3).

Db 139 RWITFCQSIIIS 149
 IL2_CANFA
 ID IL2_CANFA STANDARD; PRT; 155 AA.
 AC Q29416; Q28249;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;
 RX MEDLINE=95337423; PubMed=7612930;
 RA Dunham S.P., Argyle D.J., Onions D.E.;
 RT "The isolation and sequence of canine interleukin-2.";
 RL DNA Seq. 5:177-180(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=96016696; PubMed=8571541;
 CC Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,
 CC Henthorn P.S.;
 CC "A single nucleotide insertion in the canine interleukin-2 receptor
 CC gamma chain results in X-linked severe combined immunodeficiency
 CC disease.";
 CC Vet. Immunol. Immunopathol. 47:203-213(1995).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Beagle; TISSUE=Spleen;
 CC MEDLINE=95347614; PubMed=7622066;
 CC Knapp D.W., Williams J.S., Andrisani O.M.;
 CC "Cloning of the canine interleukin-2-encoding cDNA.";
 CC Gene 159:281-282(1995).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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 CC -----
 DR EMBL; D30710; BAA06378.1; -;
 DR EMBL; U28141; AAA68969.1; -;
 DR EMBL; U11689; AAA75360.1; -;
 DR HSP; P01585; 31NK.
 DR InterPro: IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 24 24 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 112 112 N-LINKED (GLCNA. . .) (POTENTIAL).
 FT DISULFID 79 127 BY SIMILARITY.
 FT CONFLICT 4 4 M -> I (IN REF. 3).

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FT CONFLICT 37 37 Q -> R (IN REF. 3).
FT CONFLICT 151 151 F -> Y (IN REF. 3).
FT CONFLICT 154 154 L -> M (IN REF. 3).
SQ SEQUENCE 155 AA; 17668 MW; D123E486B7F4ACID CRC64;

Query Match 25.2%; Score 502; DB 1; Length 155;
Best Local Similarity 73.3%; Pred. No. 3.2e-33;
Matches 99; Conservative 17; Mismatches 17; Indels 2; Gaps 2;

QY 249 AP-TSSSKTKQLOLEHLLDQMLANGINNYKNPKLTRMLTFKFPKPKATELKHLOCL 307
DB 21 APTSSSTKETEQMEQLLDQLLNGVNNYENPQLSRMLTFKFPKPKATEFTHLOCL 80

QY 308 EELKPLEEVLNLAQSNHFLR-PRDLISININVLLELKGSETFMCEYADETATIVFEFL 366
DB 81 AEELKNLEEVGLPQSKNVHLTDTKELISNNVTLLELKGSETSYNCEYDEETATITEFL 140

QY 367 NRWTFQOSIISTLT 381
DB 141 NKWTFQOSIFSTLT 155

RESULT 10
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN P01617;
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01887; K2HUML.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;

PRT; A01888; K2HUTW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Anyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 FRAMEWORK-3.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;

Query Match 24.0%; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.8%; Pred. No. 1.6e-31;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 127 EIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 186
DB 1 DIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 59

QY 187 SGVPDRFSGSVSGTDTFLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 239
DB 60 SGVPNRFSGSGTBTFLKISRVAZBVGVIYCMQALQTLPTLFGGNTVNEIKR 112

RESULT 12
IL2_MERON STANDARD; PRT; 155 AA.
ID IL2_MERON Q08081;
AC Q08081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

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Query Match 25.1%; Score 500; DB 1; Length 113;
Best Local Similarity 82.3%; Pred. No. 3.1e-33;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 127 EIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 186
DB 1 DIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 187 SGVPDRFSGSVSGTDTFLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 239
DB 61 SGVPDRFSGSGTDTFLKISRVAEDGVGYCMZALQAPITFGGTRLEIKR 113

RESULT 11
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID KV2C_HUMAN P01616;
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01887; K2HUML.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B2E2FA7ABE481 CRC64;

Query Match 24.0%; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.8%; Pred. No. 1.6e-31;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 127 EIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 186
DB 1 DIVLTQSPLSPLVPTGPEPASISCRSSQSLHSHNGVITYLDWYLOKPGQSPQLLIYSGSHRA 59

QY 187 SGVPDRFSGSVSGTDTFLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 239
DB 60 SGVPNRFSGSGTBTFLKISRVAZBVGVIYCMQALQTLPTLFGGNTVNEIKR 112

RESULT 12
IL2_MERON STANDARD; PRT; 155 AA.
ID IL2_MERON Q08081;
AC Q08081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

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OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RC MEDLINE=94174702; PubMed=8128610;
RA Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;
RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)
RT interleukin-2 cDNA and its expression in COS-7 cells.";
RL Vet. Immunol. Immunopathol. 40:63-71(1994).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X68779; CAA48679.1; -.
DR PIR; S33509; S33509.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 155 AA; 17602 MW; D0F74AA1A381CDDA CRC64;

Query Match 24.0%; Score 478.5; DB 1; Length 155;
Best Local Similarity 70.1%; Pred. No. 2.4e-31;
Matches 94; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRLMTFKFYMPPKATELKHLCLE 308
DB 21 APTSSPAKEAQYQLQLLLDLQQLRGINNYKNPKLPMLTFKFYMPPKATELKHLCLE 80
QY 309 EELKPLEEVLNLAQSKNFHRLPR-DLIISNIVIVLELKGSETTFMCFYADETATVEFLN 367
DB 81 EELGPLHDLVNLVQSKNLYLEDAGNFISNIRVTVMKLKGSENTLNCDFDDETVTVEFLS 140
QY 368 RWITFCQSIISTLT 381
DB 141 RWITFCQSAISTWT 154

RESULT 13
IL2_PIG
ID IL2_PIG STANDARD; PRT; 154 AA.
AC P26891;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RC MEDLINE=91274360; PubMed=2054386;
RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;
RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction.";
RL Biochim. Biophys. Acta 1089:257-258(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA Lefevre F.;
RN Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;
RT "Structure of the porcine chromosomal interleukin-2 gene.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X56750; CAA40071.1; -.
DR EMBL; X58428; CAA41330.1; -.
DR EMBL; AB041935; BAB16110.1; -.
DR PIR; S15473; S15473.
DR PIR; S16241; S16241.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17401 MW; F3B95E43D4A3D3E1 CRC64;

Query Match 23.7%; Score 472.5; DB 1; Length 154;
Best Local Similarity 71.6%; Pred. No. 7.2e-31;
Matches 96; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRLMTFKFYMPPKATELKHLCLE 308
DB 21 APTSSSTKTKKQLEPLDLLDLQLLEKVKNYENADLSRLMTFFKFYMPPKATELKHLCIV 80
QY 309 BELKPLEEVLNLAQSKNF-HLRLPRDLISNIVIVLELKGSETTFMCFYADETATVEFLN 367
DB 81 EELKALEGLVNLGOSKNSDSANIKESMNNINVTVLELKGSETSPKCEYDDETVTAVEFLN 140
QY 368 RWITFCQSIISTLT 381
DB 141 RWITFCQSIYSTLT 154

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RESULT 14
HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR HSSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
SQ
Query Match 23.7%; Score 471; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 6.6e-31;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKLEWVSIGSGGSTYY 60
Db :||||:|||||
DE 20 EVQLLESGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKLEWVSIGSGGSTYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK 98
Db :|||||
DE 80 GDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK 117
QY 117
Db :|||||
RESULT 15
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
```

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type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01885; K2HUCM.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
SQ
Query Match 23.5%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 1.2e-30;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;
QY 127 EIVLTQSLPLSPVTPGEPASISCRSSQSLHS-NGVTYLDWYLOKPGQSPQLLIYSGSHR 185
Db :||||:|||||
DE 2 DIVMTQPLSLPVTGEPASISCRSSQSLDSDGNGTYLNWYLOKAGQSPQLLIYLSYR 61
QY 186 ASGVPPDRFSGSVSGTDFTLIRSRVEADGVYVYCMQGLQSPFTFGPTKVDIKR 239
Db :|||||
DE 62 ASGVPPDRFSGSVSGTDFTLKISRVAEDGVYVYCMQRLPIPTFGGQTKLEIRR 115
Search completed: March 14, 2003, 11:48:07
Job time : 9.69202 secs
```


GenCore version 5.1.1.4.p5.4578
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OM protein - protein search, using sw model

Run On: March 14, 2003, 11:45:09 ; Search time 28.2491 Seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-5
Perfect score: 1990
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rviris.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678.5	34.1	298	11 Q9QYF0	Q9QYF0 mus musculus
2	666	33.5	150	4 Q9C001	Q9C001 homo sapien
3	660.5	33.2	156	4 Q13169	Q13169 homo sapien
4	632.5	31.8	154	6 Q9XS38	Q9XS38 papio hamad
5	617	31.0	139	4 Q16334	Q16334 homo sapien
6	544.5	27.4	241	11 Q921A6	Q921A6 mus musculus
7	541	27.2	597	4 Q96BB9	Q96BB9 homo sapien
8	517	26.0	218	11 Q925S1	Q925S1 mus musculus
9	509	25.6	155	6 Q9XT83	Q9XT83 halichoerus
10	507	25.5	121	4 Q9UL71	Q9UL71 homo sapien
11	503.5	25.3	573	4 Q8WU38	Q8WU38 homo sapien
12	503.5	25.3	613	4 Q8WU1	Q8WU1 homo sapien
13	489.5	24.6	471	4 Q8TC77	Q8TC77 homo sapien
14	483	24.3	113	4 Q9UL90	Q9UL90 homo sapien
15	481	24.2	487	11 Q99KA4	Q99KA4 mus musculus
16	480	24.1	116	4 Q9UL93	Q9UL93 homo sapien

17	479.5	24.1	118	4 Q9UL72	Q9UL72 homo sapien
18	471.5	23.7	112	4 Q9HCC1	Q9HCC1 homo sapien
19	470.5	23.6	118	4 Q9UL91	Q9UL91 homo sapien
20	470.5	23.6	147	4 Q9Y509	Q9Y509 homo sapien
21	466.5	23.4	138	11 Q70329	Q70329 mesocricetu
22	465	23.4	238	11 Q99M37	Q99M37 mus musculus
23	461.5	23.2	154	6 Q9XT84	Q9XT84 delphinapte
24	460	23.1	494	4 Q96K68	Q96K68 homo sapien
25	457	23.0	239	11 Q8VC55	Q8VC55 mus musculus
26	452.5	22.7	122	4 Q9UL84	Q9UL84 homo sapien
27	452.5	22.7	155	11 Q923T2	Q923T2 sigmodon hi
28	446	22.4	238	11 Q8VC16	Q8VC16 mus musculus
29	446	22.4	473	11 Q91Z05	Q91Z05 mus musculus
30	445	22.4	479	11 Q91WP5	Q91WP5 mus musculus
31	444	22.3	119	11 Q920E7	Q920E7 mus musculus
32	441	22.2	239	4 Q8TCD0	Q8TCD0 homo sapien
33	428.5	21.5	114	4 Q9UL80	Q9UL80 homo sapien
34	426.5	21.4	486	11 Q91Z07	Q91Z07 mus musculus
35	423.5	21.3	105	6 Q62773	Q62773 felis silve
36	423	21.3	131	4 Q9UL88	Q9UL88 homo sapien
37	423	21.3	480	11 Q91XEL	Q91XEL mus musculus
38	416.5	20.9	469	11 Q8R3V9	Q8R3V9 mus musculus
39	413.5	20.8	150	11 P70291	P70291 mus musculus
40	413.5	20.8	169	11 Q9QUS8	Q9QUS8 mus musculus
41	411.5	20.7	150	11 P70294	P70294 mus musculus
42	408.5	20.5	437	11 Q9R1A4	Q9R1A4 mus musculus
43	408	20.5	95	4 Q9ULB6	Q9ULB6 homo sapien
44	407.5	20.5	116	6 Q29138	Q29138 trichechus
45	407	20.5	155	6 Q9GL83	Q9GL83 capra hircu

ALIGNMENTS

RESULT 1

Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;

Query Match 34.1%; Score 678.5; DB 11; Length 298;
Best Local Similarity 53.1%; Pred.No. 1e-47;
Matches 138; Conservative 35; Mismatches 66; Indels 21; Gaps 4;

QY 1 QVQLVQSGGGLVPGGSLRLCAASGFTFRSNAMGWVRQAPKGLKLEWVSGISGGSTYY 60

Db 40 QVQLVQSGGGLVPGGSLRLCAASGFTFRSNAMGWVRQAPKGLKLEWVSGISGGSTYY 99

QY 61 ADSVKGRTFTSDNSKNTLYLQMNSLRAEDTAVYCAKHTGGVMDPDIWYQGCTLTVS 120

OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
QX	NCBI_TaxID=9606;
QX	[1]
RN	SEQUENCE FROM N.A.
RA	Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RP	"Expression of human IL-2 from gene transferred mouse melanoma cells
RT	and its effect on the growth of mouse melanoma.";
RT	Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL	13:78-82(1993).
RL	[2]
RN	SEQUENCE FROM N.A.
RA	Xu L.;
RA	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL	EMBL; U25676; AAA70092.1; -.
DR	HSSP; P01585; 31NK.
DR	InterPro; IPR000779; Interleukin-2.
DR	Pfam; PF00715; IL2; 1.
DR	PRINTS; PR00265; INTERLEUKIN2.
DR	ProDom; PD003649; Interleukin-2; 1.
DR	SMART; SM00189; IL2; 1.
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
DR	SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;
QY	Query Match
QY	Best Local Similarity 33.28; Score 660.5; DB 4; Length 156;
QY	Matches 132; Conservative 0; Mismatches 1; Indels 3; Gaps
QY	249 APTSSS--TTKTLQLEHLLDLQMLINGINNYKNPKLRMLTFFKYPMPKKATELKHLQ 300
QY	
QY	21 APTSSSTKTKTKTLQLEHLLDLQMLINGINNYKNPKLRMLTFFKYPMPKKATELKQLQ 80
QY	
QY	306 CLEELKPLEEVINLAQSKNPHLRPRDLISINIVILELKGSETTFMCEVADETATVEF 366
QY	
QY	81 CLEELKPLEEVINLAQSKNPHLRPRDLISINIVILELKGSETTFMCEVADETATVEF 146
QY	
QY	366 LNRWITFCQSIISTLT 381
QY	
QY	141 LNRWITFCQSIISTLT 156
QY	
QY	RESULT 4
QY	Q9XS38
QY	ID Q9XS38 PRELIMINARY; PRT; 154 AA.
QY	AC Q9XS38
QY	DT 01-NOV-1999 (TreeBLrel. 12, Created)
QY	DT 01-NOV-1999 (TreeBLrel. 12, Last sequence update)
QY	DT 01-OCT-2001 (TreeBLrel. 18, Last annotation update)
QY	DE IL-2.
QY	OS Papio hamadryas (Hamadryas baboon),
QY	OS Aotus lemurinus (Northern gray-necked night monkey),
QY	OS Aotus nancymae (Owl monkey),
QY	OS Aotus nigricaps (black-headed night monkey), and
QY	OS Aotus vociferans (noisy night monkey).
QY	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
QY	OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
QY	OC Cercopitheciae; Papio.
QY	OC NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
QY	[1]
QY	SEQUENCE FROM N.A.
QY	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
QY	RA Patartoyo M.E.;
QY	RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
QY	RL EMBL; U88365; AADA1538.1; -.
QY	DR EMBL; U88364; AADA1534.1; -.
QY	DR EMBL; U88361; AADA1535.1; -.
QY	DR EMBL; U88363; AADA1536.1; -.
QY	DR EMBL; U88362; AADA1537.1; -.
QY	DR HSSP; P01585; 31NK.
QY	DR InterPro; IPR000779; Interleukin-2.
QY	DR Pfam; PF00715; IL2; 1.
QY	DR PRINTS; PR00265; INTERLEUKIN2.
QY	DR ProDom; PD003649; Interleukin-2; 1.
QY	DR SMART; SM00189; IL2; 1.


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DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match      31.8%; Score 632.5; DB 6; Length 154;
Best Local Similarity 92.5%; Pred. No. 2.3e-44;
Matches 124; Conservative 5; Mismatches 4; Indels 1; Gaps 0;

Qy 249 APTSSSTKKTQLEHLLLDLQMLNGINNYKNPKLTRLMTFFKYPMPKKATELKHLCLE 308
    |||
Db 21 APTSSSTKKTQLEHLLLDLQMLNGINNYKNPKLTRLMTFFKYPMPKKATELKHLCLE 80

Qy 309 EELKPLEVLNLAQSKNFHLR-PRDLISNINIVLELKGSETTFMCEYADETATIVFEFLN 367
    |||
Db 81 EELKPLEVLNLAQSKNFHLR-PRDLISNINIVLELKGSETTFMCEYADETATIVFEFLN 140

Qy 368 RWITFCQSIISTLT 381
    |||
Db 141 GWITFCQSIISTLT 154

RESULT 5
Q16334 PRELIMINARY; PRT; 139 AA.
AC Q16334
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95239150; PubMed=7722480;
RA Elzenberg O., Faber-Eiman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes."
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSSP; P01585; 3INK
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match      31.0%; Score 617; DB 4; Length 139;
Best Local Similarity 98.4%; Pred. No. 3.8e-43;
Matches 121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 249 APTSSSTKKTQLEHLLLDLQMLNGINNYKNPKLTRLMTFFKYPMPKKATELKHLCLE 308
    |||
Db 17 APTSSSTKKTQLEHLLLDLQMLNGINNYKNPKLTRLMTFFKYPMPKKATELKHLCLE 76

Qy 309 EELKPLEVLNLAQSKNFHLR-PRDLISNINIVLELKGSETTFMCEYADETATIVFEFLN 368
    |||
Db 77 EELKPLEVLNLAQSKNFHLR-PRDLISNINIVLELKGSETTFMCEYADETATIVFEFLN 136

Qy 369 WIT 371
    |||
Db 137 WIT 139

RESULT 6
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match      27.4%; Score 544.5; DB 11; Length 241;
Best Local Similarity 45.5%; Pred. No. 7.8e-37;
Matches 115; Conservative 39; Mismatches 72; Indels 27; Gaps 6;

Qy 1 QVQLVQSGGGLVQPQGLRSLSCAASGFTFRSNAMGWVQAQPKGLEWVGSGSGSY 60
    |||
Db 1 QVQLQSGGPELKKPGETVKISKASGYTFTDYGMNWKQAQPKGLKMGWINTYTGPTY 60

Qy 61 ADSVKGRTFISRDNSKNTLYLQMSLRADTAIVYCAKHTGGVWDPTDYNGOGTLTVTS 120
    |||
Db 61 ADDFGKRAFAFLETSASTAYLQINLNKEDTATYFCARK---DLRYFDYWGQGTTVTS 117

Qy 121 -----SGGALVLTQSPVLPVTPGEPASISCRSSQSLLSHNGTYLDWYLOK 170
    |||
Db 118 SGGGGSGGGGGGGGDIETQSPSSLSASLGKVTITCKASQDI----NKYIAWQHK 172

Qy 171 PQQSQ---LLIYSGSHRASGVPRFSGSVGSGTFTLRISRVAEADVGVYCMQGLQSP 226
    |||
Db 173 PGKGRSAHJLHIYI----QPGIPRFGSGSGGRDYSFSISNLEPEDIATYCLH-YDNL 227

Qy 227 FTFPGTKVDIKR 239
    |||
Db 228 HTFGGKLELR 240

RESULT 7
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=B-CELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match      27.2%; Score 541; DB 4; Length 597;

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Best Local Similarity 69.0%; Pred. No. 5.8e-36;
Matches 109; Conservative 14; Mismatches 17; Indels 18; Gaps 3;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGSTYY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLIESGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSGSTYY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAK-----HTGGGVMDPIDYWGQGT 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKDPKGYASAGNTREDYWGQGT 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 VTVSSGGGALEIVLQSPSLPVTGPEGPASISCRSSQS 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 VTVSSGSAS-----APTFLPL-----VSCSNSPS 163
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q2551
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2
FT NON_TER 218; 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 26.0%; Score 517; DB 11; Length 218;
Best Local Similarity 48.0%; Pred. No. 1.2e-34;
Matches 107; Conservative 39; Mismatches 57; Indels 20; Gaps 4;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGSTYY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVKLQSGPELKPGETVTRISCKASGYTTTAGMQWQKMPGKGLKWTGWINTHSQVPE 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVND---PIDYWGQGT 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 AEEFKGRFAFSLSTSASTAYLQISLNKEDTATYFCMR-----WDYDGGFAYWGQGT 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 TVSSGG-----GALIEIVLTQSPSLPVTGPEGPASISCRSSQSLHNSGYTL 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 TVSSGGSGGGSGGGSDIVLTQSPASLAVSLQQRATISCRASES-VDNIGISFMNWF 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 168 LQKPGSPOLLVYSGSHRASGVDPFRFSGVSGTDTFLISRVE 210
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 QQKPGPPKLLIYAASKQSGVPGAGLLASGSGTDFSLNIYPME 218
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9

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Q9XT83
ID Q9XT83 PRELIMINARY; PRT; 155 AA.
AC Q9XT83;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072871; AAD40848.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 155 AA; 17860 MW; F18F49AC672241A CRC64;

Query Match 25.6%; Score 509; DB 6; Length 155;
Best Local Similarity 75.8%; Pred. No. 3.4e-34;
Matches 102; Conservative 15; Mismatches 16; Indels 2; Gaps 2;

QY 249 AP-TSSSTKTKTQLEHLLDQLMLNGINNYKNPKLTRMLTFKFPMPKATELKLQCL 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 APTSSSTKETQOQLLELLDRLLLGVNYPQLSRMLTFKFPMPKATELKLQCL 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 308 EEELKPLEEVNLQAQSNFHLRP-RDLISNINVLKLGSETTFMCEYADETATIFE 366
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 PEELKLEEVLYLAPNKNFHLTDIKELMSNINVTLLKLGSETFRKCEYDDEATITE 140
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 367 NRWITFCQSIITSLT 381
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 NKWITFCQSIIFSLT 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.

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Db 20 EVLVESGGGLVPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSSSSSSYIY 79
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG--GGVNDPIDYWGQGLTIV 118
Db 80 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDLRLQLTSYWFYDLWGRGLTIV 138
Qy 119 VSSGGGALEIVLTQSPSLSPVTPG-----EPASISCRSS----- 152
Db 139 VSSAS-----TKGPSVEPLAPSSKSTSGGTAALGCLIVKDYFPFVPTVSNWNSGALTSGV 191
Qy 153 ---QSLLHSNGYTYLDWLQKPGQS--PQLLIYSGSHRAS 187
Db 192 HTFPAVLOSGLYSUSSVTVTPSSSLGTQTYICNVNHRKPS 231

RESULT 14
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 24.3%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 3e-32;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKGLWVSGISGGSGSYIY 60
Db 1 EVLVESGGVVPQGGSLRLSCAASGFTFSYGMHVRQAPGKGLWVAFIRYDGSNKYY 60
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVNDPIDYWGQGLTIVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAK-----DLNWYGQGLTIVTS 112
Qy 121 S 121
Db 113 S 113

RESULT 15
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DDB333077B CRC64;

Query Match 24.2%; Score 481; DB 11; Length 487;
Best Local Similarity 41.5%; Pred. No. 3.7e-31;
Matches 134; Conservative 33; Mismatches 102; Indels 54; Gaps 15;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKGLWVSGISGGSGSYIY 60
Db 20 EVLVESGGGLVPGGSLRLSCAASGFTFSYAMSVVROTPEKRLWVATISDGGSYIY 79
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGG---GVNDPIDYWGQGLTIV 117
Db 80 PDNVKGRFTISRDNKNTLYLQMSHLKSEDTAMYYCARDMGSGSPYGGYSRFDYWGQGTI 139
Qy 118 TVSSGGGALEIVLTQSPSLP-VTPGEPASISCRSSQSLHS---NGYTYLDWLQKPGQ 173
Db 140 TVSESAARNPTIY---PLTLPRALSDPVTIIGC-----LIHDYFPGTWNVTW--GKSGK 189
Qy 174 S-----PQLLIYSGSHRASGVPDRFSVSGVSGTDFTL-RISRVEADV--GVVYCMOGLQ 224
Db 190 DITVNFPPAL-----ASG-----GGYTMSSQLTLPAVECPGEGSVKCSVQHDNSAVQ 237
Qy 225 SPFTFGPGTKVDIKRGSGGGGALAPTS--SSTKKTQLOLEHLL---DLQMLINGINN 278
Db 238 -----ELDYKCSGPPPPCPPPSCHPSLSLQRPALDILLGSDASLTCTLNGLRN 288
Qy 279 YKNPKLT-RMLTFKFPMPKATE 300
Db 289 PEGAVFTWEPSTGKDAVQKRAVQ 311

Search completed: March 14, 2003, 11:49:35
Job time : 31.2491 secs
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